



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number 152205

**TO: Patricia Duffy**  
**Location: rem/3b05/3c18**  
**Art Unit: 1645**  
**Wednesday, May 11, 2005**

**Case Serial Number: 10/063692**

**From: Toby Port**

**Location: Biotech-Chem Library**  
**REM1-A59**

**Phone: 272-2523**

**toby.port@uspto.gov**

### Search Notes

Dear Examiner Duffy,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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STIC-Biotech/ChemLib

~~152206~~ 152206

From: Duffy, Patricia  
Sent: Monday, May 02, 2005 1:02 PM  
To: STIC-Biotech/ChemLib  
Subject: SPDI 10/063,692

PLEASE SEARCH SEQ ID NOS:37, 38 AND OLIGOMERS THEREOF.  
PLEASE RUN THE AA OF SEQ ID NO:38 AGAINST THE NA DATABASE.

STANDARD SPDI OUTPUT.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

RECEIVED  
MAY - 2 2005  
STIC

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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Run on: May 6, 2005, 13:05:52 ; Search time 994 Seconds  
(without alignments)  
16949.280 Million cell updates/sec

Title: US-10-063-692-37  
Perfect score: 2846  
Sequence: 1 cctctgggcaccagccgcgg.....aaaaaaaaaaaaaaaaaaaaa 2846  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%

Database : N\_Geneseq\_16Dec04.\*  
Listing first 1500 summaries  
Maximum Match 100%

No.	Score	Match Length	DB	ID	Description
1	Geneseqn19808.*				
2	Geneseqn19808.*				
3	Geneseqn20008.*				
4	Geneseqn2001as.*				
5	Geneseqn2001bs.*				
6	Geneseqn2002as.*				
7	Geneseqn2002bs.*				
8	Geneseqn2003as.*				
9	Geneseqn2003bs.*				
10	Geneseqn2003cs.*				
11	Geneseqn2003ds.*				
12	Geneseqn2004as.*				
13	Geneseqn2004bs.*				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	AAZ65034 standard; cDNA; 2846 BP.				
2	Membrane-bound protein PRO1344 encoding cDNA.				
3	WO9963088/A2.				
4	09-DEC-1999.				
5	Geneseqn2004bs.*				
6	Geneseqn2004bs.*				
7	Geneseqn2004bs.*				
8	Geneseqn2004bs.*				
9	Geneseqn2004bs.*				
10	Geneseqn2004bs.*				
11	Geneseqn2004bs.*				
12	Geneseqn2004bs.*				
13	Geneseqn2004bs.*				
14	Geneseqn2004bs.*				
15	Geneseqn2004bs.*				
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19	Geneseqn2004bs.*				
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148	Geneseqn2004bs.*				
149	Geneseqn2004bs.*				
150	Geneseqn2004bs.*				

Query Match  
Best Local Similarity 100.0%; Score 2846; DB 6; Length 2846;  
RESULT 6  
ID ACA89459 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 7  
ID ACA73469 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 8  
ID ACA05784 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 9  
ID ACA66618 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO protein #85.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 10  
ID ACA64316 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 11  
ID ACA91182 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 12  
ID ACD81559 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 13  
ID ACF20193 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 14  
ID ACF19579 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 15  
ID ACD21867 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 16  
ID ACF13032 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 17  
ID ACD25135 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 18  
ID ACF00184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 19  
ID ACA60381 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 20  
ID ACA72241 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 21  
ID ACD04765 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 22  
ID ACD18226 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 23  
ID ACD08233 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 24  
ID ACA88667 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 25  
ID ACA70109 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 26  
ID ACD12331 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 27  
ID ACC74246 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 28  
ID ACD15874 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 29  
ID ACD25442 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 30  
ID ACD17919 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 31  
ID ACC88206 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 32  
ID ACD21560 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 33  
ID ACD18627 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 34  
ID ACA58828 standard; cDNA; 2846 BP.  
DE cDNA encoding human secreted polypeptide PRO1344.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 35  
ID ABX98237 standard; cDNA; 2846 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.  
PN US2003036156-A1.

PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 36  
ID ACD13988 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 37  
ID ACD09768 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 38  
ID ACC88513 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 39  
ID ACD21253 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 40  
ID ABX75625 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 41  
ID ACA64004 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 42  
ID ABX97828 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 43  
ID ACA97304 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 44  
ID ACA57767 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 45  
ID ACD14295 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032130-A1.  
PD 13-FEB-2003.

Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 46  
ID ACC91078 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 47  
ID ACC88820 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 48  
ID ACD07017 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 49  
ID ACA67468 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 50  
ID ACC81523 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 51  
ID ACA91268 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 52  
ID ACC89127 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 53  
ID ACC86483 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 54  
ID ACC89741 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 55  
ID ACC92920 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032135-A1.  
PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 56  
ID ACX80775 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 57  
ID ACX72548 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 58  
ID ACX89066 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 59  
ID ACX69802 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 60  
ID ACX6945 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 61  
ID ACX90941 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 62  
ID ACX70723 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 63  
ID ACX95233 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 64  
ID ACX44284 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 65  
ID ACX86176 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027263-A1.  
PD 06-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 66  
ID ACX45167 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 67  
ID ACC90048 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 68  
ID ACD12656 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 69  
ID ACF19886 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 70  
ID ABX76830 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 71  
ID ACA73162 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 72  
ID ACA68705 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 73  
ID ACA74549 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 74  
ID ACA70416 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 75  
ID ACD14602 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
PD 06-FEB-2003.

RESULT 76  
ID ACA93715 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 77  
ID ACA68274 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 78  
ID ABX98739 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 79  
ID ACC81216 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 80  
ID ACA95540 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 81  
ID ACD04458 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 82  
ID ACC97899 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 83  
ID ACF12561 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 84  
ID ACH66262 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 85  
ID ABX79455 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 86  
ID ACA96276 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 87  
ID ACA65050 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 88  
ID ACA73776 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 89  
ID ACA74188 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 90  
ID ACA96583 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 91  
ID ACD10689 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 92  
ID ACC91385 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 93  
ID ACA93476 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 94  
ID ACD02720 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 95  
ID ACC87285 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 96  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;



ID ACC85869 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027362-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 97  
ID ABX81158 standard; DNA; 2846 BP.  
DE Human secreted or transmembrane protein related PCR primer #50.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 98  
ID ACA65357 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 99  
ID ACA94174 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 100  
ID ACA97918 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 101  
ID ACA91420 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 102  
ID ACA90634 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 103  
ID ACD16181 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 104  
ID ACD17342 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 105  
ID ACC91999 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 106  
ID ACD02316 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183493-A1.

PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 107  
ID ACA74856 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 108  
ID ACA91727 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 109  
ID ACA71371 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 110  
ID ACC90771 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 111  
ID ACA65781 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO protein #85.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 112  
ID ACA68944 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 113  
ID ACA92974 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 114  
ID ACA94926 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 115  
ID ACD16488 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 116  
ID ACD15567 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.

Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 117  
ID AC98466 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003027993-Al.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 118  
ID ABX17058 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2002123463-Al.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 119  
ID ABX16670 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein #85.  
PN US2002127584-Al.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 120  
ID AC67913 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002177164-Al.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 121  
ID AC63391 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003023042-Al.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 122  
ID AC97611 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032115-Al.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 123  
ID AC99060 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032140-Al.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 124  
ID ACC91692 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040076-Al.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 125  
ID ACD1103 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003008352-Al.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 126

ID ACD14953 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044922-Al.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 127  
ID AC98362 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane polypeptide PRO1344 cDNA.  
PN US2002197615-Al.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 128  
ID ACB81869 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003017981-Al.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 129  
ID ACD11717 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032118-Al.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 130  
ID AC95846 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036135-Al.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 131  
ID ACF16409 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054455-Al.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 132  
ID ACF02527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049741-Al.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 133  
ID ACF02834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049743-Al.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 134  
ID ACF21421 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049769-Al.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 135  
ID ACF10105 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068743-Al.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 136  
ID ACF77998 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 137  
ID ACD46703 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 138  
ID ACD49456 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 139  
ID ACF28233 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 140  
ID ACD88923 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 141  
ID ACD84318 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 142  
ID ACD99092 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 143  
ID ADA77921 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 144  
ID ACF48834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 145  
ID ACD09154 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 146  
ID ACF11947 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 147  
ID ACF41181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 148  
ID ACF15795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 149  
ID ACF16102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 150  
ID ADB17094 standard; cDNA; 2846 BP.  
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 151  
ID ACD31929 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 152  
ID ACF18737 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 153  
ID ACF09184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 154  
ID ACF78305 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054473-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 154  
ID ACF31985 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 155  
ID ACF51904 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 156  
ID ACF26391 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 157  
ID ACF24184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 158  
ID ACF63495 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 159  
ID ACF50369 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 160  
ID ACH07840 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 161  
ID ACF13646 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 162  
ID ACD41572 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 163  
ID ADA37741 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 164  
ID ACF31985 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 165  
ID ACF23263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 166  
ID ACF39953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 167  
ID ACD45475 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 168  
ID ACF53132 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 169  
ID ACF27312 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 170  
ID ACF45150 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 171  
ID ACF29768 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 172  
ID ACD89844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ADA37741 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ACD84625 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 174  
ID ACD98785 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 175  
ID ACF77077 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 176  
ID ACF76770 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 177  
ID ACF49755 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 178  
ID ACF50062 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 179  
ID ADA21427 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 180  
ID ACD09461 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 181  
ID ACD08540 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 182  
ID ACH03594 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 183  
ID ACF12254 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 184  
ID ACC94762 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 185  
ID ACD22481 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 186  
ID ACF15181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 187  
ID ACC97276 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 188  
ID ACC92306 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 189  
ID ACF13953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 190  
ID ACF14260 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 191  
ID ADA10214 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 192  
ID ACF09491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 193  
ID ACD45782 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 194  
ID ACD47931 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 195  
ID ACD67662 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 196  
ID ACF25470 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 197  
ID ACF29154 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 198  
ID ACD84932 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 199  
ID ACD84011 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 200  
ID ACD88002 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 201  
ID ACF30689 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003069407-A1.

PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 202  
ID ACF32292 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 203  
ID ACH11952 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 204  
ID ACH12259 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 205  
ID ADA19899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 206  
ID ACD40651 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 207  
ID ADB17282 standard; cDNA; 2846 BP.  
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 208  
ID ADA17758 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 209  
ID ACF18123 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 210  
ID ACF08570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;

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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ACF31371 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ACF52211 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ACD50080 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
ID ACF38783 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ACF26698 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ACF24798 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ACF46378 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ACF77926 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ACD89230 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ACF63802 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ACF60442 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003083774-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ACHI2566 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ACH09989 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ACD03844 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ACD10382 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ACD12024 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ACF42409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADA27866 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ACF18430 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 230  
ID ACF02220 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 231  
ID ACF21728 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 232  
ID ACF10412 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 233  
ID ACF33864 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 234  
ID ACF44826 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 235  
ID ACD90458 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 236  
ID ACD91071 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 237  
ID ACF30382 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 238  
ID ACD87081 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 239  
ID ACF60135 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 240  
ID ACF46685 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 241  
ID ACF75542 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 242  
ID ADA79713 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 243  
ID ACF17202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 244  
ID ACF22956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 245  
ID ACF07956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 246  
ID ACF08263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 247  
ID ACF40567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 248  
ID ACF53746 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064456-A1.  
PD 03-APR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 249  
ID ACD47010 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 250  
ID ACF47913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 251  
ID ACF47299 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 252  
ID ACF46071 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 253  
ID ACD96160 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 254  
ID ACF52518 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 255  
ID ACF52825 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 256  
ID ACF64818 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 257  
ID ACF76463 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 258  
ID ACF61363 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 259  
ID ACF61670 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 260  
ID ACD30701 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 261  
ID ACD31622 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 262  
ID ACD32543 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 263  
ID ADA20071 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 264  
ID ACD82108 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 265  
ID ACF17509 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 266  
ID ADA94446 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 267  
ID ACF07342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049753-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 268  
ID ACF20500 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 269  
ID ACF20807 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 270  
ID ACF21114 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 271  
ID ACD47624 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 272  
ID ACF47606 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 273  
ID ACF53439 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 274  
ID ACD86774 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 275  
ID ACH05022 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 276  
ID ACF44519 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 277  
ID ADA81440 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 278  
ID ACD22174 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 279  
ID ACD24521 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 280  
ID ACD39724 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 281  
ID ACD40031 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 282  
ID ACF13339 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 283  
ID ACF03141 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 284  
ID ACF78612 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 285  
ID ACF11333 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 286  
ID ACF50676 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032121-A1.

PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 287  
ID ACH07226 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 288  
ID ACD46396 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 289  
ID ACD48238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 290  
ID ACF27619 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 291  
ID ACF24491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 292  
ID ACD85546 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 293  
ID ACD90151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 294  
ID ACD83704 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 295  
ID ACF49141 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 296  
ID ACH07226 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 297  
ID ACH07533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 298  
ID ACH08147 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 299  
ID ACH11338 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 300  
ID ACH11645 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 301  
ID ACH10296 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 302  
ID ACF01299 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 303  
ID ACF40874 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 304  
ID ACD24214 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 305  
ID ACD31315 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 306  
ID ACF17816 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 307  
ID ADA38671 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 308  
ID ACF32599 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 309  
ID ACF40260 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 310  
ID ACF48220 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 311  
ID ACF38169 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 312  
ID ACF25105 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 313  
ID ACF27005 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 314  
ID ACF29461 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 315  
ID ACD87695 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 316  
ID ACF76156 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 317  
ID ACF49448 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 318  
ID ACF43905 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 319  
ID ACH06250 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 320  
ID ACH06557 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 321  
ID ADA83238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 322  
ID ACC92613 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 323  
ID ACC93227 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 324  
ID ACF19272 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 325  
ID ACD12963 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 326  
ID ACF06421 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 327  
ID ACC94455 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 328  
ID ACC97883 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US200304932-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 329  
ID ACC94148 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 330  
ID ACF42102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 331  
ID ACD31108 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 332  
ID ACD43037 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 333  
ID ACD43344 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 334  
ID ACF14874 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003045700-A1.  
PD 06-MAR-2003.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 335  
ID ADA92792 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 336  
ID ACF01606 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 337  
ID ACF31678 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 338  
ID ACD67355 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 339  
ID ACD48545 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 340  
ID ACD48852 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 341  
ID ACF51290 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 342  
ID ACF54053 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 343  
ID ACF25777 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003045700-A1.  
PD 06-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 344  
ID ACF39090 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 345  
ID ACF28847 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 346  
ID ACD90764 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 347  
ID ACD86467 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 348  
ID ACH05329 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 349  
ID ACF65125 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 350  
ID ADB20281 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 351  
ID ACF43598 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 352  
ID ACH09068 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 353  
ID ACH09375 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 354  
ID ADA78533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 355  
ID ACF09798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 356  
ID ACF50983 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 357  
ID ACF23877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 358  
ID ACD88309 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 359  
ID ACH09682 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 360  
ID ACH10603 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 361  
ID ACD11410 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 362  
ID ACH09068 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 362

ID ACC96460 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 363  
ID ACC98490 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 364  
ID ACF41795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 365  
ID ACF16716 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 366  
ID ACD32236 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PD US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 367  
ID ACD30394 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PD US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 368  
ID ACD41265 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PD US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 369  
ID ACF07649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 370  
ID ACF31064 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 371  
ID ACF77384 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 372  
ID ACF11026 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 373  
ID ACF32906 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 374  
ID ACF26084 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 375  
ID ACD83397 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PD US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 376  
ID ACF23570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 377  
ID ACF42984 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 378  
ID ACF43291 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PD US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 379  
ID ACH05943 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PD US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 380  
ID ACH08761 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PD US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 381

ID ACC90355 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 382  
ID ACF10719 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 383  
ID ACC93534 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 384  
ID ACC96153 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 385  
ID ACD24828 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 386  
ID ACF01913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 387  
ID ACF22035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 388  
ID ACP22649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 389  
ID ACF08977 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 390  
ID ACF33213 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 391  
ID ACF54667 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 392  
ID ACF48527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 393  
ID ACD47317 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 394  
ID ACD49159 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 395  
ID ACF37862 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 396  
ID ACF30075 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 397  
ID ACD87388 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 398  
ID ACF61977 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 399  
ID ACH10910 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;



RESULT 400  
ID ACD10075 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 401  
ID ACD16800 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 402  
ID ACH65430 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 403  
ID ACC99097 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 404  
ID ACF00491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 405  
ID ACD40958 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 406  
ID ACF14567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 407  
ID ACF22342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 408  
ID ACF78919 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 409  
ID ACF11640 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073177-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
PA (GETH) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 410  
ID ADA22353 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 411  
ID ACF51597 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 412  
ID ACF33520 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 413  
ID ACD49773 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 414  
ID ACF37555 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 415  
ID ACF28540 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 416  
ID ACD8616 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 417  
ID ACF75235 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 418  
ID ACF61056 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
100.0%; Pred. No. 0;  
RESULT 419  
ID ACF44212 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 420  
ID ACF07035 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 421  
ID ACD39420 standard; DNA; 2846 BP.  
DE Human PRO 1344 PCR primer #1.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 422  
ID ACC93841 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 423  
ID ACD20946 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 424  
ID ACF06728 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 425  
ID ACD20639 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 426  
ID ACD22788 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 427  
ID ACF41488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 428  
ID ADA06519 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #65.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 429  
ID ADA39212 standard; cDNA; 2846 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 430  
ID ACF07035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 431  
ID ACF77691 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 432  
ID ACD46089 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 433  
ID ACF46992 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 434  
ID ACF54360 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 435  
ID ACF45764 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 436  
ID ACF45457 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 437  
ID ACF38476 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 438  
ID ACD89537 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068694-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 439  
ID ACD85239 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 440  
ID ACD85853 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 441  
ID ACF75849 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 442  
ID ACF60749 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 443  
ID ACH05636 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 444  
ID ADA82604 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 445  
ID ADB85610 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 446  
ID ADB96238 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 447  
ID ACF55895 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 448  
ID ACF55281 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 449  
ID ADB85912 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 450  
ID ACF56202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 451  
ID ACF56509 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 452  
ID ADB68289 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 453  
ID ADB68096 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 454  
ID ACF55588 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 455  
ID ACF54974 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 456  
ID ADB90913 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;

RESULT 457  
ID ADC57710 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 458  
ID ADC55074 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 459  
ID ADC11941 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 460  
ID ADC06993 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 461  
ID ADC56363 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 462  
ID ADC17172 standard; cDNA; 2846 BP.  
DE cDNA sequence encoding a PRO polypeptide (seqID 37).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 463  
ID ADC07418 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 464  
ID ADC11408 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 465  
ID ADC14870 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 466  
ID ADC52365 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US200313882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 467  
ID ADC14530 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 468  
ID ADD08062 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 469  
ID ADC81887 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 470  
ID ADD07529 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 471  
ID ADC82420 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 472  
ID ADD05642 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 473  
ID ADD08600 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 474  
ID ADD06849 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 475  
ID ADC83096 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 476  
ID ADD55203 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 477  
ID ADD36041 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 478  
ID ADD56161 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003077594-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 479  
ID ADD54599 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 480  
ID ADE26753 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 481  
ID ADE26220 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 482  
ID ADF67157 standard; cDNA; 2846 BP.  
DE Human PRO1344 nucleotide sequence SEQ ID NO:230.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 483  
ID ADG01042 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 484  
ID ADG08595 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 485  
ID ADG02637 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 486  
ID ADG01344 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 487  
ID ADP95519 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 488  
ID ADP95216 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 489  
ID ADG12334 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 490  
ID ADH24069 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 491  
ID ADH34095 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 492  
ID ADH29928 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 493  
ID ADH23899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 494  
ID ADH08994 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 495  
ID ADG85503 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180904-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 496  
 ID ADH24579 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180907-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 497  
 ID ADH37435 standard; cDNA; 2846 BP.  
 DE Human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181646-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 498  
 ID ADH2024 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003180837-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 499  
 ID ADH37605 standard; cDNA; 2846 BP.  
 DE Human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181648-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 500  
 ID ADG5643 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180905-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 501  
 ID ADH24239 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180914-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 502  
 ID ADH38533 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181643-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 503  
 ID ADG3654 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2003180794-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 504  
 ID ADH29462 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180860-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 505  
 ID ADH27578 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180906-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 506  
 ID ADH37775 standard; cDNA; 2846 BP.  
 DE Human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181647-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 507  
 ID ADH37952 standard; cDNA; 2846 BP.  
 DE Human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181649-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 508  
 ID ADH57372 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003180920-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 509  
 ID ADH53514 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181636-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 510  
 ID ADH53684 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181641-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 511  
 ID ADH52020 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181638-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 512  
 ID ADH49875 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181639-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 513  
 ID ADI25385 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003181696-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 10; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 514  
ID ADH90178 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 515  
ID ADI25555 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 516  
ID ADH97729 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 517  
ID ADI35411 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 518  
ID ADI03577 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 519  
ID ADI11934 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 520  
ID ADH90008 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 521  
ID ADH99903 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 522  
ID ADH98409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 523  
ID ADI11084 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 524  
ID ADI11594 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 525  
ID ADH98239 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 526  
ID ADH98579 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 527  
ID ADH98069 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 528  
ID ABX78612 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 529  
ID ACA75584 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 530  
ID ACA71064 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 531  
ID ACC87592 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 532  
ID ACC86978 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US20030316159-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 533  
ID ACD04151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 534  
ID ABX77859 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 535  
ID ABX80271 standard; DNA; 2846 BP.  
DE Human secreted or transmembrane protein related PCR primer #50.  
PN US200213252-A1.  
PD 19-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 536  
ID ACA69177 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 537  
ID ACA69482 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 538  
ID ACA90327 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 539  
ID ACC89434 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 540  
ID ABX90248 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 541  
ID ACA98225 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 542  
ID ACA93867 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 543  
ID ACD15260 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 544  
ID ACD08847 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 545  
ID ACC96767 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 546  
ID ACF15488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 547  
ID ABX64094 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH) GENENTECH LTD.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 548  
ID ACA72855 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 549  
ID ACD03027 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 550  
ID ACD01842 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 551  
ID ACA92034 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 552  
ID ADI05057 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 553



ID ADI03407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 554  
ID ADI04802 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 555  
ID ADH78256 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 556  
ID ADI19600 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 557  
ID ADH90348 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 558  
ID ADI03067 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 559  
ID ADH77916 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 560  
ID ADH97899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 561  
ID ADI01284 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 562  
ID ADI01979 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 563  
ID ADI03237 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 564  
ID ADI11424 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 565  
ID ADI02326 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 566  
ID ADI11764 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 567  
ID ADI05401 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 568  
ID ADH79473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 569  
ID ADI19430 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 570  
ID ADI05231 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 571  
ID ADH79643 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 572  
ID ADI01469 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 573  
ID ADI01639 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 574  
ID ADI01809 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 575  
ID ADH79813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 576  
ID ADI04631 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 577  
ID ADI02767 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 578  
ID ADH78086 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 579  
ID ADI25725 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 580  
ID ADI25895 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181671-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 581  
ID ADH98749 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 582  
ID ADH79990 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 583  
ID ADL32775 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 11; Length 2846;  
RESULT 584  
ID ADM30309 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 11; Length 2846;  
RESULT 585  
ID ADL93721 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 11; Length 2846;  
RESULT 586  
ID ADC52175 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
RESULT 587  
ID ADE74306 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
RESULT 588  
ID ADE74918 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
RESULT 589  
ID ADF35356 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
RESULT 590  
ID ADI25895 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181671-A1.

RESULT 590  
ID ADG11606 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003228655-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 591  
ID ADF96131 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 592  
ID ADG04402 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 593  
ID ADG00562 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 594  
ID ADH06607 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 595  
ID ADH06437 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 596  
ID ADG68858 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 597  
ID ADH27748 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 598  
ID ADH25089 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 599  
ID ADH33721 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #19.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 600  
ID ADG82818 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 601  
ID ADH02364 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 602  
ID ADH07971 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 603  
ID ADG69368 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 604  
ID ADH39189 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 605  
ID ADH26099 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 606  
ID ADG83929 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 607  
ID ADH19476 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 608  
ID ADG85473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 609  
ID ADH06267 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 610  
ID ADH30097 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 611  
ID ADH24409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 612  
ID ADH33068 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA' (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 613  
ID ADG69538 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 614  
ID ADH07801 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 615  
ID ADG85813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 616  
ID ADH39359 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 617  
ID ADH33551 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN' US2003181637-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 618  
ID ADH33891 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 619  
ID ADH01101 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 620  
ID ADG69708 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 621  
ID ADH20969 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 622  
ID ADH02194 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 623  
ID ADG69198 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 624  
ID ADG85983 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 625  
ID ADH24919 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 12; Length 2846;  
Pred. No. 0;  
RESULT 626  
ID ADH39536 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 627  
ID ADH20009 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 628  
ID ADH02534 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 629  
ID ADG69028 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 630  
ID ADH07631 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 631  
ID ADG86153 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 632  
ID ADH24749 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180308-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 633  
ID ADH25797 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 634  
ID ADH38363 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 635  
ID ADH57202 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 636  
ID ADH52190 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 637  
ID ADH49556 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 638  
ID ADH90518 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 639  
ID ADI11254 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 640  
ID ADH98919 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 641  
ID ADI02149 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 642  
ID ADH90688 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 643  
ID ADJ54807 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 644  
ID ADJ98563 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 645  
ID ADJ98733 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 646  
ID ADJ78892 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 647  
ID ADJ99126 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 648  
ID ADJ99296 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 649  
ID ADJ99914 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 650  
ID ADJ79062 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 651  
ID ADK00922 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 652  
ID ADK14443 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 653  
ID ADJ64578 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 654  
ID ADJ98733 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 655  
ID ADK00922 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 656  
ID ADK0326 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 657  
ID ADM80892 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 658  
ID ADN37934 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 659  
ID ADK55407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 660  
ID ACA89307 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 661  
ID ADA00368 standard; cDNA; 2843 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 2838; DB 8; Length 2846;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 662  
ID ACA67289 standard; cDNA; 2848 BP.  
DE cDNA encoding human secreted polypeptide PRO1344.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 99.5%; Score 2832; DB 9; Length 2843;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 663  
ID AAA39951 standard; cDNA; 2747 BP.

DE Human TANGO 215 cDNA.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 95.7%; Score 2724.6; DB 3; Length 2747;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 664  
ID AB235533 standard; cDNA; 2845 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 644.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 95.4%; Score 2714.4; DB 6; Length 2845;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 665  
ID AAH47256 standard; cDNA; 2784 BP.  
DE Human serine protease-like protein encoding cDNA (hc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 92.6%; Score 2636.8; DB 4; Length 2784;  
Best Local Similarity 98.0%; Pred. No. 0;  
RESULT 666  
ID AAH15142 standard; cDNA; 2784 BP.  
DE Human cDNA sequence SEQ ID NO:13201.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 92.6%; Score 2636.8; DB 4; Length 2784;  
Best Local Similarity 98.0%; Pred. No. 0;  
RESULT 667  
ID ADN04639 standard; cDNA; 2784 BP.  
DE Antipsoriatic cDNA sequence #529.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 92.6%; Score 2636.8; DB 12; Length 2784;  
Best Local Similarity 98.0%; Pred. No. 0;  
RESULT 668  
ID ADS85021 standard; DNA; 2784 BP.  
DE Human atopic dermatitis-related gene sequence SeqID23.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 92.6%; Score 2636.8; DB 13; Length 2784;  
Best Local Similarity 98.0%; Pred. No. 0;  
RESULT 669  
ID ADS85033 standard; DNA; 2784 BP.  
DE Human atopic dermatitis-related gene sequence SeqID35.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 92.6%; Score 2636.8; DB 13; Length 2784;  
Best Local Similarity 98.0%; Pred. No. 0;  
RESULT 670  
ID ADL06663 standard; DNA; 2650 BP.  
DE Human 3T3 cell conversion promoter FP938 DNA.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match 92.4%; Score 2630.6; DB 10; Length 2650;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 671  
ID ADL06661 standard; cDNA; 2650 BP.  
DE Human 3T3 cell conversion promoter FP938 cDNA.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match 92.4%; Score 2630.6; DB 10; Length 2650;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 672

ID ADR41309 standard; cDNA; 2311 BP.  
DE Human CD-like molecule HSXDF41 cDNA, SEQ ID NO:108.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 80.8%; Score 2298.8; DB 7; Length 2311;  
Best Local Similarity 99.6%; Pred. No. 0;  
RESULT 673  
ID AAD30584 standard; cDNA; 2632 BP.  
DE Human protease, PRYS-17 cDNA.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 80.5%; Score 2292.4; DB 6; Length 2632;  
Best Local Similarity 92.2%; Pred. No. 0;  
RESULT 674  
ID ABK30334 standard; cDNA; 2886 BP.  
DE Human G-protein-coupled protease #104.  
PN US6331427-B1.  
PD 18-DEC-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 79.4%; Score 2259.4; DB 6; Length 2886;  
Best Local Similarity 96.9%; Pred. No. 1.1e-311;  
RESULT 675  
ID AAF74433 standard; cDNA; 2306 BP.  
DE Human PRO2 nucleotide sequence SEQ ID NO:3.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 77.2%; Score 2197.6; DB 4; Length 2306;  
Best Local Similarity 99.8%; Pred. No. 6.5e-303;  
RESULT 676  
ID AAS01222 standard; cDNA; 2306 BP.  
DE DNA encoding human secreted protein, POLY13.  
PN WO200119856-A2.  
PD 22-MAR-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 77.2%; Score 2197.6; DB 5; Length 2306;  
Best Local Similarity 99.8%; Pred. No. 6.5e-303;  
RESULT 677  
ID ADH89027 standard; cDNA; 2305 BP.  
DE Human POLYX polynucleotide #13.  
PN US2003198958-A1.  
PD 23-OCT-2003.  
PA (SHIM/) SHIMKETS R. A.  
PA (FERN/) FERNANDES E.  
PA (HERR/) HERRMANN J L.  
PA (LIUX/) LIU X.  
PA (YANG/) YANG M.  
PA (BOLD/) BOLDOG F L.  
PA (SMIT/) SMITHSON G.  
PA (RAST/) RASTELLI L.  
Query Match 76.8%; Score 2185.6; DB 12; Length 2305;  
Best Local Similarity 99.8%; Pred. No. 3.3e-301;  
RESULT 678  
ID AAA39952 standard; cDNA; 2163 BP.  
DE Human TANGO 215 coding sequence cDNA.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 75.7%; Score 2155; DB 3; Length 2163;  
Best Local Similarity 99.8%; Pred. No. 7.2e-297;  
RESULT 679  
ID AAC90025 standard; cDNA; 2259 BP.  
DE Clone HFPEY75 coding sequence.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 75.3%; Score 2142.2; DB 3; Length 2259;  
Best Local Similarity 97.6%; Pred. No. 4.7e-295;  
RESULT 680  
ID AAH47258 standard; cDNA; 2289 BP.  
DE Human serine protease-like protein coding sequence.

PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 73.6%; Score 2095.8; DB 4; Length 2289;  
Best Local Similarity 97.6%; Pred. No. 1.8e-288;  
RESULT 681  
ID AAD33261 standard; cDNA; 2022 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:35.  
PD WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 70.5%; Score 2007.8; DB 6; Length 2022;  
Best Local Similarity 99.7%; Pred. No. 5.4e-276;  
RESULT 682  
ID AAI59076 standard; cDNA; 2144 BP.  
DE Human polynucleotide SEQ ID NO 1279.  
PD WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 69.9%; Score 1988.4; DB 4; Length 2144;  
Best Local Similarity 97.1%; Pred. No. 3e-273;  
RESULT 683  
ID ADQ99299 standard; cDNA; 2144 BP.  
DE DNA encoding human GPCR-like protein seqid 969.  
PD US659662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 69.9%; Score 1988.4; DB 5; Length 2144;  
Best Local Similarity 97.1%; Pred. No. 3e-273;  
RESULT 684  
ID ADB49059 standard; cDNA; 2144 BP.  
DE Novel human cDNA SEQ ID NO 969.  
PD US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRNA/) DRMANAC R T.  
Query Match 69.9%; Score 1988.4; DB 9; Length 2144;  
Best Local Similarity 97.1%; Pred. No. 3e-273;  
RESULT 685  
ID AAI59113 standard; cDNA; 2142 BP.  
DE Human polynucleotide SEQ ID NO 1316.  
PD WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 69.7%; Score 1984.8; DB 4; Length 2142;  
Best Local Similarity 97.0%; Pred. No. 9.9e-273;  
RESULT 686  
ID ADQ99336 standard; cDNA; 2142 BP.  
DE DNA encoding human GPCR-like protein seqid 1006.  
PD US659662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 69.7%; Score 1984.8; DB 5; Length 2142;  
Best Local Similarity 97.0%; Pred. No. 9.9e-273;  
RESULT 687  
ID ADB49096 standard; cDNA; 2142 BP.  
DE Novel human cDNA SEQ ID NO 1006.  
PD US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRNA/) DRMANAC R T.  
Query Match 69.7%; Score 1984.8; DB 9; Length 2142;  
Best Local Similarity 97.0%; Pred. No. 9.9e-273;  
RESULT 688  
ID AAI60862 standard; cDNA; 2040 BP.  
DE Human polynucleotide SEQ ID NO 4851.  
PD WO200153312-A1.

PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 67.7%; Score 1928; DB 4; Length 2040;  
Best Local Similarity 97.5%; Pred. No. 1.1e-264;  
RESULT 689  
ID AAA39985 standard; cDNA; 2823 BP.  
DE Murine TANGO 215 cDNA.  
PD WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 65.4%; Score 1862.4; DB 3; Length 2823;  
Best Local Similarity 80.3%; Pred. No. 2.2e-255;  
RESULT 690  
ID AAF7432 standard; cDNA; 1867 BP.  
DE Human PRO1 nucleotide sequence SEQ ID NO:1.  
PD WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 60.5%; Score 1722; DB 4; Length 1867;  
Best Local Similarity 99.2%; Pred. No. 1.8e-235;  
RESULT 691  
ID AAH47257 standard; cDNA; 2244 BP.  
DE Murine serine protease-like protein encoding cDNA (mc-PLACE1009992).  
PD WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 59.5%; Score 1692.6; DB 4; Length 2244;  
Best Local Similarity 85.5%; Pred. No. 2.7e-231;  
RESULT 692  
ID AAD33241 standard; cDNA; 1101 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:15.  
PD WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 30.9%; Score 879.8; DB 6; Length 1101;  
Best Local Similarity 94.4%; Pred. No. 5e-116;  
RESULT 693  
ID AAH99144 standard; cDNA; 1058 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 1001.  
PD WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 23.7%; Score 674.2; DB 4; Length 1058;  
Best Local Similarity 94.3%; Pred. No. 7.2e-87;  
RESULT 694  
ID AAS86826 standard; cDNA; 1058 BP.  
DE DNA encoding novel human diagnostic protein #22630.  
PD WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 23.7%; Score 674.2; DB 5; Length 1058;  
Best Local Similarity 94.3%; Pred. No. 7.2e-87;  
RESULT 695  
ID AAH08069 standard; cDNA; 705 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:4904.  
PD EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 22.8%; Score 648; DB 4; Length 705;  
Best Local Similarity 98.5%; Pred. No. 3.8e-83;  
RESULT 696  
ID AB234917 standard; cDNA; 548 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 29.  
PD WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 18.9%; Score 538.8; DB 6; Length 548;  
Best Local Similarity 98.5%; Pred. No. 1.2e-67;  
RESULT 697  
ID ABK30409 standard; cDNA; 505 BP.  
DE Human G-protein-coupled protease #179.  
PD US6331427-B1.  
PD 18-DEC-2001.



PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 479.4; DB 6; Length 505;  
Best Local Similarity 99.4%; Pred. No. 3.1e-59;  
RESULT 698  
ID AAI60899 standard; cDNA; 438 BP.  
DE Human polynucleotide SEQ ID NO 4888.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.6%; Score 414.6; DB 4; Length 438;  
Best Local Similarity 98.8%; Pred. No. 4.9e-50;  
RESULT 699  
ID ABN74148 standard; cDNA; 997 BP.  
DE Bovine embryonic germ (EG) cell cDNA EST #199.  
PN WO200194550-A2.  
PD 13-DEC-2001.  
PA (INFI-) INFIGEN INC.  
Query Match 14.4%; Score 409.4; DB 6; Length 997;  
Best Local Similarity 83.9%; Pred. No. 2.6e-49;  
RESULT 700  
ID AAHL3031 standard; cDNA; 532 BP.  
DE Human cDNA clone (3'-primer) SEQ ID NO:9866.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 14.3%; Score 408.2; DB 4; Length 532;  
Best Local Similarity 88.5%; Pred. No. 3.9e-49;  
RESULT 701  
ID ABL63519 standard; DNA; 337 BP.  
DE Breast cancer related gene sequence SEQ ID NO:1856.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 11.8%; Score 337; DB 6; Length 337;  
Best Local Similarity 100.0%; Pred. No. 5e-39;  
RESULT 702  
ID ABL63953 standard; DNA; 337 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2290.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 11.8%; Score 337; DB 6; Length 337;  
Best Local Similarity 100.0%; Pred. No. 5e-39;  
RESULT 703  
ID AAX40465 standard; cDNA; 340 BP.  
DE Human secreted protein 5' EST SEQ ID No: 65.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 11.7%; Score 332; DB 2; Length 340;  
Best Local Similarity 98.5%; Pred. No. 2.6e-38;  
RESULT 704  
ID AAD33260 standard; cDNA; 477 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:34.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.3%; Score 321; DB 6; Length 477;  
Best Local Similarity 99.1%; Pred. No. 9.1e-37;  
RESULT 705  
ID ACH19532 standard; cDNA; 403 BP.  
DE Human adult lung cDNA #535.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 9.9%; Score 283; DB 9; Length 403;  
Best Local Similarity 97.6%; Pred. No. 2.3e-31;  
RESULT 706  
ID ABN73761 standard; cDNA; 432 BP.

DE Bovine embryonic germ (EG) cell cDNA EST 990928a CONTIG 32.  
PN WO200194550-A2.  
PD 13-DEC-2001.  
PA (INFI-) INFIGEN INC.  
Query Match 8.9%; Score 253.8; DB 6; Length 432;  
Best Local Similarity 85.5%; Pred. No. 3.1e-27;  
RESULT 707  
ID ADQ21818 standard; DNA; 286 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4638.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 7.7%; Score 218.4; DB 12; Length 286;  
Best Local Similarity 99.5%; Pred. No. 3.3e-22;  
RESULT 708  
ID AAD37042 standard; DNA; 369 BP.  
DE Mouse limulus-clotting factor protease-like EST gene.  
PN WO200203787-A2.  
PD 17-JAN-2002.  
PA (DELT-) DELTAGEN INC.  
Query Match 7.5%; Score 213.6; DB 6; Length 369;  
Best Local Similarity 82.7%; Pred. No. 1.6e-21;  
RESULT 709  
ID AAZ43781 standard; cDNA; 2685 BP.  
DE Human fetal brain cDNA clone vb6\_1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 5.2%; Score 148; DB 3; Length 2685;  
Best Local Similarity 84.7%; Pred. No. 2.9e-12;  
RESULT 710  
ID AAD07722 standard; cDNA; 938 BP.  
DE Human secreted protein-encoding gene 18 cDNA clone HLYDU43, SEQ ID NO:28.  
PN WO200134800-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.1%; Score 146.2; DB 5; Length 938;  
Best Local Similarity 78.5%; Pred. No. 5.4e-12;  
RESULT 711  
ID ACN58522 standard; cDNA; 476 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-010-Q6-K6-C11, SEQ:13303.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.1%; Score 145.8; DB 13; Length 476;  
Best Local Similarity 85.7%; Pred. No. 6.4e-12;  
RESULT 712  
ID ADR62569 standard; cDNA; 1423 BP.  
DE Cotton cDNA sequence, SEQ ID 3350.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 5.1%; Score 145.8; DB 13; Length 1423;  
Best Local Similarity 85.7%; Pred. No. 6.1e-12;  
RESULT 713  
ID AAF72803 standard; DNA; 2057 BP.  
DE Secreted protein gene #5.  
PN WO200107459-A1.  
PD 01-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.1%; Score 145.6; DB 4; Length 2057;  
Best Local Similarity 79.6%; Pred. No. 6.4e-12;  
RESULT 714  
ID AAI87708 standard; cDNA; 903 BP.  
DE Human polynucleotide SEQ ID NO 7768.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 5.1%; Score 145.4; DB 4; Length 903;  
Best Local Similarity 90.6%; Pred. No. 7.1e-12;  
RESULT 715  
ID ACN45855 standard; cDNA; 608 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.1%; Score 144.8; DB 13; Length 608;  
Best Local Similarity 87.8%; Pred. No. 8.8e-12;  
RESULT 716  
ID ACN61841 standard; cDNA; 483 BP.  
DE Cotton gynecium tissue EST Clone ID: LIB3829-021-Q6-N6-F8, SEQ:16622.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.1%; Score 144.4; DB 13; Length 483;  
Best Local Similarity 84.0%; Pred. No. 1e-11;  
RESULT 717  
ID ABA93725 standard; cDNA; 3028 BP.  
DE Human differentiation/development cDNA clone amy2\_2b19.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 5.1%; Score 144.2; DB 6; Length 3028;  
Best Local Similarity 75.5%; Pred. No. 9.9e-12;  
RESULT 718  
ID ACF34512 standard; DNA; 3028 BP.  
DE Gene encoding angiogenesis protein BN0146.  
PN WO2003027285-A1.  
PD 03-APR-2003.  
PA (BION-) BIONOMICS LTD.  
Query Match 5.1%; Score 144.2; DB 8; Length 3028;  
Best Local Similarity 75.5%; Pred. No. 9.9e-12;  
RESULT 719  
ID ABV58662 standard; cDNA; 381 BP.  
DE Human prostate expression marker cDNA 58653.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 5.1%; Score 144; DB 5; Length 381;  
Best Local Similarity 84.4%; Pred. No. 1.2e-11;  
RESULT 720  
ID ACN45357 standard; cDNA; 597 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A11, SEQ:138.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.1%; Score 144; DB 13; Length 597;  
Best Local Similarity 84.4%; Pred. No. 1.1e-11;  
RESULT 721  
ID ABV44911 standard; cDNA; 375 BP.  
DE Human prostate expression marker cDNA 44902.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 5.1%; Score 143.8; DB 5; Length 375;  
Best Local Similarity 87.7%; Pred. No. 1.2e-11;  
RESULT 722  
ID ACN56273 standard; cDNA; 517 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.1%; Score 143.8; DB 13; Length 517;  
Best Local Similarity 83.6%; Pred. No. 1.2e-11;  
RESULT 723  
ID ACN3890 standard; cDNA; 547 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.1%; Score 143.8; DB 13; Length 547;  
Best Local Similarity 90.1%; Pred. No. 1.2e-11;  
RESULT 724  
ID ADN95834 standard; DNA; 1999 BP.  
DE Human BEC/LEC-related gene sequence SeqID758.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 5.1%; Score 143.8; DB 11; Length 1999;  
Best Local Similarity 83.6%; Pred. No. 1.2e-11;  
RESULT 725  
ID ADQ24947 standard; DNA; 1999 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7767.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.1%; Score 143.8; DB 12; Length 1999;  
Best Local Similarity 83.6%; Pred. No. 1.2e-11;  
RESULT 726  
ID ADP23790 standard; cDNA; 1999 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:968.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 5.1%; Score 143.8; DB 13; Length 1999;  
Best Local Similarity 83.6%; Pred. No. 1.2e-11;  
RESULT 727  
ID ADP23585 standard; cDNA; 733 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:763.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 5.0%; Score 143.4; DB 13; Length 733;  
Best Local Similarity 88.1%; Pred. No. 1.4e-11;  
RESULT 728  
ID ACN51414 standard; cDNA; 547 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-K6-G6, SEQ:6195.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 5.0%; Score 143.2; DB 13; Length 547;  
Best Local Similarity 87.2%; Pred. No. 1.5e-11;  
RESULT 729  
ID ADI43251 standard; DNA; 2226 BP.  
DE Plant transcription factor polynucleotide #1150.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.

PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match  
Best Local Similarity 5.0%; Score 143; DB 12; Length 2226;  
88.6%; Pred. No. 1.5e-11;  
RESULT 730  
ID AD002941 standard; cDNA; 2226 BP.  
DE Soybean orthologue of Thalecress transcription factor, cDNA #174.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match  
Best Local Similarity 5.0%; Score 143; DB 12; Length 2226;  
88.6%; Pred. No. 1.5e-11;  
RESULT 731  
ID ACN56223 standard; cDNA; 458 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-A12, SEQ:11004.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 5.0%; Score 142.8; DB 13; Length 458;  
95.5%; Pred. No. 1.7e-11;  
RESULT 732  
ID ACN47028 standard; cDNA; 528 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-B12, SEQ:1809.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 5.0%; Score 142.8; DB 13; Length 528;  
83.5%; Pred. No. 1.7e-11;  
RESULT 733  
ID ACN56344 standard; cDNA; 565 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:11125.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 5.0%; Score 142.8; DB 13; Length 565;  
83.5%; Pred. No. 1.7e-11;  
RESULT 734  
ID AAC59297 standard; cDNA; 887 BP.  
DE Human secreted protein cDNA #21.  
PN WO200056753-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match  
Best Local Similarity 5.0%; Score 142.8; DB 3; Length 887;  
83.5%; Pred. No. 1.7e-11;  
RESULT 735  
ID ACN62109 standard; cDNA; 547 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 5.0%; Score 142.6; DB 13; Length 547;  
81.0%; Pred. No. 1.8e-11;  
RESULT 736  
ID AAQ04107 standard; cDNA; 2427 BP.  
DE Human pro-urokinase cDNA of clone pcUK176.  
PN EP365894-A.  
PD 02-MAY-1990.  
PA (FARM) FARMITALIA ERBA SPA CARLO.  
Query Match  
Best Local Similarity 5.0%; Score 142.6; DB 2; Length 2427;  
75.1%; Pred. No. 1.7e-11;  
RESULT 737  
ID ABV23160 standard; cDNA; 2922 BP.  
DE Human prostate expression marker cDNA 23151.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 5.0%; Score 142.6; DB 5; Length 2922;  
91.5%; Pred. No. 1.7e-11;  
RESULT 738  
ID ACN47472 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 5.0%; Score 142.4; DB 13; Length 560;  
83.9%; Pred. No. 1.9e-11;  
RESULT 739  
ID ABX48619 standard; cDNA; 397 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13784.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 5.0%; Score 142.2; DB 8; Length 397;  
89.5%; Pred. No. 2.1e-11;  
RESULT 740  
ID ABK34899 standard; cDNA; 409 BP.  
DE Human cDNA encoding secreted protein #37.  
PN WO200177288-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 5.0%; Score 142.2; DB 6; Length 409;  
89.5%; Pred. No. 2.1e-11;  
RESULT 741  
ID ABV56624 standard; cDNA; 544 BP.  
DE Human prostate expression marker cDNA 56615.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 5.0%; Score 142.2; DB 5; Length 544;  
85.0%; Pred. No. 2.1e-11;  
RESULT 742  
ID AAS62239 standard; cDNA; 681 BP.  
DE cDNA sequence #26 encoding novel human secreted protein.  
PN WO200177291-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.

Query Match 5.0%; Score 142.2; DB 6; Length 681;  
 Best Local Similarity 92.0%; Pred. No. 2e-11;  
 RESULT 743  
 ID ABZ82489 standard; cDNA; 805 BP.  
 DE Human secreted protein cDNA #SEQ ID 36.  
 PN WO200268628-A1.  
 PD 06-SEP-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 5.0%; Score 142.2; DB 6; Length 805;  
 Best Local Similarity 92.0%; Pred. No. 2e-11;  
 RESULT 744  
 ID ACN62281 standard; cDNA; 496 BP.  
 DE Cotton Gynoecium tissue EST Clone ID: LIB3829-027-Q6-N6-E4, SEQ:17062.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 5.0%; Score 142; DB 13; Length 496;  
 Best Local Similarity 91.0%; Pred. No. 2.2e-11;  
 RESULT 745  
 ID ADQ22434 standard; DNA; 1215 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5254.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 5.0%; Score 142; DB 12; Length 1215;  
 Best Local Similarity 76.1%; Pred. No. 2.1e-11;  
 RESULT 746  
 ID ADL26832 standard; cDNA; 12178 BP.  
 DE Rat L-NAME-related actin-associated cytoskeleton protein LACS cDNA.  
 PN WO2004022753-A1.  
 PD 18-MAR-2004.  
 PA (ANGE-) ANGES MG INC.  
 Query Match 5.0%; Score 142; DB 13; Length 12178;  
 Best Local Similarity 91.0%; Pred. No. 1.9e-11;  
 RESULT 747  
 ID ABX43725 standard; cDNA; 257 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #8890.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 5.0%; Score 141.8; DB 8; Length 257;  
 Best Local Similarity 87.6%; Pred. No. 2.4e-11;  
 RESULT 748  
 ID ADQ24863 standard; DNA; 2575 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7683.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 5.0%; Score 141.8; DB 12; Length 2575;  
 Best Local Similarity 81.6%; Pred. No. 2.2e-11;  
 RESULT 749  
 ID ACN48060 standard; cDNA; 487 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-018-Q1-N6-F4, SEQ:2841.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 5.0%; Score 141.6; DB 13; Length 487;  
 Best Local Similarity 80.5%; Pred. No. 2.5e-11;  
 RESULT 750  
 ID ADK57243 standard; DNA; 774 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #4626.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.

PA (DOWC) DOW AGROSCIENCES LLC.  
 Query Match 5.0%; Score 141.6; DB 10; Length 774;  
 Best Local Similarity 91.5%; Pred. No. 2.5e-11;  
 RESULT 751  
 ID ABL33490 standard; DNA; 8392 BP.  
 DE Human immune system associated gene SEQ ID NO: 1463.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 141.6; DB 6; Length 8392;  
 Best Local Similarity 86.7%; Pred. No. 2.2e-11;  
 RESULT 752  
 ID ABL32118 standard; DNA; 11416 BP.  
 DE Human immune system associated gene SEQ ID NO: 91.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 141.6; DB 6; Length 11416;  
 Best Local Similarity 84.6%; Pred. No. 2.2e-11;  
 RESULT 753  
 ID ABL70135 standard; DNA; 11416 BP.  
 DE Chemically treated cell signalling DNA sequence#13.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 141.6; DB 6; Length 11416;  
 Best Local Similarity 84.6%; Pred. No. 2.2e-11;  
 RESULT 754  
 ID AAS61063 standard; DNA; 11416 BP.  
 DE Human gene regulation-associated gene oligonucleotide #18.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 141.6; DB 6; Length 11416;  
 Best Local Similarity 84.6%; Pred. No. 2.2e-11;  
 RESULT 755  
 ID ABL33404 standard; DNA; 16033 BP.  
 DE Human immune system associated gene SEQ ID NO: 1377.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 141.6; DB 6; Length 16033;  
 Best Local Similarity 84.6%; Pred. No. 2.2e-11;  
 RESULT 756  
 ID ABX48177 standard; cDNA; 286 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #13342.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 5.0%; Score 141.4; DB 8; Length 286;  
 Best Local Similarity 90.4%; Pred. No. 2.7e-11;  
 RESULT 757  
 ID AAI87526 standard; cDNA; 382 BP.  
 DE Human polynucleotide SEQ ID NO 7586.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.0%; Score 141.2; DB 4; Length 382;  
 Best Local Similarity 87.1%; Pred. No. 2.9e-11;  
 RESULT 758  
 ID ABQ67159 standard; DNA; 6775 BP.  
 DE Human angiotensin associated polynucleotide SEQ ID NO 189.  
 PN WO200246454-A2.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 141.2; DB 6; Length 6775;  
 Best Local Similarity 87.1%; Pred. No. 2.6e-11;  
 RESULT 759  
 ID ADS89685 standard; DNA; 8900 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:701.

PD WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 5.0%; Score 141.2; DB 13; Length 8900;  
Best Local Similarity 87.1%; Pred. No. 2.5e-11;  
RESULT 760  
ID ADS89411 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO:427.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 5.0%; Score 141.2; DB 13; Length 8900;  
Best Local Similarity 87.1%; Pred. No. 2.5e-11;  
RESULT 761  
ID AAI88514 standard; cDNA; 389 BP.  
DE Human polynucleotide SEQ ID NO 8574.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYGE-) HYSEQ INC.  
Query Match 5.0%; Score 141; DB 4; Length 389;  
Best Local Similarity 86.2%; Pred. No. 3.1e-11;  
RESULT 762  
ID AAC59098 standard; cDNA; 667 BP.  
DE Human secreted protein coding sequence SEQ ID NO: 60.  
PN WO200055171-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.0%; Score 141; DB 3; Length 667;  
Best Local Similarity 76.0%; Pred. No. 3e-11;  
RESULT 763  
ID ADQ22371 standard; DNA; 4824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.0%; Score 141; DB 12; Length 4824;  
Best Local Similarity 90.9%; Pred. No. 2.8e-11;  
RESULT 764  
ID AAK89974 standard; DNA; 165 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3550.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 765  
ID AAK90168 standard; DNA; 165 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3744.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 766  
ID AAK89381 standard; DNA; 165 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 2957.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 767  
ID AAK73944 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28756.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 768  
ID AAK78761 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33573.  
PN WO200157182-A2.

PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 769  
ID AAK81312 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36124.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 770  
ID AAK79574 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34386.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 771  
ID AAL07127 standard; DNA; 165 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9815.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 772  
ID AAL04803 standard; DNA; 165 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7491.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 773  
ID ABA08161 standard; DNA; 165 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 956.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 774  
ID ABL97697 standard; DNA; 165 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2349.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 4; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 775  
ID AAS29235 standard; DNA; 165 BP.  
DE Genomic sequence #78 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 5; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 776  
ID ABA17044 standard; DNA; 165 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9375.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 5; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 777  
ID AAD16672 standard; DNA; 165 BP.  
DE Human pancreatic related protein-encoding exon, SEQ ID NO:36.  
PN WO200155327-A2.  
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 5; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 778  
ID AAS39812 standard; DNA; 165 BP.  
DE Genomic sequence #231 encoding human colon associated polypeptide.  
PN WO200155302-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 5; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 779  
ID ABS68375 standard; DNA; 165 BP.  
DE Human DNA-binding protein genomic DNA sequence #78.  
PN US2002102638-A1.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.9%; Score 140.8; DB 6; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 780  
ID ADB32772 standard; DNA; 165 BP.  
DE Human novel colon related polypeptide DNA SEQ ID NO 709.  
PN US2003050231-A1.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.9%; Score 140.8; DB 9; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 781  
ID ADC25497 standard; cDNA; 165 BP.  
DE Human cDNA from extracellular matrix gene 80 #9.  
PN US2003049650-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 140.8; DB 10; Length 165;  
Best Local Similarity 95.4%; Pred. No. 3.4e-11;  
RESULT 782  
ID ACN56670 standard; cDNA; 341 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-C8, SEQ:451.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 341;  
Best Local Similarity 83.3%; Pred. No. 3.3e-11;  
RESULT 783  
ID ACN53869 standard; cDNA; 355 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-B10, SEQ:8650.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 355;  
Best Local Similarity 87.5%; Pred. No. 3.3e-11;  
RESULT 784  
ID ACN51993 standard; cDNA; 478 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E1, SEQ:6774.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 478;  
Best Local Similarity 83.3%; Pred. No. 3.3e-11;  
RESULT 785

ID ACN54384 standard; cDNA; 489 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-K6-F9, SEQ:9165.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 489;  
Best Local Similarity 91.4%; Pred. No. 3.3e-11;  
RESULT 786  
ID ABV57765 standard; cDNA; 502 BP.  
DE Human prostate expression marker cDNA 57756.  
PN WO200160860-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 140.8; DB 5; Length 502;  
Best Local Similarity 87.0%; Pred. No. 3.3e-11;  
RESULT 787  
ID ACN62215 standard; cDNA; 516 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-026-Q6-N6-F3, SEQ:16996.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 516;  
Best Local Similarity 83.3%; Pred. No. 3.3e-11;  
RESULT 788  
ID ACN53333 standard; cDNA; 517 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-E7, SEQ:10114.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 517;  
Best Local Similarity 89.9%; Pred. No. 3.3e-11;  
RESULT 789  
ID ACN52090 standard; cDNA; 571 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B9, SEQ:6871.  
PN US2004123340-A1.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 140.8; DB 13; Length 571;  
Best Local Similarity 83.3%; Pred. No. 3.2e-11;  
RESULT 790  
ID AAD50017 standard; cDNA; 1696 BP.  
DE Human secreted protein cDNA.  
PN WO200283914-A2.  
PA (PEKE) PE CORP NY.  
Query Match 4.9%; Score 140.8; DB 8; Length 1696;  
Best Local Similarity 87.5%; Pred. No. 3.1e-11;  
RESULT 791  
ID AAA48576 standard; cDNA; 2604 BP.  
DE cDNA encoding wheat protein phosphatase 2A regulatory subunit A.  
PN WO200036121-A2.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 4.9%; Score 140.8; DB 3; Length 2604;  
Best Local Similarity 92.5%; Pred. No. 3e-11;  
RESULT 792  
ID ABL92313 standard; DNA; 8079 BP.  
DE Chemically treated DNA repair gene fragment complementary to #61.  
PN WO200181622-A2.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 4.9%; Score 140.8; DB 6; Length 9079;  
 Best Local Similarity 85.3%; Pred. No. 2.9e-11;  
 RESULT 793  
 ID ACN62049 standard; cDNA; 469 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FING/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 140.6; DB 13; Length 469;  
 Best Local Similarity 86.6%; Pred. No. 3.5e-11;  
 RESULT 794  
 ID ADD69623 standard; cDNA; 1343 BP.  
 DE Human REMAP cDNA - SEQ ID 52.  
 PN WO2003048305-A2.  
 PD 12-JUN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.9%; Score 140.6; DB 10; Length 1343;  
 Best Local Similarity 86.6%; Pred. No. 3.3e-11;  
 RESULT 795  
 ID ADD69624 standard; cDNA; 1464 BP.  
 DE Human REMAP cDNA - SEQ ID 53.  
 PN WO2003048305-A2.  
 PD 12-JUN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.9%; Score 140.6; DB 10; Length 1464;  
 Best Local Similarity 86.6%; Pred. No. 3.3e-11;  
 RESULT 796  
 ID ADR25589 standard; DNA; 1521 BP.  
 DE Breast cancer prognosis marker #1450.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 4.9%; Score 140.6; DB 13; Length 1521;  
 Best Local Similarity 86.6%; Pred. No. 3.3e-11;  
 RESULT 797  
 ID ADP55051 standard; cDNA; 1521 BP.  
 DE Human PRO cDNA sequence SEQ ID NO:1027.  
 PN WO2004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.9%; Score 140.6; DB 13; Length 1521;  
 Best Local Similarity 86.6%; Pred. No. 3.3e-11;  
 RESULT 798  
 ID ADQ22988 standard; DNA; 1576 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.9%; Score 140.6; DB 12; Length 1576;  
 Best Local Similarity 88.9%; Pred. No. 3.3e-11;  
 RESULT 799  
 ID ADI42816 standard; DNA; 1803 BP.  
 DE Plant transcription factor polynucleotide #820.  
 PN US2004019927-A1.  
 PD 29-JAN-2004.  
 PA (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIAN/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAK/) HAAKE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.  
 PA (PILG/) PILGRIM M L.  
 PA (DUBE/) DUBELL A N.  
 PA (PINE/) PINEDA O.

PA (YUGG/) YU G.  
 Query Match 4.9%; Score 140.6; DB 12; Length 1803;  
 Best Local Similarity 86.6%; Pred. No. 3.3e-11;  
 RESULT 800  
 ID ADO03025 standard; cDNA; 1803 BP.  
 DE Corn orthologue of Thalecress transcription factor, cDNA #126.  
 PN US2004045049-A1.  
 PD 04-MAR-2004.  
 PA (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PILG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KUMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 Query Match 4.9%; Score 140.6; DB 12; Length 1803;  
 Best Local Similarity 86.6%; Pred. No. 3.3e-11;  
 RESULT 801  
 ID ADR24479 standard; DNA; 2809 BP.  
 DE Breast cancer prognosis marker #340.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 4.9%; Score 140.6; DB 13; Length 2809;  
 Best Local Similarity 86.6%; Pred. No. 3.2e-11;  
 RESULT 802  
 ID ADK00688 standard; DNA; 3226 BP.  
 DE HOMO protein encoding sequence #33.  
 PN WO2004014946-A1.  
 PD 19-FEB-2004.  
 PA (NEWO-) NEWORGEN LTD.  
 Query Match 4.9%; Score 140.6; DB 12; Length 3226;  
 Best Local Similarity 86.6%; Pred. No. 3.2e-11;  
 RESULT 803  
 ID ADJ48200 standard; DNA; 3505 BP.  
 DE Maize oil-associated gene #18.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C.  
 PA (RAVA/) RAVANELLO M.  
 PA (SAVA/) SAVAGE T.  
 PA (LEDE/) LEDEAUX J R.  
 PA (ROGE/) ROGERS J A.  
 Query Match 4.9%; Score 140.6; DB 12; Length 3505;  
 Best Local Similarity 88.9%; Pred. No. 3.2e-11;  
 RESULT 804  
 ID ABK31495 standard; DNA; 15954 BP.  
 DE Signal transduction associated gene modified complementary DNA #169.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 140.6; DB 6; Length 15954;  
 Best Local Similarity 91.4%; Pred. No. 3e-11;  
 RESULT 805  
 ID ABL70468 standard; DNA; 15954 BP.  
 DE Chemically treated cell signalling DNA sequence complementary to#179.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 140.6; DB 6; Length 15954;  
 Best Local Similarity 91.4%; Pred. No. 3e-11;

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RESULT 806
ID ABX39465 standard; cDNA; 327 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #4630.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.9%; Score 140.4; DB 8; Length 327;
Best Local Similarity 90.4%; Pred. No. 3.8e-11;
RESULT 807
ID ACN55708 standard; cDNA; 381 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-N6-E10, SEQ:10489.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.4; DB 13; Length 381;
Best Local Similarity 90.4%; Pred. No. 3.8e-11;
RESULT 808
ID ACN47898 standard; cDNA; 495 BP.
DE Cotton primed seed EST Clone ID: LIB3825-016-Q1-N6-E4, SEQ:2679.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140.4; DB 13; Length 495;
Best Local Similarity 81.4%; Pred. No. 3.7e-11;
RESULT 809
ID AAF91902 standard; cDNA; 1198 BP.
DE Human secreted protein-encoding gene 45 cDNA clone HRAC126, SEQ ID NO:55.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 4.9%; Score 140.4; DB 4; Length 1198;
Best Local Similarity 87.9%; Pred. No. 3.6e-11;
RESULT 810
ID AAX33181 standard; DNA; 6644 BP.
DE Base sequence of the plasmid prx-ires-bsr.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 6644;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 811
ID AAX33182 standard; DNA; 7372 BP.
DE Base sequence of the plasmid prx-Bcl-xl-bsr.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 7372;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 812
ID AAX33180 standard; DNA; 7797 BP.
DE Cowpox virus bsr full length gene sequence.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 7797;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 813
ID AAX33184 standard; DNA; 7996 BP.
DE Base sequence of the plasmid prx-Bcl 2-i-hcd 25.
PN WO913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 4.9%; Score 140.4; DB 2; Length 7996;
Best Local Similarity 71.0%; Pred. No. 3.3e-11;
RESULT 814
ID ABL32895 standard; DNA; 11729 BP.
DE Human immune system associated gene SEQ ID NO: 868.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 4.9%; Score 140.4; DB 6; Length 11729;
Best Local Similarity 85.7%; Pred. No. 3.2e-11;
RESULT 815
ID AAT76782 standard; DNA; 240 BP.
DE Staphylococcus aureus exfoliative toxin A gene capture probe.
PN US5627054-A.
PD 06-MAY-1997.
PA (USAA-) US SEC OF ARMY.
Query Match 4.9%; Score 140; DB 2; Length 240;
Best Local Similarity 86.1%; Pred. No. 4.4e-11;
RESULT 816
ID ABX38708 standard; cDNA; 242 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3873.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 4.9%; Score 140; DB 8; Length 242;
Best Local Similarity 88.4%; Pred. No. 4.4e-11;
RESULT 817
ID ACN53191 standard; cDNA; 564 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-B10, SEQ:7972.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 4.9%; Score 140; DB 13; Length 564;
Best Local Similarity 88.4%; Pred. No. 4.2e-11;
RESULT 818
ID ABV29481 standard; cDNA; 760 BP.
DE Human prostate expression marker cDNA 29472.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 760;
Best Local Similarity 86.1%; Pred. No. 4.2e-11;
RESULT 819
ID ABV28953 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 28944.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 1603;
Best Local Similarity 82.1%; Pred. No. 4e-11;
RESULT 820
ID ABV22100 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 22091.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 1603;
Best Local Similarity 82.1%; Pred. No. 4e-11;
RESULT 821
ID ABV23114 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 23105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 4.9%; Score 140; DB 5; Length 1603;
Best Local Similarity 82.1%; Pred. No. 4e-11;
RESULT 822
ID ABV27940 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 27931.
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PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.9%; Score 140; DB 5; Length 1603;  
 Best Local Similarity 82.1%; Pred. No. 4e-11;  
 RESULT 823  
 ID ADQ22192 standard; DNA; 3931 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5012.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.9%; Score 140; DB 12; Length 3931;  
 Best Local Similarity 86.1%; Pred. No. 3.9e-11;  
 RESULT 824  
 ID ABL32171 standard; DNA; 3973 BP.  
 DE Human immune system associated gene SEQ ID NO: 144.  
 PD WO200200928-A2.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 140; DB 6; Length 3973;  
 Best Local Similarity 84.0%; Pred. No. 3.9e-11;  
 RESULT 825  
 ID ABQ67149 standard; DNA; 40324 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 179.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 140; DB 6; Length 40324;  
 Best Local Similarity 90.9%; Pred. No. 3.5e-11;  
 RESULT 826  
 ID ACN52108 standard; cDNA; 545 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-P7, SEQ:6889.  
 PD US2004123340-A1.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.8; DB 13; Length 545;  
 Best Local Similarity 83.2%; Pred. No. 4.5e-11;  
 RESULT 827  
 ID ACN53565 standard; cDNA; 619 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-C10, SEQ:8346.  
 PD US2004123340-A1.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.8; DB 13; Length 619;  
 Best Local Similarity 83.2%; Pred. No. 4.5e-11;  
 RESULT 828  
 ID AA64638 standard; DNA; 801 BP.  
 DE Partial sequence MEL3 associated with melanoma and thyroid tumors.  
 PD WO200005095-A2.  
 PD 31-AUG-2000.  
 PA (GOUT/) GOUT I.  
 PA (RODN/) RODIN N.  
 PA (FILO/) FILOENKO V.  
 PA (MATS/) MATSUKA G.  
 PA (SCAN/) SCANLAN M.  
 PA (OLDL/) OLD L.  
 PA (BILY/) BILYNSKY B.  
 Query Match 4.9%; Score 139.8; DB 3; Length 801;  
 Best Local Similarity 92.9%; Pred. No. 4.4e-11;  
 RESULT 829  
 ID ADE40468 standard; DNA; 1047 BP.  
 DE Human granzyme H (gene ID 1793) DNA.  
 PD WO200307083-A2.  
 PD 28-AUG-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 4.9%; Score 139.8; DB 10; Length 1047;  
 Best Local Similarity 89.8%; Pred. No. 4.4e-11;

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PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.9%; Score 140; DB 5; Length 1603;  
 Best Local Similarity 82.1%; Pred. No. 4e-11;  
 RESULT 823  
 ID ADQ22192 standard; DNA; 3931 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5012.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.9%; Score 140; DB 12; Length 3931;  
 Best Local Similarity 86.1%; Pred. No. 3.9e-11;  
 RESULT 824  
 ID ABL32171 standard; DNA; 3973 BP.  
 DE Human immune system associated gene SEQ ID NO: 144.  
 PD WO200200928-A2.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 140; DB 6; Length 3973;  
 Best Local Similarity 84.0%; Pred. No. 3.9e-11;  
 RESULT 825  
 ID ABQ67149 standard; DNA; 40324 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 179.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 140; DB 6; Length 40324;  
 Best Local Similarity 90.9%; Pred. No. 3.5e-11;  
 RESULT 826  
 ID ACN52108 standard; cDNA; 545 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-P7, SEQ:6889.  
 PD US2004123340-A1.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.8; DB 13; Length 545;  
 Best Local Similarity 83.2%; Pred. No. 4.5e-11;  
 RESULT 827  
 ID ACN53565 standard; cDNA; 619 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-C10, SEQ:8346.  
 PD US2004123340-A1.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.8; DB 13; Length 619;  
 Best Local Similarity 83.2%; Pred. No. 4.5e-11;  
 RESULT 828  
 ID AA64638 standard; DNA; 801 BP.  
 DE Partial sequence MEL3 associated with melanoma and thyroid tumors.  
 PD WO200005095-A2.  
 PD 31-AUG-2000.  
 PA (GOUT/) GOUT I.  
 PA (RODN/) RODIN N.  
 PA (FILO/) FILOENKO V.  
 PA (MATS/) MATSUKA G.  
 PA (SCAN/) SCANLAN M.  
 PA (OLDL/) OLD L.  
 PA (BILY/) BILYNSKY B.  
 Query Match 4.9%; Score 139.8; DB 3; Length 801;  
 Best Local Similarity 92.9%; Pred. No. 4.4e-11;  
 RESULT 829  
 ID ADE40468 standard; DNA; 1047 BP.  
 DE Human granzyme H (gene ID 1793) DNA.  
 PD WO200307083-A2.  
 PD 28-AUG-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 4.9%; Score 139.8; DB 10; Length 1047;  
 Best Local Similarity 89.8%; Pred. No. 4.4e-11;

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RESULT 830  
 ID ADN39370 standard; cDNA; 1416 BP.  
 DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:854.  
 PN WO2003042661-A2.  
 PD 22-MAY-2003.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 4.9%; Score 139.8; DB 11; Length 1416;  
 Best Local Similarity 89.8%; Pred. No. 4.3e-11;  
 RESULT 831  
 ID ACN41008 standard; cDNA; 1416 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA327030, SEQ ID NO:6163.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.9%; Score 139.8; DB 13; Length 1416;  
 Best Local Similarity 89.8%; Pred. No. 4.3e-11;  
 RESULT 832  
 ID ADQ24552 standard; DNA; 7115 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7372.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.9%; Score 139.8; DB 12; Length 7115;  
 Best Local Similarity 83.2%; Pred. No. 4e-11;  
 RESULT 833  
 ID ABV57059 standard; cDNA; 490 BP.  
 DE Human prostate expression marker cDNA 57050.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.9%; Score 139.6; DB 5; Length 490;  
 Best Local Similarity 91.4%; Pred. No. 4.8e-11;  
 RESULT 834  
 ID ACN55464 standard; cDNA; 540 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-N6-A3, SEQ:10245.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.6; DB 13; Length 540;  
 Best Local Similarity 82.5%; Pred. No. 4.8e-11;  
 RESULT 835  
 ID ACN51318 standard; cDNA; 545 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-P6, SEQ:6099.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.6; DB 13; Length 545;  
 Best Local Similarity 76.1%; Pred. No. 4.8e-11;  
 RESULT 836  
 ID ACN52669 standard; cDNA; 578 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-A11, SEQ:7450.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.6; DB 13; Length 578;  
 Best Local Similarity 76.1%; Pred. No. 4.8e-11;  
 RESULT 837  
 ID AAK88206 standard; cDNA; 698 BP.  
 DE Human digestive system antigen coding sequence SEQ ID NO: 522.  
 PN WO200155314-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.9%; Score 139.6; DB 4; Length 698;  
 Best Local Similarity 83.5%; Pred. No. 4.8e-11;

RESULT 838  
ID AAS29150 standard; cDNA; 698 BP.  
DE cDNA encoding for human DNA-binding protein #121.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.6; DB 5; Length 698;  
Best Local Similarity 83.5%; Pred. No. 4.8e-11;  
RESULT 839  
ID AAD16659 standard; cDNA; 698 BP.  
DE Human novel protein-encoding cDNA clone HVAET61, SEQ ID NO:13.  
PN WO200155327-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.6; DB 5; Length 698;  
Best Local Similarity 83.5%; Pred. No. 4.8e-11;  
RESULT 840  
ID ABS68290 standard; cDNA; 698 BP.  
DE cDNA encoding human DNA-binding protein #121.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.9%; Score 139.6; DB 6; Length 698;  
Best Local Similarity 83.5%; Pred. No. 4.8e-11;  
RESULT 841  
ID ADC25284 standard; cDNA; 698 BP.  
DE Human cDNA from extracellular matrix gene 121.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.6; DB 10; Length 698;  
Best Local Similarity 83.5%; Pred. No. 4.8e-11;  
RESULT 842  
ID AAC68125 standard; cDNA; 809 BP.  
DE Human secreted protein cDNA sequence #45.  
PN WO200059335-A1.  
PD 05-OCT-2000.  
PA (ROSE/) ROSEN C A.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.6; DB 3; Length 809;  
Best Local Similarity 91.4%; Pred. No. 4.7e-11;  
RESULT 843  
ID AAA64642 standard; DNA; 905 BP.  
DE Partial sequence MEL7 associated with melanoma and thyroid tumors.  
PN WO200050595-A2.  
PD 31-AUG-2000.  
PA (GOUT/) GOUT I.  
PA (RODN/) RODIN N.  
PA (FILO/) FILONENKO V.  
PA (MATS/) MATSUKA G.  
PA (SCAN/) SCANLAN M.  
PA (OLDL/) OLD L.  
PA (BILY/) BILYNSKY B.  
Query Match 4.9%; Score 139.6; DB 3; Length 905;  
Best Local Similarity 65.9%; Pred. No. 4.7e-11;  
RESULT 844  
ID ADQ22618 standard; DNA; 2499 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5438.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.9%; Score 139.6; DB 12; Length 2499;  
Best Local Similarity 82.5%; Pred. No. 4.5e-11;  
RESULT 845  
ID ADQ32662 standard; DNA; 15749 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6482.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.9%; Score 139.6; DB 12; Length 15749;  
Best Local Similarity 91.4%; Pred. No. 4.2e-11;

RESULT 846  
ID ACN51926 standard; cDNA; 509 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-G11, SEQ:6707.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 139.4; DB 13; Length 509;  
Best Local Similarity 81.7%; Pred. No. 5.1e-11;  
RESULT 847  
ID ACN55753 standard; cDNA; 516 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-B12, SEQ:10534.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 139.4; DB 13; Length 516;  
Best Local Similarity 85.6%; Pred. No. 5.1e-11;  
RESULT 848  
ID ACN62570 standard; cDNA; 552 BP.  
DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A1, SEQ:17351.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 139.4; DB 13; Length 552;  
Best Local Similarity 90.3%; Pred. No. 5.1e-11;  
RESULT 849  
ID ABZ73285 standard; cDNA; 667 BP.  
DE Secreted protein-encoding gene 5 cDNA clone HADDE71, SEQ ID NO:15.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.4; DB 8; Length 667;  
Best Local Similarity 75.5%; Pred. No. 5.1e-11;  
RESULT 850  
ID ABT16763 standard; DNA; 667 BP.  
DE Human secreted protein gene sequence - SEQ ID NO 12.  
PN WO200277188-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.4; DB 10; Length 667;  
Best Local Similarity 75.5%; Pred. No. 5.1e-11;  
RESULT 851  
ID ABZ66896 standard; cDNA; 667 BP.  
DE Human secreted protein encoding cDNA SEQ ID NO 16.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.4; DB 10; Length 667;  
Best Local Similarity 75.5%; Pred. No. 5.1e-11;  
RESULT 852  
ID AAD05318 standard; cDNA; 671 BP.  
DE Human secreted protein-encoding gene 19 cDNA clone HWLFQ64, SEQ ID NO:29.  
PN WO200134626-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 139.4; DB 4; Length 671;  
Best Local Similarity 90.3%; Pred. No. 5.1e-11;  
RESULT 853  
ID ACN60479 standard; cDNA; 431 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-023-Q6-K6-D10, SEQ:15260.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.2; DB 13; Length 431;  
 Best Local Similarity 91.9%; Pred. No. 5.5e-11;  
 RESULT 854  
 ID ACN52334 standard; cDNA; 571 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139.2; DB 13; Length 571;  
 Best Local Similarity 82.8%; Pred. No. 5.5e-11;  
 RESULT 855  
 ID AAC80551 standard; cDNA; 658 BP.  
 DE Human secreted protein gene 21 SEQ ID NO:31.  
 PN WO200058467-A1.  
 PD 05-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.9%; Score 139.2; DB 3; Length 658;  
 Best Local Similarity 84.8%; Pred. No. 5.4e-11;  
 RESULT 856  
 ID ABV78042 standard; DNA; 1071 BP.  
 DE Hypoxia-regulated protein coding sequence #62.  
 PN WO200246465-A2.  
 PD 13-JUN-2002.  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 Query Match 4.9%; Score 139.2; DB 6; Length 1071;  
 Best Local Similarity 81.0%; Pred. No. 5.3e-11;  
 RESULT 857  
 ID ABQ92014 standard; cDNA; 4236 BP.  
 DE Human polynucleotide SEQ ID NO 11.  
 PN US2002065394-A1.  
 PD 30-MAY-2002.  
 PA (JACO/) JACOBS K.  
 PA (MCCO/) MCCOY J M.  
 PA (LAVA/) LAVALLIE E R.  
 PA (COLL/) COLLINS-RACIE L A.  
 PA (EVAN/) EVANS C.  
 PA (MERB/) MERBERG D.  
 PA (TREAC/) TREACY M.  
 PA (SPAU/) SPAULDING V.  
 Query Match 4.9%; Score 139.2; DB 6; Length 4236;  
 Best Local Similarity 82.8%; Pred. No. 5e-11;  
 RESULT 858  
 ID AAS46815 standard; DNA; 21354 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #512.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 139.2; DB 4; Length 21354;  
 Best Local Similarity 89.3%; Pred. No. 4.7e-11;  
 RESULT 859  
 ID ABV57512 standard; cDNA; 439 BP.  
 DE Human prostate expression marker cDNA 57503.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.9%; Score 139; DB 5; Length 439;  
 Best Local Similarity 83.5%; Pred. No. 5.9e-11;  
 RESULT 860  
 ID ACN52447 standard; cDNA; 537 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-015-Q1-N6-E10, SEQ:7228.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 139; DB 13; Length 537;  
 Best Local Similarity 86.0%; Pred. No. 5.9e-11;  
 RESULT 861

ID ADQ23617 standard; DNA; 2050 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6437.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.9%; Score 139; DB 12; Length 2050;  
 Best Local Similarity 86.0%; Pred. No. 5.5e-11;  
 RESULT 862  
 ID AAF22346 standard; cDNA; 2058 BP.  
 DE Human secreted protein gene 31 SEQ ID NO:41.  
 PN WO200061748-A1.  
 PD 19-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.9%; Score 139; DB 3; Length 2058;  
 Best Local Similarity 89.7%; Pred. No. 5.5e-11;  
 RESULT 863  
 ID ADJ48201 standard; DNA; 2520 BP.  
 DE Maize oil-associated gene #19.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C.  
 PA (RAVA/) RAVANELLO M.  
 PA (SAVA/) SAVAGE T.  
 PA (LEDE/) LEDEUX J R.  
 PA (ROGE/) ROGERS J A.  
 Query Match 4.9%; Score 139; DB 12; Length 2520;  
 Best Local Similarity 86.0%; Pred. No. 5.5e-11;  
 RESULT 864  
 ID ABL33662 standard; DNA; 5845 BP.  
 DE Human immune system associated gene SEQ ID NO: 1635.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 139; DB 6; Length 5845;  
 Best Local Similarity 88.3%; Pred. No. 5.3e-11;  
 RESULT 865  
 ID ABL33637 standard; DNA; 7306 BP.  
 DE Human immune system associated gene SEQ ID NO: 1610.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 139; DB 6; Length 7306;  
 Best Local Similarity 90.8%; Pred. No. 5.2e-11;  
 RESULT 866  
 ID ABL32717 standard; DNA; 12007 BP.  
 DE Human immune system associated gene SEQ ID NO: 690.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 139; DB 6; Length 12007;  
 Best Local Similarity 88.3%; Pred. No. 5.1e-11;  
 RESULT 867  
 ID ACN51606 standard; cDNA; 486 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-F5, SEQ:8387.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 138.8; DB 13; Length 486;  
 Best Local Similarity 89.8%; Pred. No. 6.3e-11;  
 RESULT 868  
 ID ACN49328 standard; cDNA; 496 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-K6-E6, SEQ:4109.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.9%; Score 138.8; DB 13; Length 496;  
 Best Local Similarity 89.8%; Pred. No. 6.3e-11;

RESULT 869  
ID AAZ06226 standard; DNA; 936 BP.  
DE Human secreted protein gene No. 8.  
PN WO9935158-A1.  
PD 15-JUL-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 138.8; DB 2; Length 936;  
Best Local Similarity 89.8%; Pred. No. 6.1e-11;  
RESULT 870  
ID ADM32854 standard; DNA; 1084 BP.  
DE DNA sequence of a human adenosine monophosphate deaminase (AMPD).  
PN WO2004024880-A2.  
PD 25-MAR-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 4.9%; Score 138.8; DB 12; Length 1084;  
Best Local Similarity 92.4%; Pred. No. 6.1e-11;  
RESULT 871  
ID AAF91862 standard; cDNA; 2753 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HDP1885, SEQ ID NO:15.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 138.8; DB 4; Length 2753;  
Best Local Similarity 89.8%; Pred. No. 5.8e-11;  
RESULT 872  
ID AAS45399 standard; DNA; 15832 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #52.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.8; DB 4; Length 15832;  
Best Local Similarity 92.4%; Pred. No. 5.4e-11;  
RESULT 873  
ID ABL33343 standard; DNA; 15832 BP.  
DE Human immune system associated gene SEQ ID NO: 1316.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.8; DB 6; Length 15832;  
Best Local Similarity 92.4%; Pred. No. 5.4e-11;  
RESULT 874  
ID ABK28244 standard; DNA; 15832 BP.  
DE DNA transcription associated complementary genomic DNA #59.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.8; DB 6; Length 15832;  
Best Local Similarity 92.4%; Pred. No. 5.4e-11;  
RESULT 875  
ID AAT13475 standard; RNA; 191 BP.  
DE Capture probe for detection of target sequence by chimaeric probe.  
PN EP707076-A1.  
PD 17-APR-1996.  
PA (STAD) AMOCO CORP.  
Query Match 4.9%; Score 138.6; DB 2; Length 191;  
Best Local Similarity 91.3%; Pred. No. 7e-11;  
RESULT 876  
ID ABV44994 standard; cDNA; 309 BP.  
DE Human prostate expression marker cDNA 44995.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 138.6; DB 5; Length 309;  
Best Local Similarity 91.3%; Pred. No. 6.8e-11;  
RESULT 877  
ID ACN58609 standard; cDNA; 313 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-010-Q6-N6-C11, SEQ:13390.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 6; Length 14006;  
Best Local Similarity 84.3%; Pred. No. 5.8e-11;  
RESULT 878  
ID ACN60136 standard; cDNA; 481 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 13; Length 481;  
Best Local Similarity 88.8%; Pred. No. 6.7e-11;  
RESULT 879  
ID ACN46089 standard; cDNA; 538 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A6, SEQ:870.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 13; Length 538;  
Best Local Similarity 82.4%; Pred. No. 6.7e-11;  
RESULT 880  
ID ADR59353 standard; cDNA; 583 BP.  
DE Cotton cDNA sequence, SEQ ID 134.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 4.9%; Score 138.6; DB 13; Length 583;  
Best Local Similarity 94.1%; Pred. No. 6.6e-11;  
RESULT 881  
ID ACN54072 standard; cDNA; 640 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 13; Length 640;  
Best Local Similarity 94.1%; Pred. No. 6.6e-11;  
RESULT 882  
ID ABV04793 standard; cDNA; 893 BP.  
DE Human prostate expression marker cDNA 4784.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 138.6; DB 5; Length 893;  
Best Local Similarity 80.6%; Pred. No. 6.5e-11;  
RESULT 883  
ID ACN86075 standard; DNA; 893 BP.  
DE Breast cancer related marker, seq id 7225.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.9%; Score 138.6; DB 11; Length 893;  
Best Local Similarity 65.0%; Pred. No. 6.5e-11;  
RESULT 884  
ID ABL33958 standard; DNA; 14006 BP.  
DE Human immune system associated gene SEQ ID NO: 1931.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.6; DB 6; Length 14006;  
Best Local Similarity 84.3%; Pred. No. 5.8e-11;  
RESULT 885  
ID AAF94862 standard; cDNA; 396 BP.  
DE Human ovarian cancer associated coding sequence SEQ ID NO: 53.  
PN WO200118046-A2.

Query Match 4.9%; Score 138.6; DB 13; Length 313;  
Best Local Similarity 84.3%; Pred. No. 6.8e-11;  
RESULT 878  
ID ACN60136 standard; cDNA; 481 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 13; Length 481;  
Best Local Similarity 88.8%; Pred. No. 6.7e-11;  
RESULT 879  
ID ACN46089 standard; cDNA; 538 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A6, SEQ:870.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 13; Length 538;  
Best Local Similarity 82.4%; Pred. No. 6.7e-11;  
RESULT 880  
ID ADR59353 standard; cDNA; 583 BP.  
DE Cotton cDNA sequence, SEQ ID 134.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 4.9%; Score 138.6; DB 13; Length 583;  
Best Local Similarity 94.1%; Pred. No. 6.6e-11;  
RESULT 881  
ID ACN54072 standard; cDNA; 640 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.6; DB 13; Length 640;  
Best Local Similarity 94.1%; Pred. No. 6.6e-11;  
RESULT 882  
ID ABV04793 standard; cDNA; 893 BP.  
DE Human prostate expression marker cDNA 4784.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 138.6; DB 5; Length 893;  
Best Local Similarity 80.6%; Pred. No. 6.5e-11;  
RESULT 883  
ID ACN86075 standard; DNA; 893 BP.  
DE Breast cancer related marker, seq id 7225.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.9%; Score 138.6; DB 11; Length 893;  
Best Local Similarity 65.0%; Pred. No. 6.5e-11;  
RESULT 884  
ID ABL33958 standard; DNA; 14006 BP.  
DE Human immune system associated gene SEQ ID NO: 1931.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.6; DB 6; Length 14006;  
Best Local Similarity 84.3%; Pred. No. 5.8e-11;  
RESULT 885  
ID AAF94862 standard; cDNA; 396 BP.  
DE Human ovarian cancer associated coding sequence SEQ ID NO: 53.  
PN WO200118046-A2.

PD 15-MAR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.4; DB 4; Length 396;  
Best Local Similarity 79.3%; Pred. No. 7.2e-11;  
RESULT 886  
ID ABL48812 standard; cDNA; 396 BP.  
DE Ovarian carcinoma sequence isolate 24368.  
PN US2002004491-A1.  
PD 10-JAN-2002.  
PA (XUJ/) XU J.  
PA (STOL/) STOLK J A.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
Query Match 4.9%; Score 138.4; DB 6; Length 396;  
Best Local Similarity 79.3%; Pred. No. 7.2e-11;  
RESULT 887  
ID ABT03129 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 53.  
PN WO200239885-A2.  
PD 23-MAY-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.4; DB 6; Length 396;  
Best Local Similarity 79.3%; Pred. No. 7.2e-11;  
RESULT 888  
ID ADM10722 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma-associated cDNA 24368.  
PN US2003206918-A1.  
PD 06-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.4; DB 11; Length 396;  
Best Local Similarity 79.3%; Pred. No. 7.2e-11;  
RESULT 889  
ID ADJ11052 standard; cDNA; 396 BP.  
DE Representative human ovarian carcinoma cDNA SeqID 53.  
PN US2003232056-A1.  
PD 18-DEC-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.4; DB 12; Length 396;  
Best Local Similarity 79.3%; Pred. No. 7.2e-11;  
RESULT 890  
ID ADM43313 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma cDNA #53.  
PN US2003129192-A1.  
PD 10-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.4; DB 12; Length 396;  
Best Local Similarity 79.3%; Pred. No. 7.2e-11;  
RESULT 891  
ID ACN53459 standard; cDNA; 567 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-A7, SEQ:8240.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.4; DB 13; Length 567;  
Best Local Similarity 85.6%; Pred. No. 7.1e-11;  
RESULT 892  
ID ACN51300 standard; cDNA; 583 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-C2, SEQ:6081.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.4; DB 13; Length 583;  
Best Local Similarity 79.9%; Pred. No. 7.1e-11;  
RESULT 893  
ID AAC77829 standard; cDNA; 2921 BP.  
DE Human cancer associated gene sequence SEQ ID NO:223.  
PN WO200055350-A1.

PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.9%; Score 138.4; DB 3; Length 2921;  
Best Local Similarity 91.8%; Pred. No. 6.6e-11;  
RESULT 894  
ID ABQ67050 standard; DNA; 6486 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 80.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.4; DB 6; Length 6486;  
Best Local Similarity 87.8%; Pred. No. 6.4e-11;  
RESULT 895  
ID ACF62785 standard; DNA; 7369 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:34.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.4; DB 8; Length 7369;  
Best Local Similarity 90.2%; Pred. No. 6.4e-11;  
RESULT 896  
ID ABZ09991 standard; DNA; 7369 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #131.  
PN WO20027772-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.4; DB 8; Length 7369;  
Best Local Similarity 90.2%; Pred. No. 6.4e-11;  
RESULT 897  
ID AAS46303 standard; DNA; 10369 BP.  
DE Tumour suppressor gene derived chemically modified sequence #25.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.4; DB 4; Length 10369;  
Best Local Similarity 90.2%; Pred. No. 6.3e-11;  
RESULT 898  
ID ABL32392 standard; DNA; 10369 BP.  
DE Human immune system associated gene SEQ ID NO: 365.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.4; DB 6; Length 10369;  
Best Local Similarity 90.2%; Pred. No. 6.3e-11;  
RESULT 899  
ID ACN33877 standard; cDNA; 325 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-C7, SEQ:8658.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.2; DB 13; Length 325;  
Best Local Similarity 86.9%; Pred. No. 7.8e-11;  
RESULT 900  
ID ADL43689 standard; DNA; 351 BP.  
DE Human ovarian cancer DNA marker #17579.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 138.2; DB 5; Length 351;  
Best Local Similarity 89.2%; Pred. No. 7.7e-11;  
RESULT 901  
ID AAI88388 standard; cDNA; 398 BP.  
DE Human polynucleotide SEQ ID NO 8448.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 138.2; DB 4; Length 398;  
Best Local Similarity 91.8%; Pred. No. 7.7e-11;  
RESULT 902  
ID ACN49987 standard; cDNA; 452 BP.

DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-P5, SEQ:4768.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.2; DB 13; Length 452;  
Best Local Similarity 79.2%; Pred. No. 7.7e-11;  
RESULT 903  
ID ACN52021 standard; cDNA; 485 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-G4, SEQ:6802.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.9%; Score 138.2; DB 13; Length 485;  
Best Local Similarity 80.9%; Pred. No. 7.6e-11;  
RESULT 904  
ID ADM47653 standard; DNA; 1708 BP.  
DE Polynucleotide sequence #71 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCEITI L B.  
Query Match 4.9%; Score 138.2; DB 12; Length 1708;  
Best Local Similarity 86.9%; Pred. No. 7.2e-11;  
RESULT 905  
ID AAA23441 standard; cDNA; 1954 BP.  
DE cDNA encoding human secreted protein vc51\_1, SEQ ID NO:37.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 4.9%; Score 138.2; DB 3; Length 1954;  
Best Local Similarity 86.9%; Pred. No. 7.2e-11;  
RESULT 906  
ID ADQ22627 standard; DNA; 2785 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5447.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.9%; Score 138.2; DB 12; Length 2785;  
Best Local Similarity 89.2%; Pred. No. 7.1e-11;  
RESULT 907  
ID AAZ07192 standard; cDNA; 3275 BP.  
DE Human lung tumour protein SAL-25 5' cDNA sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.2; DB 2; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 7e-11;  
RESULT 908  
ID AAC79145 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific cDNA #98.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.2; DB 3; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 7e-11;  
RESULT 909  
ID AAD23220 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific protein SAL-25 cDNA.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.2; DB 4; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 7e-11;  
RESULT 910  
ID ADD66459 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific related cDNA, SEQ ID No 151.

PN WO200292001-A2.  
PD 21-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.2; DB 10; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 7e-11;  
RESULT 911  
ID ADE87713 standard; cDNA; 3275 BP.  
DE Human lung tumour antigen cDNA #98.  
PN US2003118599-A1.  
PD 26-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 138.2; DB 10; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 7e-11;  
RESULT 912  
ID ADQ23592 standard; DNA; 3454 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6412.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.9%; Score 138.2; DB 12; Length 3454;  
Best Local Similarity 86.9%; Pred. No. 7e-11;  
RESULT 913  
ID ABL32681 standard; DNA; 6436 BP.  
DE Human immune system associated gene SEQ ID NO: 654.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.9%; Score 138.2; DB 6; Length 6436;  
Best Local Similarity 91.8%; Pred. No. 6.8e-11;  
RESULT 914  
ID AAI80464 standard; cDNA; 456 BP.  
DE Human polynucleotide SEQ ID NO 524.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 138; DB 4; Length 456;  
Best Local Similarity 96.6%; Pred. No. 8.2e-11;  
RESULT 915  
ID ACN46935 standard; cDNA; 499 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 138; DB 13; Length 499;  
Best Local Similarity 82.0%; Pred. No. 8.1e-11;  
RESULT 916  
ID ACN48235 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-021-Q1-N6-B5, SEQ:3016.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 138; DB 13; Length 560;  
Best Local Similarity 82.0%; Pred. No. 8.1e-11;  
RESULT 917  
ID ACN52610 standard; cDNA; 574 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-G6, SEQ:7391.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 138; DB 13; Length 574;  
Best Local Similarity 83.9%; Pred. No. 8.1e-11;  
RESULT 918  
ID ACN87190 standard; DNA; 592 BP.  
DE Breast cancer related marker, seq id 8340.

PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.8%; Score 138; DB 11; Length 592;  
Best Local Similarity 78.9%; Pred. No. 8.1e-11;  
RESULT 919  
ID AAH72860 standard; cDNA; 2771 BP.  
DE Human cervical cancer marker nucleic acid 4134.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 138; DB 4; Length 2771;  
Best Local Similarity 90.7%; Pred. No. 7.6e-11;  
RESULT 920  
ID ABL32911 standard; DNA; 8946 BP.  
DE Human immune system associated gene SEQ ID NO: 884.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 138; DB 6; Length 8946;  
Best Local Similarity 90.7%; Pred. No. 7.2e-11;  
RESULT 921  
ID ABL34174 standard; DNA; 113515 BP.  
DE Human immune system associated gene SEQ ID NO: 2147.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 138; DB 6; Length 113515;  
Best Local Similarity 90.7%; Pred. No. 6.4e-11;  
RESULT 922  
ID ACN46088 standard; cDNA; 522 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A5, SEQ:869.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.8; DB 13; Length 522;  
Best Local Similarity 87.3%; Pred. No. 8.7e-11;  
RESULT 923  
ID ADM19286 standard; cDNA; 1167 BP.  
DE Novel human channel/transporter gene #83.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.8; DB 5; Length 1167;  
Best Local Similarity 92.4%; Pred. No. 8.4e-11;  
RESULT 924  
ID AAS20587 standard; cDNA; 1798 BP.  
DE Human methionine aminopeptidase protease cDNA.  
PN US6329188-B1.  
PD 11-DEC-2001.  
PA (PEKE) PE CORP NY.  
Query Match 4.8%; Score 137.8; DB 6; Length 1798;  
Best Local Similarity 95.3%; Pred. No. 8.2e-11;  
RESULT 925  
ID ADB54096 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 20.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.8; DB 10; Length 4316;  
Best Local Similarity 85.1%; Pred. No. 7.9e-11;  
RESULT 926  
ID ADS89248 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:264.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.8; DB 13; Length 4316;  
Best Local Similarity 85.1%; Pred. No. 7.9e-11;  
RESULT 927

ID ABL32921 standard; DNA; 5195 BP.  
DE Human immune system associated gene SEQ ID NO: 894.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.8; DB 6; Length 5195;  
Best Local Similarity 85.1%; Pred. No. 7.8e-11;  
RESULT 928  
ID ABK34027 standard; DNA; 6944 BP.  
DE Human DNA for staging of Astrocytomas, complement, #57.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.8; DB 6; Length 6944;  
Best Local Similarity 85.1%; Pred. No. 7.8e-11;  
RESULT 929  
ID ADA20447 standard; DNA; 6944 BP.  
DE Prostate tumour related genomic DNA complement sample #56.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.8; DB 8; Length 6944;  
Best Local Similarity 85.1%; Pred. No. 7.8e-11;  
RESULT 930  
ID ADA84254 standard; DNA; 6944 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.8; DB 8; Length 6944;  
Best Local Similarity 85.1%; Pred. No. 7.8e-11;  
RESULT 931  
ID AAI87804 standard; cDNA; 398 BP.  
DE Human Polynucleotide SEQ ID NO 7864.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 137.6; DB 4; Length 398;  
Best Local Similarity 91.2%; Pred. No. 9.4e-11;  
RESULT 932  
ID ADL37305 standard; DNA; 406 BP.  
DE Human ovarian cancer DNA marker #11195.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137.6; DB 5; Length 406;  
Best Local Similarity 88.0%; Pred. No. 9.4e-11;  
RESULT 933  
ID ADI72158 standard; DNA; 406 BP.  
DE Human ovarian cancer DNA marker #4900.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137.6; DB 5; Length 406;  
Best Local Similarity 88.0%; Pred. No. 9.4e-11;  
RESULT 934  
ID ACN52913 standard; cDNA; 411 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ:7694.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.6; DB 13; Length 411;  
Best Local Similarity 82.3%; Pred. No. 9.4e-11;  
RESULT 935  
ID ABX46069 standard; cDNA; 419 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11234.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.8%; Score 137.6; DB 8; Length 419;  
Best Local Similarity 86.4%; Pred. No. 9.3e-11;  
RESULT 936  
ID ACN53393 standard; cDNA; 485 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-C5, SEQ:8174.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.6; DB 13; Length 485;  
Best Local Similarity 97.2%; Pred. No. 9.3e-11;  
RESULT 937  
ID ACN61416 standard; cDNA; 490 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.6; DB 13; Length 490;  
Best Local Similarity 84.2%; Pred. No. 9.3e-11;  
RESULT 938  
ID ACN59971 standard; cDNA; 538 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-036-Q1-K6-H1, SEQ:14752.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.6; DB 13; Length 538;  
Best Local Similarity 91.2%; Pred. No. 9.2e-11;  
RESULT 939  
ID ABV40163 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 40154.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137.6; DB 5; Length 556;  
Best Local Similarity 82.3%; Pred. No. 9.2e-11;  
RESULT 940  
ID ABV40063 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 40054.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137.6; DB 5; Length 556;  
Best Local Similarity 82.3%; Pred. No. 9.2e-11;  
RESULT 941  
ID ABV42105 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 42096.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137.6; DB 5; Length 556;  
Best Local Similarity 82.3%; Pred. No. 9.2e-11;  
RESULT 942  
ID ABV43601 standard; cDNA; 556 BP.  
DE Human prostate expression marker cDNA 43592.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137.6; DB 5; Length 556;  
Best Local Similarity 82.3%; Pred. No. 9.2e-11;  
RESULT 943  
ID ACN58977 standard; cDNA; 563 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-014-Q6-N6-C12, SEQ:13758.  
PN US2004123340-A1.

PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.6; DB 13; Length 563;  
Best Local Similarity 82.3%; Pred. No. 9.2e-11;  
RESULT 944  
ID ADF81828 standard; DNA; 873 BP.  
DE Leukaemia-related DNA sequence #2384.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
Query Match 4.8%; Score 137.6; DB 10; Length 873;  
Best Local Similarity 85.9%; Pred. No. 9.1e-11;  
RESULT 945  
ID AAV61487 standard; cDNA; 4237 BP.  
DE Human secreted protein fe366\_1 cDNA.  
PN WO9841539-A2.  
PD 24-SEP-1998.  
PA (GENY-) GENETICS INST INC.  
Query Match 4.8%; Score 137.6; DB 2; Length 4237;  
Best Local Similarity 82.3%; Pred. No. 8.5e-11;  
RESULT 946  
ID ABL32788 standard; DNA; 6171 BP.  
DE Human immune system associated gene SEQ ID NO: 761.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.6; DB 6; Length 6171;  
Best Local Similarity 84.2%; Pred. No. 8.3e-11;  
RESULT 947  
ID AAL83750 standard; cDNA; 463 BP.  
DE Human polynucleotide SEQ ID NO 3810.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.8%; Score 137.4; DB 4; Length 463;  
Best Local Similarity 90.2%; Pred. No. 9.9e-11;  
RESULT 948  
ID AAH33241 standard; cDNA; 464 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:297.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.4; DB 4; Length 464;  
Best Local Similarity 65.3%; Pred. No. 9.9e-11;  
RESULT 949  
ID ACN47530 standard; cDNA; 506 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-012-Q1-K6-F1, SEQ:2311.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.4; DB 13; Length 506;  
Best Local Similarity 92.9%; Pred. No. 9.9e-11;  
RESULT 950  
ID ABL70492 standard; DNA; 5241 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#191.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.4; DB 6; Length 5241;  
Best Local Similarity 90.2%; Pred. No. 8.9e-11;  
RESULT 951  
ID AAS61450 standard; DNA; 5241 BP.  
DE Human gene regulation-associated gene oligonucleotide #405.



PD WO200177375-A2.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.4; DB 6; Length 5241;  
Best Local Similarity 90.2%; Pred. No. 8.9e-11;  
RESULT 952  
ID ABX39417 standard; cDNA; 393 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4582.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.8%; Score 137.2; DB 8; Length 393;  
Best Local Similarity 89.2%; Pred. No. 1.1e-10;  
RESULT 953  
ID ABX41098 standard; cDNA; 408 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6263.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.8%; Score 137.2; DB 8; Length 408;  
Best Local Similarity 89.2%; Pred. No. 1.1e-10;  
RESULT 954  
ID ACN56650 standard; cDNA; 502 BP.  
DE Cotton gynoecium tissue EST clone ID: LIB3829-001-Q1-N6-H7, SEQ:11431.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.2; DB 13; Length 502;  
Best Local Similarity 89.2%; Pred. No. 1.1e-10;  
RESULT 955  
ID ACN52320 standard; cDNA; 549 BP.  
DE Cotton androecium tissue EST clone ID: LIB3828-014-Q1-N6-B10, SEQ:7101.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.2; DB 13; Length 549;  
Best Local Similarity 89.2%; Pred. No. 1.1e-10;  
RESULT 956  
ID ACN54487 standard; cDNA; 671 BP.  
DE Cotton androecium tissue EST clone ID: LIB3828-006-Q1-K6-F12, SEQ:9268.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137.2; DB 13; Length 671;  
Best Local Similarity 83.7%; Pred. No. 1e-10;  
RESULT 957  
ID AAC95569 standard; cDNA; 1036 BP.  
DE Human secreted protein gene 49 SEQ ID NO:59.  
PN WO200061596-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 4.8%; Score 137.2; DB 3; Length 1036;  
Best Local Similarity 83.2%; Pred. No. 1e-10;  
RESULT 958  
ID ADA98058 standard; cDNA; 1036 BP.  
DE Human secreted protein cDNA sequence #152.  
PN WO2003004623-A2.

PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.2; DB 8; Length 1036;  
Best Local Similarity 83.2%; Pred. No. 1e-10;  
RESULT 959  
ID ADA43944 standard; cDNA; 1036 BP.  
DE Human secreted protein cDNA SEQ ID 132.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.2; DB 8; Length 1036;  
Best Local Similarity 83.2%; Pred. No. 1e-10;  
RESULT 960  
ID ADC20214 standard; DNA; 1036 BP.  
DE Human secreted protein coding sequence #153.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.2; DB 10; Length 1036;  
Best Local Similarity 83.2%; Pred. No. 1e-10;  
RESULT 961  
ID ADF10630 standard; DNA; 1036 BP.  
DE Human secreted protein encoding sequence #83.  
PN WO200299085-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.2; DB 10; Length 1036;  
Best Local Similarity 83.2%; Pred. No. 1e-10;  
RESULT 962  
ID ADP07638 standard; DNA; 1244 BP.  
DE Human secreted protein encoding DNA, seq id 121.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.8%; Score 137.2; DB 12; Length 1244;  
Best Local Similarity 91.8%; Pred. No. 1e-10;  
RESULT 963  
ID ADQ25148 standard; DNA; 1533 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7968.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 137.2; DB 12; Length 1533;  
Best Local Similarity 79.1%; Pred. No. 1e-10;  
RESULT 964  
ID ABX92004 standard; cDNA; 1808 BP.  
DE Lung specific nucleic acid (LSNA) #46.  
PN WO200268633-A2.  
PD 06-SEP-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 4.8%; Score 137.2; DB 6; Length 1808;  
Best Local Similarity 89.2%; Pred. No. 1e-10;  
RESULT 965  
ID ABJ32651 standard; DNA; 12177 BP.  
DE Human immune system associated gene SEQ ID NO: 624.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137.2; DB 6; Length 12177;  
Best Local Similarity 89.2%; Pred. No. 9.2e-11;  
RESULT 966  
ID ACN51559 standard; cDNA; 318 BP.  
DE Cotton androecium tissue EST clone ID: LIB3828-004-Q1-N6-B3, SEQ:6340.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 137; DB 13; Length 318;  
Best Local Similarity 90.7%; Pred. No. 1.2e-10;  
RESULT 967  
ID ABV58273 standard; cDNA; 497 BP.

DE Human prostate expression marker cDNA 58264.  
PN WO200160860-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 137; DB 5; Length 497;  
Best Local Similarity 88.2%; Pred. No. 1.1e-10;  
RESULT 968  
ID AAF31060 standard; cDNA; 872 BP.  
DE Rat clone 701291473H1 coding sequence.  
PN WO200102557-A1.  
PD 11-JAN-2001.  
PA (JANC ) JANSSEN PHARM NV.  
Query Match 4.8%; Score 137; DB 4; Length 872;  
Best Local Similarity 96.6%; Pred. No. 1.1e-10;  
RESULT 969  
ID AAQ04690 standard; cDNA; 1834 BP.  
DE Encodes Mammalian amino acid dehydrogenase activating factor-eta.  
PN JP02111796-A.  
PD 24-APR-1990.  
PA (TOFU ) TOA NENRYO KOGYO KK.  
Query Match 4.8%; Score 137; DB 2; Length 1834;  
Best Local Similarity 85.9%; Pred. No. 1.1e-10;  
RESULT 970  
ID ABL59287 standard; cDNA; 1957 BP.  
DE Nucleotide sequence of AA233368 protein (from first ORF).  
PN WO200246362-A2.  
PD 13-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISB ) JAPAN TOBACCO INC.  
Query Match 4.8%; Score 137; DB 6; Length 1957;  
Best Local Similarity 88.2%; Pred. No. 1.1e-10;  
RESULT 971  
ID ABL59288 standard; cDNA; 1957 BP.  
DE Nucleotide sequence of AA233368 protein (from second ORF).  
PN WO200246362-A2.  
PD 13-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISB ) JAPAN TOBACCO INC.  
Query Match 4.8%; Score 137; DB 13; Length 2401;  
Best Local Similarity 78.5%; Pred. No. 1.1e-10;  
RESULT 973  
ID AAV54587 standard; cDNA; 2447 BP.  
DE Human secretory protein encoding cDNA clone CO1020-1.  
PN WO9833916-A2.  
PD 06-AUG-1998.  
PA (GEMY ) GENETICS INST INC.  
Query Match 4.8%; Score 137; DB 2; Length 2447;  
Best Local Similarity 84.9%; Pred. No. 1.1e-10;  
RESULT 974  
ID AA225607 standard; cDNA; 2447 BP.  
DE Human secreted protein clone CO1020\_1 nucleotide sequence.  
PN US965397-A.  
PD 12-OCT-1999.  
PA (GEMY ) GENETICS INST INC.  
Query Match 4.8%; Score 137; DB 2; Length 2447;  
Best Local Similarity 84.9%; Pred. No. 1.1e-10;  
RESULT 975  
ID ADQ22306 standard; DNA; 2700 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5126.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 137; DB 12; Length 2700;  
Best Local Similarity 88.2%; Pred. No. 1e-10;  
RESULT 976

ID ADD18806 standard; DNA; 3232 BP.  
DE Human disease related protein DNA sequence SeqID238.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 4.8%; Score 137; DB 10; Length 3232;  
Best Local Similarity 85.9%; Pred. No. 1e-10;  
RESULT 977  
ID ABL34573 standard; DNA; 6172 BP.  
DE Human metastasis associated gene SEQ ID NO: 126.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 137; DB 6; Length 6172;  
Best Local Similarity 88.2%; Pred. No. 1e-10;  
RESULT 978  
ID ADS99834 standard; DNA; 6172 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #63.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIRP/) PIERPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 4.8%; Score 137; DB 7; Length 6172;  
Best Local Similarity 88.2%; Pred. No. 1e-10;  
RESULT 979  
ID ABX40612 standard; cDNA; 241 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #5777.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.8%; Score 136.8; DB 8; Length 241;  
Best Local Similarity 85.0%; Pred. No. 1.2e-10;  
RESULT 980  
ID ACNS2877 standard; cDNA; 421 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.8; DB 13; Length 421;  
Best Local Similarity 85.0%; Pred. No. 1.2e-10;  
RESULT 981  
ID ABX44494 standard; cDNA; 456 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9659.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.8%; Score 136.8; DB 8; Length 456;  
Best Local Similarity 95.3%; Pred. No. 1.2e-10;  
RESULT 982  
ID ABV59114 standard; cDNA; 570 BP.  
DE Human prostate expression marker cDNA 59105.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 136.8; DB 5; Length 570;  
Best Local Similarity 95.3%; Pred. No. 1.2e-10;  
RESULT 983  
ID ACNS8226 standard; cDNA; 591 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-008-Q6-K6-G6, SEQ:13007.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E. 4.8%; Score 136.8; DB 13; Length 591;  
 Query Match  
 Best Local Similarity 94.6%; Pred. No. 1.2e-10;  
 RESULT 984  
 ID AAX89609 standard; cDNA; 831 BP.  
 DE Human secreted protein clone bg570\_1 encoding cDNA.  
 PN WO9315253-A1.  
 PD 15-JUL-1999.  
 PA (GEMY) GENETICS INST INC.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 2; Length 831;  
 RESULT 985  
 ID AAS59240 standard; cDNA; 831 BP.  
 DE Human cDNA encoding a secreted protein bg570\_1.  
 PN WO200175068-A2.  
 PD 11-OCT-2001.  
 PA (GEMY) GENETICS INST INC.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 4; Length 831;  
 RESULT 986  
 ID ABA90909 standard; cDNA; 831 BP.  
 DE Human polynucleotide seq ID NO 67.  
 PN US2001039335-A1.  
 PD 08-NOV-2001.  
 PA (JACO/) JACOBS K.  
 PA (MCCO/) MCCOY J M.  
 PA (LAVA/) LAVALLE E R.  
 PA (COLL/) COLLINS-RACIE L A.  
 PA (EVAN/) EVANS C.  
 PA (MERB/) MERBERG D.  
 PA (TREA/) TREACY M.  
 PA (AGOS/) AGOSTINO M J.  
 PA (STEI/) STEININGER R J.  
 PA (SPAU/) SPAULDING V.  
 PA (WONG/) WONG G G.  
 PA (CLAR/) CLARK H.  
 PA (FECH/) FECHTEL K.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 6; Length 831;  
 RESULT 987  
 ID ADQ23195 standard; DNA; 1091 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6015.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 12; Length 1091;  
 RESULT 988  
 ID ABL32411 standard; DNA; 6161 BP.  
 DE Human immune system associated gene SEQ ID NO: 384.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 6; Length 6161;  
 RESULT 989  
 ID ACF62807 standard; DNA; 7369 BP.  
 DE Colon cancer analysis related genomic DNA SEQ ID NO:56.  
 PN WO2003014388-A2.  
 PD 20-FEB-2003.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 8; Length 7369;  
 RESULT 990  
 ID ABZ10137 standard; DNA; 7369 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #277.  
 PN WO20027272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match  
 Best Local Similarity 89.6%; Score 136.8; DB 8; Length 7369;  
 RESULT 991

ID AAV09036 standard; RNA; 12827 BP.  
 DE Equine arteritis virus partial RNA genome sequence.  
 PN WO9802549-A1.  
 PD 22-JAN-1998.  
 PA (UYLE-) RIJKSUNIV LEIDEN.  
 Query Match  
 Best Local Similarity 98.6%; Score 136.8; DB 2; Length 12827;  
 RESULT 992  
 ID AAV09039 standard; DNA; 15528 BP.  
 DE Equine arteritis virus expression vector pEAV030.  
 PN WO9802549-A1.  
 PD 22-JAN-1998.  
 PA (UYLE-) RIJKSUNIV LEIDEN.  
 Query Match  
 Best Local Similarity 98.6%; Score 136.8; DB 2; Length 15528;  
 RESULT 993  
 ID ABX49357 standard; cDNA; 220 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #14522.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match  
 Best Local Similarity 88.6%; Score 136.6; DB 8; Length 220;  
 RESULT 994  
 ID AAI87163 standard; cDNA; 394 BP.  
 DE Human polynucleotide seq ID NO 7223.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 86.3%; Score 136.6; DB 4; Length 394;  
 RESULT 995  
 ID ABVI3564 standard; cDNA; 394 BP.  
 DE Human prostate expression marker cDNA 13555.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 90.1%; Score 136.6; DB 5; Length 394;  
 RESULT 996  
 ID ABV43535 standard; cDNA; 408 BP.  
 DE Human prostate expression marker cDNA 43526.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 90.1%; Score 136.6; DB 5; Length 408;  
 RESULT 997  
 ID ABV34679 standard; cDNA; 408 BP.  
 DE Human prostate expression marker cDNA 34670.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match  
 Best Local Similarity 90.1%; Score 136.6; DB 5; Length 408;  
 RESULT 998  
 ID ACNS4703 standard; cDNA; 426 BP.  
 DE Cotton androecium tissue EST Clone ID: LTB3828-033-Q6-K6-D2, SEQ:9484.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match  
 Best Local Similarity 97.2%; Score 136.6; DB 13; Length 426;  
 RESULT 999  
 ID ABV58008 standard; cDNA; 484 BP.  
 DE Human prostate expression marker cDNA 57999.  
 PN WO200160860-A2.

PD, 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 136.6; DB 5; Length 484;  
Best Local Similarity 88.6%; Pred. No. 1.3e-10;  
RESULT 1000  
ID ACN87735 standard; DNA; 599 BP.  
DE Breast cancer related marker, seq id 8885.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.8%; Score 136.6; DB 11; Length 599;  
Best Local Similarity 85.5%; Pred. No. 1.3e-10;  
RESULT 1001  
ID ACN45292 standard; cDNA; 627 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-A11, SEQ:73.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.6; DB 13; Length 627;  
Best Local Similarity 97.2%; Pred. No. 1.3e-10;  
RESULT 1002  
ID ADE79027 standard; DNA; 1064 BP.  
DE Human protein modification and maintenance molecule (PMM) -7 gene.  
Query Match 4.8%; Score 136.6; DB 10; Length 1064;  
Best Local Similarity 88.6%; Pred. No. 1.2e-10;  
RESULT 1003  
ID AAZ52560 standard; cDNA; 2262 BP.  
DE Human secreted protein clone yel\_1 nucleotide sequence SEQ ID NO:171.  
PN WO958642-A2.  
PD 18-NOV-1999.  
PA (GENY) GENETICS INST INC.  
Query Match 4.8%; Score 136.6; DB 3; Length 2262;  
Best Local Similarity 91.2%; Pred. No. 1.2e-10;  
RESULT 1004  
ID ABK28222 standard; DNA; 11394 BP.  
DE DNA transcription associated complementary genomic DNA #48.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.6; DB 6; Length 11394;  
Best Local Similarity 88.6%; Pred. No. 1.1e-10;  
RESULT 1005  
ID ABX38235 standard; cDNA; 446 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3400.  
PN US200237139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.8%; Score 136.4; DB 8; Length 446;  
Best Local Similarity 90.1%; Pred. No. 1.4e-10;  
RESULT 1006  
ID ACN51887 standard; cDNA; 469 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.4; DB 13; Length 469;  
Best Local Similarity 83.3%; Pred. No. 1.4e-10;  
RESULT 1007  
ID ABV55889 standard; cDNA; 516 BP.  
DE Human prostate expression marker cDNA 55880.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 136.4; DB 5; Length 516;

Best Local Similarity 90.1%; Pred. No. 1.4e-10;  
RESULT 1008  
ID ADL43972 standard; DNA; 539 BP.  
DE Human ovarian cancer DNA marker #17862.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 136.4; DB 5; Length 539;  
Best Local Similarity 83.3%; Pred. No. 1.4e-10;  
RESULT 1009  
ID ACN53206 standard; cDNA; 553 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-D8, SEQ:7987.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.4; DB 13; Length 553;  
Best Local Similarity 83.3%; Pred. No. 1.4e-10;  
RESULT 1010  
ID ACN92384 standard; cDNA; 700 BP.  
DE Human colon cancer cell expressed cDNA #796.  
PN US2002155438-A1.  
PD 24-OCT-2002.  
PA (SIMP/) SIMPSON A J G.  
PA (NETO/) NETO E D.  
PA (BREN/) BRENTANI R R.  
Query Match 4.8%; Score 136.4; DB 10; Length 700;  
Best Local Similarity 90.1%; Pred. No. 1.4e-10;  
RESULT 1011  
ID AAL45656 standard; cDNA; 1762 BP.  
DE Human cancer cell growth inhibitor related DNA SEQ ID NO: 16.  
PN CN1324819-A.  
PD 05-DEC-2001.  
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.  
Query Match 4.8%; Score 136.4; DB 6; Length 1762;  
Best Local Similarity 95.9%; Pred. No. 1.3e-10;  
RESULT 1012  
ID AAL45657 standard; DNA; 1762 BP.  
DE Human cancer cell growth inhibitor related DNA SEQ ID NO: 18.  
PN CN1324819-A.  
PD 05-DEC-2001.  
PA (SHAN-) SHANGHAI CITY INST ONCOLOGY.  
Query Match 4.8%; Score 136.4; DB 6; Length 1762;  
Best Local Similarity 95.9%; Pred. No. 1.3e-10;  
RESULT 1013  
ID ADI43478 standard; DNA; 1875 BP.  
DE Plant transcription factor polynucleotide #1329.  
PN US200401927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HRAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 4.8%; Score 136.4; DB 12; Length 1875;  
Best Local Similarity 99.3%; Pred. No. 1.3e-10;  
RESULT 1014  
ID ADB54224 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 148.  
PN WO2003072821-A2.  
PD 04-SEP-2003.

PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.4; DB 10; Length 4316;  
Best Local Similarity 85.4%; Pred. No. 1.2e-10;  
RESULT 1015  
ID ADS89522 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:538.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.4; DB 13; Length 4316;  
Best Local Similarity 85.4%; Pred. No. 1.2e-10;  
RESULT 1016  
ID ABN80099 standard; DNA; 5368 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 116.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.4; DB 6; Length 5369;  
Best Local Similarity 85.4%; Pred. No. 1.2e-10;  
RESULT 1017  
ID ABK40004 standard; DNA; 5586 BP.  
DE Human chemically pretreated gene sequence #43 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.4; DB 6; Length 5586;  
Best Local Similarity 90.1%; Pred. No. 1.2e-10;  
RESULT 1018  
ID AAS46692 standard; DNA; 24259 BP.  
DE Tumour suppressor gene derived chemically modified sequence #415.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.4; DB 4; Length 24259;  
Best Local Similarity 83.3%; Pred. No. 1.2e-10;  
RESULT 1019  
ID ACN48604 standard; cDNA; 249 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-023-Q6-K6-G7, SEQ:3385.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.2; DB 13; Length 249;  
Best Local Similarity 88.6%; Pred. No. 1.5e-10;  
RESULT 1020  
ID ACN49835 standard; cDNA; 450 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-E4, SEQ:4616.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.2; DB 13; Length 450;  
Best Local Similarity 94.6%; Pred. No. 1.5e-10;  
RESULT 1021  
ID ABV54284 standard; cDNA; 459 BP.  
DE Human prostate expression marker cDNA 54275.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 136.2; DB 5; Length 459;  
Best Local Similarity 82.5%; Pred. No. 1.5e-10;  
RESULT 1022  
ID ABV56248 standard; cDNA; 481 BP.  
DE Human prostate expression marker cDNA 56239.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.8%; Score 136.2; DB 5; Length 481;  
Best Local Similarity 77.5%; Pred. No. 1.5e-10;

RESULT 1023  
ID ADR64316 standard; cDNA; 510 BP.  
DE Cotton cDNA sequence, SEQ ID 5097.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 4.8%; Score 136.2; DB 13; Length 510;  
Best Local Similarity 94.6%; Pred. No. 1.5e-10;  
RESULT 1024  
ID ACN49853 standard; cDNA; 518 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-G11, SEQ:4634.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.2; DB 13; Length 518;  
Best Local Similarity 94.6%; Pred. No. 1.5e-10;  
RESULT 1025  
ID ACN53350 standard; cDNA; 528 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.2; DB 13; Length 528;  
Best Local Similarity 94.6%; Pred. No. 1.5e-10;  
RESULT 1026  
ID ACN57165 standard; cDNA; 541 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-014-Q6-N6-G1, SEQ:11946.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136.2; DB 13; Length 541;  
Best Local Similarity 94.6%; Pred. No. 1.5e-10;  
RESULT 1027  
ID ABN80041 standard; DNA; 5387 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 58.  
PN WO200200927-A2.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.2; DB 6; Length 5387;  
Best Local Similarity 97.9%; Pred. No. 1.3e-10;  
RESULT 1028  
ID AAS46691 standard; DNA; 24259 BP.  
DE Tumour suppressor gene derived chemically modified sequence #414.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIC-) EPIGENOMICS AG.  
Query Match 4.8%; Score 136.2; DB 4; Length 24259;  
Best Local Similarity 84.5%; Pred. No. 1.2e-10;  
RESULT 1029  
ID ACN61227 standard; cDNA; 486 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-034-Q1-N6-A7, SEQ:16008.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.8%; Score 136; DB 13; Length 486;  
Best Local Similarity 75.4%; Pred. No. 1.6e-10;  
RESULT 1030  
ID ACN49736 standard; cDNA; 489 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-026-Q6-N6-B11, SEQ:4517.

PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 136; DB 13; Length 489;  
 Best Local Similarity 81.8%; Pred. No. 1.6e-10;  
 RESULT 1031  
 ID ACN50622 standard; cDNA; 508 BP.  
 DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-E9, SEQ:5403.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 136; DB 13; Length 508;  
 Best Local Similarity 81.8%; Pred. No. 1.6e-10;  
 RESULT 1032  
 ID ACN59983 standard; cDNA; 526 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-036-Q1-N6-A4, SEQ:14764.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 136; DB 13; Length 526;  
 Best Local Similarity 81.8%; Pred. No. 1.6e-10;  
 RESULT 1033  
 ID ACN61425 standard; cDNA; 527 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H7, SEQ:16206.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 136; DB 13; Length 527;  
 Best Local Similarity 85.8%; Pred. No. 1.6e-10;  
 RESULT 1034  
 ID ADRA4025 standard; DNA; 1806 BP.  
 DE Human colon tumour associated gene clone-36 SEQ ID NO:35.  
 PN WO2004074506-A2.  
 PD 02-SEP-2004.  
 PA (MERG-) MERGEN LTD.  
 Query Match 4.8%; Score 136; DB 13; Length 1806;  
 Best Local Similarity 90.6%; Pred. No. 1.5e-10;  
 RESULT 1035  
 ID ADN05367 standard; cDNA; 1913 BP.  
 DE Antipsoriatic cDNA sequence #906.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.8%; Score 136; DB 12; Length 1913;  
 Best Local Similarity 96.5%; Pred. No. 1.5e-10;  
 RESULT 1036  
 ID ADQ08601 standard; DNA; 3030 BP.  
 DE Ciona intestinalis nervous system associated gene SeqID3.  
 PN JP2004057127-A.  
 PD 26-FEB-2004.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match 4.8%; Score 136; DB 12; Length 3030;  
 Best Local Similarity 81.8%; Pred. No. 1.4e-10;  
 RESULT 1037  
 ID ABV57596 standard; cDNA; 396 BP.  
 DE Human prostate expression marker cDNA 57587.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.8%; Score 135.8; DB 5; Length 396;  
 Best Local Similarity 98.6%; Pred. No. 1.7e-10;

RESULT 1038  
 ID ACN52033 standard; cDNA; 443 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-H4, SEQ:6814.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 135.8; DB 13; Length 443;  
 Best Local Similarity 98.6%; Pred. No. 1.7e-10;  
 RESULT 1039  
 ID ABV5662 standard; cDNA; 549 BP.  
 DE Human prostate expression marker cDNA 56653.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.8%; Score 135.8; DB 5; Length 549;  
 Best Local Similarity 92.3%; Pred. No. 1.7e-10;  
 RESULT 1040  
 ID ACN56366 standard; cDNA; 574 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-D1, SEQ:11147.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 135.8; DB 13; Length 574;  
 Best Local Similarity 84.9%; Pred. No. 1.7e-10;  
 RESULT 1041  
 ID ACN52339 standard; cDNA; 593 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-F10, SEQ:7120.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.8%; Score 135.8; DB 13; Length 593;  
 Best Local Similarity 84.9%; Pred. No. 1.7e-10;  
 RESULT 1042  
 ID ADM47812 standard; DNA; 1383 BP.  
 DE Polynucleotide sequence #230 useful in producing transgenic plants.  
 PN US2003233670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE/) EDGERTON M D.  
 PA (CHOM/) CHOMET P S.  
 PA (LACC/) LACCRETI L B.  
 Query Match 4.8%; Score 135.8; DB 12; Length 1383;  
 Best Local Similarity 98.6%; Pred. No. 1.6e-10;  
 RESULT 1043  
 ID ACN39804 standard; cDNA; 2074 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA325989, SEQ ID NO:4174.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.8%; Score 135.8; DB 13; Length 2074;  
 Best Local Similarity 89.6%; Pred. No. 1.6e-10;  
 RESULT 1044  
 ID ABZ10078 standard; DNA; 2501 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #218.  
 PN WO20027272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.8%; Score 135.8; DB 8; Length 2501;  
 Best Local Similarity 98.6%; Pred. No. 1.6e-10;  
 RESULT 1045  
 ID ABZ10224 standard; DNA; 2501 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #364.  
 PN WO20027272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.

Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 2501;  
RESULT 1046  
ID ABL333928 standard; DNA; 4001 BP.  
DE Human DNA for staging of Astrocytomas, complement, #5.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 4001;  
RESULT 1047  
ID ADA20431 standard; DNA; 4001 BP.  
DE Prostate tumour related genomic DNA complement sample #48.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 4001;  
RESULT 1048  
ID ADA84238 standard; DNA; 4001 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:96.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 4001;  
RESULT 1049  
ID ABL32511 standard; DNA; 5306 BP.  
DE Human immune system associated gene SEQ ID NO: 484.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 5306;  
RESULT 1050  
ID ABOQ7140 standard; DNA; 6134 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 170.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 6134;  
RESULT 1051  
ID ABL32996 standard; DNA; 7061 BP.  
DE Human immune system associated gene SEQ ID NO: 969.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 7061;  
RESULT 1052  
ID ABL70247 standard; DNA; 7061 BP.  
DE Chemically treated cell signalling DNA sequence#69.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 7061;  
RESULT 1053  
ID AAS61188 standard; DNA; 7061 BP.  
DE Human gene regulation-associated gene oligonucleotide #143.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 7061;  
RESULT 1054  
ID ABL33032 standard; DNA; 14798 BP.  
DE Human immune system associated gene SEQ ID NO: 1005.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 14798;

Best Local Similarity 98.6%; Pred. No. 1.4e-10;  
RESULT 1055  
ID ABL80146 standard; DNA; 14920 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 163.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 14920;  
RESULT 1056  
ID ABL79984 standard; DNA; 16633 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 1.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 16633;  
RESULT 1057  
ID ABL33719 standard; DNA; 17934 BP.  
DE Human immune system associated gene SEQ ID NO: 1692.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 6; Length 17934;  
RESULT 1058  
ID ABL20958 standard; DNA; 35962 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #98.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 35962;  
RESULT 1059  
ID ABL210104 standard; DNA; 35962 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #244.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.8; DB 8; Length 35962;  
RESULT 1060  
ID AAI85202 standard; cDNA; 390 BP.  
DE Human polynucleotide SEQ ID NO 5262.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 4; Length 390;  
RESULT 1061  
ID ACH21249 standard; cDNA; 429 BP.  
DE Human adult liver cDNA #861.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 9; Length 429;  
RESULT 1062  
ID ACS53490 standard; cDNA; 468 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-D3, SEQ:8271.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 13; Length 468;  
RESULT 1063

ID ACN47785 standard; cDNA; 557 BP.  
DE - Cotton primed seed EST Clone ID: LTB3825-015-Q1-N6-A5, SEQ:2566.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 13; Length 557;  
84.1%; Pred. No. 1.8e-10;  
RESULT 1064  
ID AAL16123 standard; cDNA; 831 BP.  
DE Human breast cancer expressed polynucleotide 8580.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 4; Length 831;  
64.8%; Pred. No. 1.7e-10;  
RESULT 1065  
ID AAD02119 standard; cDNA; 1459 BP.  
DE Maize RAD51 orthologue #2 cDNA.  
PN WO200068370-A2.  
PD 16-NOV-2000.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 4; Length 1459;  
97.2%; Pred. No. 1.7e-10;  
RESULT 1066  
ID ABN80138 standard; DNA; 6484 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 155.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 6; Length 6484;  
86.2%; Pred. No. 1.6e-10;  
RESULT 1067  
ID ABQ87061 standard; DNA; 9095 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 91.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 6; Length 9095;  
82.1%; Pred. No. 1.6e-10;  
RESULT 1068  
ID ABL70544 standard; DNA; 15649 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#217.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 6; Length 15649;  
86.2%; Pred. No. 1.5e-10;  
RESULT 1069  
ID ABL34072 standard; DNA; 40862 BP.  
DE Human immune system associated gene SEQ ID NO: 2045.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 4.8%; Score 135.6; DB 6; Length 40862;  
84.1%; Pred. No. 1.5e-10;  
RESULT 1070  
ID ABX36136 standard; cDNA; 181 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #1301.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 4.8%; Score 135.4; DB 8; Length 181;  
99.3%; Pred. No. 2e-10;  
RESULT 1071  
ID ABV54282 standard; cDNA; 412 BP.  
DE Human prostate expression marker cDNA 54273.  
PN WO200160860-A2.

PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.4; DB 5; Length 412;  
92.8%; Pred. No. 1.9e-10;  
RESULT 1072  
ID ADH39852 standard; cDNA; 2146 BP.  
DE Guayule fructan:fructan 1-fructosyltransferase (1-FFT) cDNA.  
PN US2002170086-A1.  
PD 14-NOV-2002.  
PA (ALLE/) ALLEN S M.  
PA (CAIM/) CAIMI P G.  
PA (STOO/) STOOP J M.  
Query Match  
Best Local Similarity 4.8%; Score 135.4; DB 10; Length 2146;  
85.3%; Pred. No. 1.8e-10;  
RESULT 1073  
ID ABK34669 standard; cDNA; 3415 BP.  
DE Human cDNA for novel secreted protein, SEQ ID 438.  
PN WO200177290-A2.  
PD 18-OCT-2001.  
PA (GENY) GENETICS INST INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.4; DB 6; Length 3415;  
95.9%; Pred. No. 1.8e-10;  
RESULT 1074  
ID ABV54241 standard; cDNA; 385 BP.  
DE Human prostate expression marker cDNA 54232.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.2; DB 5; Length 385;  
83.5%; Pred. No. 2.1e-10;  
RESULT 1075  
ID ABV49895 standard; cDNA; 522 BP.  
DE Human prostate expression marker cDNA 49886.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.2; DB 5; Length 522;  
82.6%; Pred. No. 2e-10;  
RESULT 1076  
ID ADN04959 standard; cDNA; 1999 BP.  
DE Antiposoriatic cDNA sequence #694.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.2; DB 12; Length 1999;  
91.7%; Pred. No. 1.9e-10;  
RESULT 1077  
ID AAF97906 standard; cDNA; 2394 BP.  
DE Human secreted protein cDNA, SEQ ID NO: 33.  
PN WO200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.8%; Score 135.2; DB 4; Length 2394;  
89.0%; Pred. No. 1.9e-10;  
RESULT 1078  
ID ADPO4916 standard; cDNA; 2789 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 511.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 4.8%; Score 135.2; DB 12; Length 2789;  
86.6%; Pred. No. 1.9e-10;  
RESULT 1079  
ID ACA25512 standard; DNA; 195 BP.  
DE Prokaryotic essential gene #7169.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 8; Length 195;  
93.4%; Pred. No. 2.3e-10;  
RESULT 1080  
ID ACN50243 standard; cDNA; 368 BP.  
DE Cotton non-primed seed EST Clone ID: LTB3826-002-Q1-K6-B12, SEQ:5024.



PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 135; DB 13; Length 368;  
Best Local Similarity 72.8%; Pred. No. 2.2e-10;  
RESULT 1081  
ID AAI83197 standard; cDNA; 403 BP.  
DE Human polynucleotide SEQ ID NO 3257.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 135; DB 4; Length 403;  
Best Local Similarity 81.7%; Pred. No. 2.2e-10;  
RESULT 1082  
ID ABV09124 standard; cDNA; 417 BP.  
DE Human prostate expression marker cDNA 9115.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 135; DB 5; Length 417;  
Best Local Similarity 69.6%; Pred. No. 2.2e-10;  
RESULT 1083  
ID AAI83052 standard; cDNA; 452 BP.  
DE Human polynucleotide SEQ ID NO 3112.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 135; DB 4; Length 452;  
Best Local Similarity 96.5%; Pred. No. 2.2e-10;  
RESULT 1084  
ID ACN53254 standard; cDNA; 578 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-F11, SEQ:8035.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 135; DB 13; Length 578;  
Best Local Similarity 85.7%; Pred. No. 2.2e-10;  
RESULT 1085  
ID AA23442 standard; cDNA; 1333 BP.  
DE cDNA encoding human secreted protein vc52\_1, SEQ ID NO:39.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 4.7%; Score 135; DB 3; Length 1933;  
Best Local Similarity 96.5%; Pred. No. 2e-10;  
RESULT 1086  
ID ADH61306 standard; DNA; 3420 BP.  
DE INTSIG encoding DNA 7512389CB1, SEQ ID 23.  
PN WO2004001005-A2.  
PD 31-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 4.7%; Score 135; DB 12; Length 3420;  
Best Local Similarity 88.0%; Pred. No. 2e-10;  
RESULT 1087  
ID ABX49356 standard; cDNA; 411 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #14521.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.7%; Score 134.8; DB 8; Length 411;  
Best Local Similarity 92.2%; Pred. No. 2.3e-10;  
RESULT 1088  
ID ACN56895 standard; cDNA; 435 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-011-Q6-N6-E2, SEQ:11676.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134.8; DB 13; Length 435;  
Best Local Similarity 89.5%; Pred. No. 2.3e-10;  
RESULT 1089  
ID ABV54519 standard; cDNA; 515 BP.  
DE Human prostate expression marker cDNA 54510.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 134.8; DB 5; Length 515;  
Best Local Similarity 84.8%; Pred. No. 2.3e-10;  
RESULT 1090  
ID ADQ22502 standard; DNA; 1389 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5322.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 134.8; DB 12; Length 1389;  
Best Local Similarity 92.2%; Pred. No. 2.2e-10;  
RESULT 1091  
ID AAD05087 standard; cDNA; 2297 BP.  
DE Human secreted protein-encoding gene 7 cDNA clone HHMM74, SEQ ID NO: 45.  
PN WO200134768-A2.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 134.8; DB 4; Length 2297;  
Best Local Similarity 78.4%; Pred. No. 2.2e-10;  
RESULT 1092  
ID ADA40350 standard; cDNA; 2297 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 134.8; DB 8; Length 2297;  
Best Local Similarity 78.4%; Pred. No. 2.2e-10;  
RESULT 1093  
ID ADA56516 standard; DNA; 2297 BP.  
DE Gene encoding human secreted protein #223.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 134.8; DB 10; Length 2297;  
Best Local Similarity 78.4%; Pred. No. 2.2e-10;  
RESULT 1094  
ID ACN53258 standard; cDNA; 353 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-F9, SEQ:8039.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134.6; DB 13; Length 353;  
Best Local Similarity 80.2%; Pred. No. 2.5e-10;  
RESULT 1095  
ID ABV59054 standard; cDNA; 360 BP.  
DE Human prostate expression marker cDNA 59045.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 134.6; DB 5; Length 360;  
Best Local Similarity 97.2%; Pred. No. 2.5e-10;  
RESULT 1096  
ID ABV08149 standard; cDNA; 391 BP.  
DE Human prostate expression marker cDNA 8140.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

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Query Match      4.7%; Score 134.6; DB 5; Length 391;
Best Local Similarity 80.0%; Pred. No. 2.5e-10;
RESULT 1097
ID ABV58690 standard; cDNA; 579 BP.
DE Human prostate expression marker cDNA 58681.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      4.7%; Score 134.6; DB 5; Length 579;
Best Local Similarity 86.1%; Pred. No. 2.5e-10;
RESULT 1098
ID AAC98734 standard; cDNA; 225 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:744.
PN WO20005351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      4.7%; Score 134.4; DB 3; Length 225;
Best Local Similarity 92.8%; Pred. No. 2.7e-10;
RESULT 1099
ID ACN53166 standard; cDNA; 319 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-N6-G10, SEQ:7947.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match      4.7%; Score 134.4; DB 13; Length 319;
Best Local Similarity 81.2%; Pred. No. 2.7e-10;
RESULT 1100
ID ACN53082 standard; cDNA; 398 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-021-Q1-N6-F7, SEQ:7863.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match      4.7%; Score 134.4; DB 13; Length 398;
Best Local Similarity 95.8%; Pred. No. 2.7e-10;
RESULT 1101
ID ABV16128 standard; cDNA; 416 BP.
DE Human prostate expression marker cDNA 16119.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      4.7%; Score 134.4; DB 5; Length 416;
Best Local Similarity 76.5%; Pred. No. 2.7e-10;
RESULT 1102
ID ACH19935 standard; cDNA; 423 BP.
DE Human adult lung cDNA #938.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRNAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match      4.7%; Score 134.4; DB 9; Length 423;
Best Local Similarity 77.1%; Pred. No. 2.7e-10;
RESULT 1103
ID ACN55408 standard; cDNA; 499 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-023-Q6-N6-C10, SEQ:10189.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match      4.7%; Score 134.4; DB 13; Length 499;
Best Local Similarity 75.0%; Pred. No. 2.6e-10;
RESULT 1104
ID ACN52918 standard; cDNA; 520 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D6, SEQ:7699.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match      4.7%; Score 134.4; DB 13; Length 520;
Best Local Similarity 85.2%; Pred. No. 2.6e-10;
RESULT 1105
ID ACN61238 standard; cDNA; 548 BP.
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-034-Q1-N6-C12, SEQ:16019.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match      4.7%; Score 134.4; DB 13; Length 548;
Best Local Similarity 81.2%; Pred. No. 2.6e-10;
RESULT 1106
ID ADL37588 standard; DNA; 608 BP.
DE Human ovarian cancer DNA marker #11478.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      4.7%; Score 134.4; DB 5; Length 608;
Best Local Similarity 80.6%; Pred. No. 2.6e-10;
RESULT 1107
ID ADI72448 standard; DNA; 608 BP.
DE Human ovarian cancer DNA marker #5190.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match      4.7%; Score 134.4; DB 5; Length 608;
Best Local Similarity 80.6%; Pred. No. 2.6e-10;
RESULT 1108
ID ACN50609 standard; cDNA; 616 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-D5, SEQ:5390.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match      4.7%; Score 134.4; DB 13; Length 616;
Best Local Similarity 81.2%; Pred. No. 2.6e-10;
RESULT 1109
ID ABK47997 standard; DNA; 6409 BP.
DE Human kinesin motor protein Kinf1-3 DNA.
PN WO200226929-A2.
PD 04-APR-2002.
PA (CYTO-) CYTOKINETICS INC.
Query Match      4.7%; Score 134.4; DB 6; Length 6409;
Best Local Similarity 87.5%; Pred. No. 2.4e-10;
RESULT 1110
ID ACA62846 standard; DNA; 6409 BP.
DE DNA encoding human kinesin motor protein Kinf1-3.
PN US2003036075-A1.
PD 20-FEB-2003.
PA (CYTO-) CYTOKINETICS INC.
Query Match      4.7%; Score 134.4; DB 8; Length 6409;
Best Local Similarity 87.5%; Pred. No. 2.4e-10;
RESULT 1111
ID ACA62960 standard; DNA; 6409 BP.
DE DNA encoding human kinesin motor protein, Kinf1-3.
PN US6514738-B1.
PD 04-FEB-2003.
PA (CYTO-) CYTOKINETICS INC.
Query Match      4.7%; Score 134.4; DB 9; Length 6409;
Best Local Similarity 87.5%; Pred. No. 2.4e-10;
RESULT 1112
ID ADF50896 standard; DNA; 11097 BP.
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DE Chemically modified promoter region of human melastatin gene (SeqID 4).  
PN EP1344832-A1.  
PD 17-SEP-2003.  
PA (EP1G-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134.4; DB 10; Length 11097;  
Best Local Similarity 83.2%; Pred. No. 2.3e-10;  
RESULT 1113  
ID AAF24360 standard; DNA; 160 BP.  
DE Retroviral recombination assay coding sequence fragment #5.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match 4.7%; Score 134.2; DB 5; Length 160;  
Best Local Similarity 97.8%; Pred. No. 3e-10;  
RESULT 1114  
ID AAF24361 standard; DNA; 178 BP.  
DE Retroviral recombination assay coding sequence fragment #6.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match 4.7%; Score 134.2; DB 5; Length 178;  
Best Local Similarity 97.8%; Pred. No. 2.9e-10;  
RESULT 1115  
ID ADP85921 standard; DNA; 196 BP.  
DE Synthetic construct #5.  
PN US2004110205-A1.  
PD 10-JUN-2004.  
PA (WANG/) WANG H.  
Query Match 4.7%; Score 134.2; DB 12; Length 196;  
Best Local Similarity 97.8%; Pred. No. 2.9e-10;  
RESULT 1116  
ID AAF24363 standard; DNA; 208 BP.  
DE Retroviral recombination assay coding sequence fragment #8.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match 4.7%; Score 134.2; DB 5; Length 208;  
Best Local Similarity 97.8%; Pred. No. 2.9e-10;  
RESULT 1117  
ID ABX41374 standard; cDNA; 217 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #6539.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.7%; Score 134.2; DB 8; Length 217;  
Best Local Similarity 97.8%; Pred. No. 2.9e-10;  
RESULT 1118  
ID ACN53426 standard; cDNA; 403 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-F9, SEQ:8207.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134.2; DB 13; Length 403;  
Best Local Similarity 89.0%; Pred. No. 2.8e-10;  
RESULT 1119  
ID AAI89032 standard; cDNA; 416 BP.  
DE Human polynucleotide SEQ ID NO 9092.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 134.2; DB 4; Length 416;  
Best Local Similarity 89.0%; Pred. No. 2.8e-10;  
RESULT 1120  
ID AAI87701 standard; cDNA; 491 BP.

DE Human polynucleotide SEQ ID NO 7761.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 134.2; DB 4; Length 491;  
Best Local Similarity 71.9%; Pred. No. 2.8e-10;  
RESULT 1121  
ID ACH24750 standard; cDNA; 491 BP.  
DE Human adult ovary cDNA #3130.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match 4.7%; Score 134.2; DB 9; Length 491;  
Best Local Similarity 71.9%; Pred. No. 2.8e-10;  
RESULT 1122  
ID ABV59092 standard; cDNA; 501 BP.  
DE Human prostate expression marker cDNA 59083.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 134.2; DB 5; Length 501;  
Best Local Similarity 97.8%; Pred. No. 2.8e-10;  
RESULT 1123  
ID ACN56029 standard; cDNA; 529 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-C8, SEQ:10810.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134.2; DB 13; Length 529;  
Best Local Similarity 86.5%; Pred. No. 2.8e-10;  
RESULT 1124  
ID ACN52102 standard; cDNA; 542 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-E12, SEQ:6883.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134.2; DB 13; Length 542;  
Best Local Similarity 97.8%; Pred. No. 2.8e-10;  
RESULT 1125  
ID ACN45362 standard; cDNA; 570 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134.2; DB 13; Length 570;  
Best Local Similarity 97.8%; Pred. No. 2.8e-10;  
RESULT 1126  
ID ADQ62833 standard; RNA; 1000 BP.  
DE Homopoly-A contaminant for RNaseH activity assay.  
PN WO2004059012-A1.  
PD 15-JUL-2004.  
PA (AMHP) WYETH.  
Query Match 4.7%; Score 134.2; DB 12; Length 1000;  
Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
RESULT 1127  
ID ADQ62832 standard; RNA; 1000 BP.  
DE Homopoly-U contaminant for RNaseH activity assay.  
PN WO2004059012-A1.  
PD 15-JUL-2004.  
PA (AMHP) WYETH.

Query Match 4.7%; Score 134.2; DB 12; Length 1000;  
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
 RESULT 1128  
 ID ADP85917 standard; DNA; 1300 BP.  
 DE Synthetic construct #1.  
 PN US2004110205-A1.  
 PD 10-JUN-2004.  
 PA (WANG/) WANG H.  
 Query Match 4.7%; Score 134.2; DB 12; Length 1300;  
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
 RESULT 1129  
 ID ACC50413 standard; cDNA; 1663 BP.  
 DE Human secreted protein coding sequence, SEQ ID 80.  
 PN WO200295010-A2.  
 PD 28-NOV-2002.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 134.2; DB 8; Length 1663;  
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
 RESULT 1130  
 ID ABZ71230 standard; cDNA; 1663 BP.  
 DE Human secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:51.  
 PN WO200276488-A1.  
 PD 03-OCT-2002.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 134.2; DB 8; Length 1663;  
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
 RESULT 1131  
 ID ADB91122 standard; cDNA; 1663 BP.  
 DE Human secreted protein cDNA #SEQ ID 68.  
 PN WO2003004622-A2.  
 PD 16-JAN-2003.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 134.2; DB 9; Length 1663;  
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
 RESULT 1132  
 ID ADC73466 standard; DNA; 1663 BP.  
 DE Human secreted protein-related DNA - SEQ ID 99.  
 PN WO2003038063-A2.  
 PD 08-MAY-2003.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 134.2; DB 10; Length 1663;  
 Best Local Similarity 97.8%; Pred. No. 2.7e-10;  
 RESULT 1133  
 ID AAS45477 standard; DNA; 7657 BP.  
 DE Chemically pretreated complementary DNA associated with cell cycle #91.  
 PN WO200168911-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134.2; DB 4; Length 7657;  
 Best Local Similarity 97.8%; Pred. No. 2.5e-10;  
 RESULT 1134  
 ID ABL34022 standard; DNA; 7657 BP.  
 DE Human immune system associated gene SEQ ID NO: 1995.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134.2; DB 6; Length 7657;  
 Best Local Similarity 97.8%; Pred. No. 2.5e-10;  
 RESULT 1135  
 ID ABK31429 standard; DNA; 9814 BP.  
 DE Signal transduction associated gene modified complementary DNA #136.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134.2; DB 6; Length 9814;  
 Best Local Similarity 97.8%; Pred. No. 2.5e-10;  
 RESULT 1136  
 ID ABL34196 standard; DNA; 37973 BP.  
 DE Human immune system associated gene SEQ ID NO: 2169.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134.2; DB 6; Length 37973;

Best Local Similarity 97.8%; Pred. No. 2.3e-10;  
 RESULT 1137  
 ID ABX38052 standard; cDNA; 242 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #3217.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 4.7%; Score 134; DB 8; Length 242;  
 Best Local Similarity 96.5%; Pred. No. 3.1e-10;  
 RESULT 1138  
 ID ADL35477 standard; DNA; 305 BP.  
 DE Human filamin A alpha-related functional screen hit DNA 3.  
 PN WO2004019893-A2.  
 PD 11-MAR-2004.  
 PA (RIGE-) RIGEL PHARM INC.  
 Query Match 4.7%; Score 134; DB 12; Length 305;  
 Best Local Similarity 96.5%; Pred. No. 3.1e-10;  
 RESULT 1139  
 ID ACN55002 standard; cDNA; 342 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.7%; Score 134; DB 13; Length 342;  
 Best Local Similarity 85.6%; Pred. No. 3.1e-10;  
 RESULT 1140  
 ID ABV57020 standard; cDNA; 472 BP.  
 DE Human prostate expression marker cDNA 57011.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 472;  
 Best Local Similarity 90.5%; Pred. No. 3e-10;  
 RESULT 1141  
 ID ACN49504 standard; cDNA; 593 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-034-Q6-K6-G11, SEQ:4285.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.7%; Score 134; DB 13; Length 593;  
 Best Local Similarity 96.5%; Pred. No. 3e-10;  
 RESULT 1142  
 ID ACN56642 standard; cDNA; 598 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.7%; Score 134; DB 13; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 3e-10;  
 RESULT 1143  
 ID ADI73484 standard; DNA; 756 BP.  
 DE Human ovarian cancer DNA marker #6226.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 756;  
 Best Local Similarity 82.5%; Pred. No. 3e-10;  
 RESULT 1144  
 ID ADL38614 standard; DNA; 756 BP.  
 DE Human ovarian cancer DNA marker #12504.  
 PN WO200170979-A2.

PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 756;  
 Best Local Similarity 82.5%; Pred. No. 3e-10;  
 RESULT 1145  
 ID ADQ22074 standard; DNA; 980 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.7%; Score 134; DB 12; Length 980;  
 Best Local Similarity 85.6%; Pred. No. 2.9e-10;  
 RESULT 1146  
 ID ADF94940 standard; cDNA; 1311 BP.  
 DE Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.  
 PN WO2003031586-A2.  
 PD 17-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (BLON/) BLONDEL O.  
 PA (RUBE/) RUBEN S M.  
 Query Match 4.7%; Score 134; DB 10; Length 1311;  
 Best Local Similarity 98.5%; Pred. No. 2.9e-10;  
 RESULT 1147  
 ID ABL49347 standard; DNA; 5152 BP.  
 DE Human polynucleotide associated with DNA replication SEQ ID NO 47.  
 PN WO200177377-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134; DB 6; Length 5152;  
 Best Local Similarity 95.8%; Pred. No. 2.7e-10;  
 RESULT 1148  
 ID ABK40074 standard; DNA; 8899 BP.  
 DE Human chemically pretreated gene sequence #78 strand 2.  
 PN WO200202806-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134; DB 6; Length 8899;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 RESULT 1149  
 ID ABL32837 standard; DNA; 8899 BP.  
 DE Human immune system associated gene SEQ ID NO: 810.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 134; DB 6; Length 8899;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;  
 RESULT 1150  
 ID ABX43930 standard; cDNA; 283 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #9095.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 4.7%; Score 133.8; DB 8; Length 283;  
 Best Local Similarity 97.1%; Pred. No. 3.3e-10;  
 RESULT 1151  
 ID ABX37058 standard; cDNA; 415 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #2223.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 4.7%; Score 133.8; DB 8; Length 415;  
 Best Local Similarity 92.2%; Pred. No. 3.2e-10;  
 RESULT 1152  
 ID ABV54238 standard; cDNA; 474 BP.  
 DE Human prostate expression marker cDNA 54229.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 133.8; DB 5; Length 474;  
 Best Local Similarity 83.3%; Pred. No. 3.2e-10;  
 RESULT 1153  
 ID AAL16112 standard; cDNA; 817 BP.  
 DE Human breast cancer expressed polynucleotide 8569.  
 PN WO200151628-A2.  
 PD 19-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 133.8; DB 4; Length 817;  
 Best Local Similarity 73.2%; Pred. No. 3.1e-10;  
 RESULT 1154  
 ID ACN86064 standard; DNA; 861 BP.  
 DE Breast cancer related marker, seq id 7214.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 4.7%; Score 133.8; DB 11; Length 861;  
 Best Local Similarity 73.2%; Pred. No. 3.1e-10;  
 RESULT 1155  
 ID ADL63529 standard; DNA; 874 BP.  
 DE Human ovarian cancer DNA marker #21741.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 133.8; DB 5; Length 874;  
 Best Local Similarity 89.4%; Pred. No. 3.1e-10;  
 RESULT 1156  
 ID ADQ29621 standard; DNA; 2566 BP.  
 DE Human colorectal cancer-associated protein coding sequence #43.  
 PN EP1439393-A2.  
 PD 21-JUL-2004.  
 PA (FARB) BAYER HEALTHCARE LLC.  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 Query Match 4.7%; Score 133.8; DB 12; Length 2566;  
 Best Local Similarity 98.5%; Pred. No. 3e-10;  
 RESULT 1157  
 ID ABL33801 standard; DNA; 6115 BP.  
 DE Human immune system associated gene SEQ ID NO: 1774.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 133.8; DB 6; Length 6115;  
 Best Local Similarity 87.0%; Pred. No. 2.9e-10;  
 RESULT 1158  
 ID ABN80102 standard; DNA; 8712 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 119.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 133.8; DB 6; Length 8712;  
 Best Local Similarity 95.2%; Pred. No. 2.8e-10;  
 RESULT 1159  
 ID ABX42068 standard; cDNA; 259 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #7233.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 4.7%; Score 133.6; DB 8; Length 259;  
 Best Local Similarity 86.0%; Pred. No. 3.5e-10;  
 RESULT 1160  
 ID ACH28630 standard; cDNA; 477 BP.  
 DE Human adult ovary cDNA #7010.  
 PN US2003073623-A1.  
 PD 17-APR-2003.  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.

Query Match 4.7%; Score 133.6; DB 9; Length 477;  
Best Local Similarity 86.0%; Pred. No. 3.4e-10;  
RESULT 1161  
ID ADPO4748 standard; cDNA; 1352 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 343.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGAKU) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 4.7%; Score 133.6; DB 12; Length 1352;  
Best Local Similarity 88.4%; Pred. No. 3.3e-10;  
RESULT 1162  
ID AAF98380 standard; cDNA; 2178 BP.  
DE Human cDNA clone BL187\_4 sequence SEQ ID NO. 2178.  
PN WO200119988-A1.  
PD 22-MAR-2001.  
PA (GENY) GENETICS INST INC.  
Query Match 4.7%; Score 133.6; DB 5; Length 2178;  
Best Local Similarity 91.0%; Pred. No. 3.2e-10;  
RESULT 1163  
ID AAS45339 standard; DNA; 6025 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #22.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.6; DB 4; Length 6025;  
Best Local Similarity 88.4%; Pred. No. 3.1e-10;  
RESULT 1164  
ID AAS46794 standard; DNA; 56153 BP.  
DE Tumour suppressor gene derived chemically modified sequence #520.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.6; DB 4; Length 56153;  
Best Local Similarity 83.9%; Pred. No. 2.8e-10;  
RESULT 1165  
ID AAS35937 standard; DNA; 148 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1437.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1166  
ID AAK89970 standard; DNA; 148 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3546.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1167  
ID AAI62624 standard; DNA; 148 BP.  
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 274.  
PN WO200155324-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1168  
ID AAK78753 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33565.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1169  
ID AAK81310 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36122.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;

Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1170  
ID AAK73937 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28749.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1171  
ID AAK79569 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34381.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1172  
ID AAL04801 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7489.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1173  
ID AAL06718 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9406.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1174  
ID AAL07121 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9809.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1175  
ID AAL05015 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7703.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1176  
ID ABA08155 standard; DNA; 148 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 950.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1177  
ID ABL97695 standard; DNA; 148 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2347.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1178  
ID ABL97908 standard; DNA; 148 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2560.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;

RESULT 1179  
ID AAS29186 standard; DNA; 148 BP.  
DE Genomic sequence #29 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1180  
ID AAS29163 standard; DNA; 148 BP.  
DE Genomic sequence #6 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1181  
ID AAS29228 standard; DNA; 148 BP.  
DE Genomic sequence #71 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1182  
ID AAS29176 standard; DNA; 148 BP.  
DE Genomic sequence #19 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1183  
ID ABAL7037 standard; DNA; 148 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9368.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1184  
ID AAD16668 standard; DNA; 148 BP.  
DE Human pancreatic related protein-encoding exon, SEQ ID NO:32.  
PN WO200155327-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1185  
ID ABS68316 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #19.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133.4; DB 6; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1186  
ID ABS68303 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #6.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133.4; DB 6; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1187  
ID ABS68326 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #29.  
PN US2002102638-A1.  
PD 01-AUG-2002.

PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133.4; DB 6; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1188  
ID ABS68368 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #71.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133.4; DB 6; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1189  
ID ADA41651 standard; DNA; 148 BP.  
DE Human secreted protein related DNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 8; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1190  
ID ADC25448 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 53 #4.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1191  
ID ADC25490 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 80 #2.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1192  
ID ADC25425 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 14 #3.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1193  
ID ADC25438 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 25 #2.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1194  
ID ADC74709 standard; DNA; 148 BP.  
DE Human secreted protein-related DNA - SEQ ID 1342.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1195  
ID ADE46631 standard; DNA; 148 BP.  
DE Human cardiovascular system related genomic DNA #197.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1196  
ID ADA57783 standard; DNA; 148 BP.

DE BAC fragment containing human secreted protein gene #537.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 10; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1197  
ID ADNA1714 standard; DNA; 148 BP.  
DE Novel human secreted protein polynucleotide seqid 836.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYV/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFU/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 4.7%; Score 133.4; DB 12; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1198  
ID ADJ08049 standard; DNA; 148 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID1437.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUNA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133.4; DB 13; Length 148;  
Best Local Similarity 99.3%; Pred. No. 3.9e-10;  
RESULT 1199  
ID AAF24365 standard; DNA; 172 BP.  
DE Retroviral recombination assay coding sequence fragment #10.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 172;  
Best Local Similarity 99.3%; Pred. No. 3.8e-10;  
RESULT 1200  
ID AAV41451 standard; cDNA; 202 BP.  
DE Nucleotide sequence of the 3' portion of the BL229\_22 clone.  
PN WO921332-A2.  
PD 22-MAY-1998.  
PA (GENY) GENETICS INST INC.  
Query Match 4.7%; Score 133.4; DB 2; Length 202;  
Best Local Similarity 99.3%; Pred. No. 3.8e-10;  
RESULT 1201  
ID AAF98423 standard; cDNA; 202 BP.  
DE Human cDNA clone BL229\_22 3' sequence SEQ ID 81.  
PN WO200119988-A1.  
PD 22-MAR-2001.  
PA (GENY) GENETICS INST INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 202;  
Best Local Similarity 99.3%; Pred. No. 3.8e-10;  
RESULT 1202  
ID AAI82950 standard; cDNA; 402 BP.  
DE Human polynucleotide SEQ ID NO 3010.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 402;  
Best Local Similarity 95.8%; Pred. No. 3.7e-10;  
RESULT 1203  
ID AAI85952 standard; cDNA; 420 BP.  
DE Human polynucleotide SEQ ID NO 6012.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 4.7%; Score 133.4; DB 4; Length 420;  
Best Local Similarity 96.4%; Pred. No. 3.7e-10;  
RESULT 1204  
ID ABV57899 standard; cDNA; 565 BP.  
DE Human prostate expression marker cDNA 57890.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133.4; DB 5; Length 565;  
Best Local Similarity 99.3%; Pred. No. 3.6e-10;  
RESULT 1205  
ID AAH71472 standard; cDNA; 597 BP.  
DE Human cervical cancer marker nucleic acid 2746.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 597;  
Best Local Similarity 89.9%; Pred. No. 3.6e-10;  
RESULT 1206  
ID ACN87353 standard; DNA; 611 BP.  
DE Breast cancer related marker, seq id 8503.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.7%; Score 133.4; DB 11; Length 611;  
Best Local Similarity 78.6%; Pred. No. 3.6e-10;  
RESULT 1207  
ID ACN87667 standard; DNA; 617 BP.  
DE Breast cancer related marker, seq id 8817.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.7%; Score 133.4; DB 11; Length 617;  
Best Local Similarity 78.0%; Pred. No. 3.6e-10;  
RESULT 1208  
ID AAH71551 standard; cDNA; 621 BP.  
DE Human cervical cancer marker nucleic acid 2825.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133.4; DB 4; Length 621;  
Best Local Similarity 79.4%; Pred. No. 3.6e-10;  
RESULT 1209  
ID ABX49378 standard; cDNA; 237 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #14543.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.7%; Score 133.2; DB 8; Length 237;  
Best Local Similarity 86.5%; Pred. No. 4e-10;  
RESULT 1210  
ID ACN48457 standard; cDNA; 424 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-K6-E6, SEQ:3238.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133.2; DB 13; Length 424;  
Best Local Similarity 88.9%; Pred. No. 3.9e-10;  
RESULT 1211  
ID ACN55951 standard; cDNA; 543 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-030-Q6-N6-F11, SEQ:10732.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.



Query Match 4.7%; Score 133.2; DB 13; Length 543;  
Best Local Similarity 91.6%; Pred. No. 3.9e-10;  
RESULT 1212  
ID ADG33178 standard; DNA; 1381 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID502.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 4.7%; Score 133.2; DB 10; Length 1381;  
Best Local Similarity 97.8%; Pred. No. 3.7e-10;  
RESULT 1213  
ID ABN80090 standard; DNA; 8166 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 107.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.2; DB 6; Length 8186;  
Best Local Similarity 88.9%; Pred. No. 3.5e-10;  
RESULT 1214  
ID ABK40075 standard; DNA; 9021 BP.  
DE Human chemically pretreated gene sequence #79 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.2; DB 6; Length 9021;  
Best Local Similarity 86.5%; Pred. No. 3.4e-10;  
RESULT 1215  
ID ABL34232 standard; DNA; 9021 BP.  
DE Human immune system associated gene SEQ ID NO: 2205.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.2; DB 6; Length 9021;  
Best Local Similarity 86.5%; Pred. No. 3.4e-10;  
RESULT 1216  
ID ABK33988 standard; DNA; 9021 BP.  
DE Human DNA for staging of Astrocytomas #37.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.2; DB 6; Length 9021;  
Best Local Similarity 86.5%; Pred. No. 3.4e-10;  
RESULT 1217  
ID ADA20388 standard; DNA; 9021 BP.  
DE Prostate tumour related genomic DNA sample #27.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.2; DB 8; Length 9021;  
Best Local Similarity 86.5%; Pred. No. 3.4e-10;  
RESULT 1218  
ID ADA84195 standard; DNA; 9021 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:53.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133.2; DB 8; Length 9021;  
Best Local Similarity 86.5%; Pred. No. 3.4e-10;  
RESULT 1219  
ID ABX43106 standard; cDNA; 365 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8271.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.7%; Score 133; DB 8; Length 365;  
Best Local Similarity 100.0%; Pred. No. 4.2e-10;  
RESULT 1220  
ID ABV38062 standard; cDNA; 425 BP.  
DE Human prostate expression marker cDNA 38053.  
PN WO200160860-A2.

PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 425;  
Best Local Similarity 90.4%; Pred. No. 4.2e-10;  
RESULT 1221  
ID ACN49708 standard; cDNA; 554 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 554;  
Best Local Similarity 100.0%; Pred. No. 4.1e-10;  
RESULT 1222  
ID ABV16074 standard; cDNA; 843 BP.  
DE Human prostate expression marker cDNA 16065.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 843;  
Best Local Similarity 79.2%; Pred. No. 4.1e-10;  
RESULT 1223  
ID ABQ54211 standard; cDNA; 970 BP.  
DE Human ovarian antigen HHFBY53 cDNA, SEQ ID NO:91.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 6; Length 970;  
Best Local Similarity 90.4%; Pred. No. 4e-10;  
RESULT 1224  
ID ABZ71397 standard; cDNA; 1687 BP.  
DE Secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:218.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 8; Length 1687;  
Best Local Similarity 88.2%; Pred. No. 4e-10;  
RESULT 1225  
ID ADM67116 standard; DNA; 2090 BP.  
DE Human homologue of murine adipocyte specific DNA SeqID 252.  
PN WO2004011618-A2.  
PD 05-FEB-2004.  
PA (HMGF-) HMGNE INC.  
Query Match 4.7%; Score 133; DB 12; Length 2090;  
Best Local Similarity 90.4%; Pred. No. 3.9e-10;  
RESULT 1226  
ID ABK31264 standard; DNA; 6794 BP.  
DE Signal transduction associated gene modified DNA #54.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 6794;  
Best Local Similarity 79.7%; Pred. No. 3.7e-10;  
RESULT 1227  
ID ABL70219 standard; DNA; 6794 BP.  
DE Chemically treated cell signalling DNA sequence#55.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 6794;  
Best Local Similarity 79.7%; Pred. No. 3.7e-10;  
RESULT 1228  
ID AAS61174 standard; DNA; 6794 BP.  
DE Human gene regulation-associated gene oligonucleotide #129.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 6794;  
Best Local Similarity 79.7%; Pred. No. 3.7e-10;  
RESULT 1229  
ID ABL32230 standard; DNA; 14568 BP.

DE Human immune system associated gene SEQ ID NO: 203.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIC-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 133; DB 6; Length 14568;  
 Best Local Similarity 85.5%; Pred. No. 3.6e-10;  
 RESULT 1230  
 ID ABV08830 standard; cDNA; 420 BP.  
 DE Human prostate expression marker cDNA 8821.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 132.8; DB 5; Length 420;  
 Best Local Similarity 72.7%; Pred. No. 4.5e-10;  
 RESULT 1231  
 ID AAI87434 standard; cDNA; 454 BP.  
 DE Human polynucleotide SEQ ID NO 7494.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 132.8; DB 4; Length 454;  
 Best Local Similarity 89.4%; Pred. No. 4.5e-10;  
 RESULT 1232  
 ID ACN59858 standard; cDNA; 531 BP.  
 DE CotCon gynoecium tissue EST Clone ID: LIB3829-035-Q1-K6-D8, SEQ:14639.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 4.7%; Score 132.8; DB 13; Length 531;  
 Best Local Similarity 98.5%; Pred. No. 4.4e-10;  
 RESULT 1233  
 ID AAF72410 standard; cDNA; 1985 BP.  
 DE Human PRO271 cDNA.  
 PN WO200104311-A1.  
 PD 18-JAN-2001.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 4; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1234  
 ID AAS45938 standard; cDNA; 1985 BP.  
 DE Human DNA encoding PRO polypeptide sequence #14.  
 PN WO200168848-A2.  
 PD 20-SEP-2001.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 4; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1235  
 ID ACA60174 standard; cDNA; 1985 BP.  
 DE Human cDNA for secreted/transmembrane protein PRO271.  
 PN US2003003530-A1.  
 PD 02-JAN-2003.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1236  
 ID ACA9398 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003036141-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1237  
 ID ACA73398 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036146-A1.  
 PD 20-FEB-2003.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1238  
 ID ACA5713 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036162-A1.  
 PD 20-FEB-2003.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1239  
 ID ACA66547 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO protein #14.  
 PN US2003036137-A1.  
 PD 20-FEB-2003.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1240  
 ID ACD07574 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1241  
 ID ACF20122 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040063-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1242  
 ID ACF19508 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040064-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1243  
 ID ACD21796 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003027267-A1.  
 PD 06-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1244  
 ID ACF12961 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003036160-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1245  
 ID ACD25064 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003044925-A1.  
 PD 06-MAR-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1246  
 ID ACF00113 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054474-A1.  
 PD 20-MAR-2003.  
 PA (GETH-) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1247  
 ID ACA72170 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2003032114-A1.  
 PD 13-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;

RESULT 1248  
ID ACD04694 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1249  
ID ACD18155 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1250  
ID ACD08162 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1251  
ID ABX71622 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO271.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1252  
ID ACA88596 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1253  
ID ACA70038 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1254  
ID ACD12260 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1255  
ID AC74175 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1256  
ID ACD15803 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1257  
ID ACD25371 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1258

ID ACD17848 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1259  
ID ACC88135 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1260  
ID ACD21489 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1261  
ID ACD18556 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1262  
ID ACH06954 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane polypeptide PRO271 cDNA.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1263  
ID ABX98166 standard; cDNA; 1985 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1264  
ID ACD13917 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1265  
ID ACD09697 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1266  
ID ACC88442 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1267  
ID ACD21182 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1268  
ID ABX75554 standard; cDNA; 1985 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO271.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1269  
ID ABX97757 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1270  
ID ACA97233 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1271  
ID ACA57696 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1272  
ID ACD14224 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1273  
ID ACC91007 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1274  
ID ACC88749 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1275  
ID ACD06946 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1276  
ID ACA67397 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1277  
ID ACC81452 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1278  
ID ACC89056 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1279  
ID ACC86412 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1280  
ID ACC89670 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1281  
ID ACC92849 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1282  
ID ACA72477 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1283  
ID ACA88995 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1284  
ID ACA69731 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1285  
ID ACA96874 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1286  
ID ACA90870 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1287  
ID ACA70652 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1288  
ID ACA95162 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1289  
 ID ACA86105 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003027263-A1.  
 PD 06-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1290  
 ID ACC89977 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003027271-A1.  
 PD 06-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1291  
 ID ACD12585 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US20030316125-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1292  
 ID ACF19815 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040068-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1293  
 ID ABX76759 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #14.  
 PN US2003027280-A1.  
 PD 06-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1294  
 ID ABX96191 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein cDNA, #40.  
 PN US2002160374-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1295  
 ID ACA73091 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2003022300-A1.  
 PD 30-JAN-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1296  
 ID ACA05512 standard; cDNA; 1985 BP.  
 DE cDNA encoding human secreted protein PRO271.  
 PN US2003023054-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1297  
 ID ACA68634 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US20030316136-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1298  
 ID ACA74478 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US20030316138-A1.  
 PD 20-FEB-2003.

Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1299  
 ID ACA70345 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003032109-A1.  
 PD 13-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1300  
 ID ACD14531 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #14.  
 PN US2003040066-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1301  
 ID ACD20179 standard; cDNA; 1985 BP.  
 DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
 PN US20030316060-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1302  
 ID ACA68203 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2003032104-A1.  
 PD 13-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1303  
 ID ABX98668 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US20030316157-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1304  
 ID ACC81145 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003032120-A1.  
 PD 13-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1305  
 ID ACA95469 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US20030316155-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1306  
 ID ACD04387 standard; cDNA; 1985 BP.  
 DE Novel human secreted and transmembrane protein PRO271 cDNA.  
 PN US2003022296-A1.  
 PD 30-JAN-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1307  
 ID ACC87828 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003027281-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1308  
 ID ACF12490 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040058-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 8; Length 1985;

Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1309  
ID ACA96205 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1310  
ID ACA64979 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1311  
ID ACA73705 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1312  
ID ACA74117 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1313  
ID ACA96512 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1314  
ID ACD10618 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1315  
ID ACC91314 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1316  
ID ACD02649 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US20030322301-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1317  
ID ACC87214 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1318  
ID ACC85798 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1319

ID ACA5286 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1320  
ID ACA94103 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1321  
ID ACA97847 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1322  
ID ACA91349 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1323  
ID ACA90563 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1324  
ID ACD16110 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1325  
ID ACD17271 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1326  
ID ACC91928 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1327  
ID ACA74785 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1328  
ID ACA91656 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1329  
ID ACA71300 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032116-A1.

PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1330  
ID ACC90700 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1331  
ID ACA65710 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1332  
ID ACA54982 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1333  
ID ACA94855 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1334  
ID ACD16417 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1335  
ID ACD15496 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1336  
ID ABX16599 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 8; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1337  
ID ACA97540 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1338  
ID ACA98989 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1339  
ID ACG91621 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040076-A1.  
PD 27-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1340  
ID ACD11032 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US200308352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1341  
ID ACD14882 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1342  
ID ACD19817 standard; cDNA; 1985 BP.  
DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1343  
ID ACD11646 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1344  
ID ACC95775 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1345  
ID ACF16338 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1346  
ID ACF02456 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1347  
ID ACF02763 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1348  
ID ACF21350 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1349

ID ACF10034 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068743-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1350  
 ID ACF77927 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054479-A1.  
 PD 20-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1351  
 ID ACD4632 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068685-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1352  
 ID ACD49395 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068725-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1353  
 ID ACF28162 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068752-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1354  
 ID ACD8852 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068682-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1355  
 ID ACD84247 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #14.  
 PN US2003068701-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1356  
 ID ACD99021 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003068755-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1357  
 ID ADA77779 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003073180-A1.  
 PD 17-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1358  
 ID ACF48763 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104539-A1.  
 PD 05-JUN-2003.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1359  
 ID ADB29417 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein cDNA, #42.  
 PN US2003092002-A1.  
 PD 15-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1360  
 ID ACD09083 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036131-A1.  
 PD 20-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1361  
 ID ACF11876 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040075-A1.  
 PD 27-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1362  
 ID ACF41110 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054459-A1.  
 PD 20-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1363  
 ID ACF15724 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003044930-A1.  
 PD 06-MAR-2003.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1364  
 ID ACF16031 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040071-A1.  
 PD 27-FEB-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1365  
 ID ACD31858 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003054471-A1.  
 PD 20-MAR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1366  
 ID ACF18666 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003064452-A1.  
 PD 03-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1367  
 ID ACF09113 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068705-A1.  
 PD 10-APR-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;



Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
ID ACF78234 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1369  
ID ACF51833 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1370  
ID ACF26320 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1371  
ID ACF24113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1372  
ID ACF63424 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1373  
ID ACF50298 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1374  
ID ACH07769 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1375  
ID ACF13575 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1376  
ID ACD41501 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1377

ID ACF31914 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1378  
ID ACF23192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1379  
ID ACF39882 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1380  
ID ACD45404 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1381  
ID ACF53061 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1382  
ID ACF27241 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1383  
ID ACF45079 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1384  
ID ACF29697 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1385  
ID ACD89773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1386  
ID ACD84554 standard; cDNA; 1985 BP.

DE Human PRO polynucleotide #14.  
 PN US2003068703-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1387  
 ID ACD98714 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003068732-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1388  
 ID ACF77006 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003082717-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1389  
 ID ACF76699 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104548-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1390  
 ID ACF49684 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104542-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1391  
 ID ACF49991 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104543-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1392  
 ID ACD09390 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036127-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1393  
 ID ACD08469 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003040061-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1394  
 ID ACF12183 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003036130-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1395  
 ID ACC94691 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054468-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1396  
 ID ACD45711 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003064454-A1.

ID ACD22410 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003054470-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1397  
 ID ACF15110 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003044917-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1398  
 ID ACC97205 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003044929-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1399  
 ID ADA18273 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein cDNA, #42.  
 PN US2003039971-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1400  
 ID ACD66964 standard; cDNA; 1985 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO271.  
 PN US2003045693-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1401  
 ID ACC92235 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003059880-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1402  
 ID ACF13982 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003064465-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1403  
 ID ACF14189 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054478-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1404  
 ID ACF09420 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068718-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1405  
 ID ACD45711 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003064454-A1.

PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1406  
 ID ACD47860 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003064461-A1.  
 PD 03-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1407  
 ID ACD67591 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003068724-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1408  
 ID ACF25399 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068727-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1409  
 ID ACF29083 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068772-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1410  
 ID ACD84861 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068714-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1411  
 ID ACD83940 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #14.  
 PN US2003068758-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1412  
 ID ACD87931 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068776-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1413  
 ID ACF30618 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003069407-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1414  
 ID ACF32221 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104555-A1.  
 PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1415  
 ID ACH11881 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003049768-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1416  
 ID ACH12188 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003049771-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1417  
 ID ACD40580 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003032134-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1418  
 ID ACF18052 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054481-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1419  
 ID ACF08499 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049778-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1420  
 ID ACF31300 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049782-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1421  
 ID ACF52140 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054476-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1422  
 ID ACD50009 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068733-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1423  
 ID ACF38712 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068592-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1424  
 ID ACF38712 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068592-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;

Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1424  
 ID ACF26627 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068709-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1425  
 ID ACF24727 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068716-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1426  
 ID ACF46307 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068740-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1427  
 ID ACF27855 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068751-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1428  
 ID ACD89159 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068684-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1429  
 ID ACF63731 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003073179-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1430  
 ID ACF60371 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003087374-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1431  
 ID ACHI2495 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003049773-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1432  
 ID ACH09918 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003049777-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1433  
 ID ACF10341 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003073169-A1.  
 PD 17-APR-2003.

ID ACD03773 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003040055-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1434  
 ID ACD10311 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036164-A1.  
 PD 20-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1435  
 ID ACD11953 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003040074-A1.  
 PD 27-FEB-2003.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1436  
 ID ACD83125 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #38.  
 PN US2003044793-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1437  
 ID ACF42338 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054480-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1438  
 ID ADA16248 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein cDNA, #42.  
 PN US2003049621-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1439  
 ID ACF18359 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003059885-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1440  
 ID ACF02149 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049740-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1441  
 ID ACF21657 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003049770-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
 Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
 RESULT 1442  
 ID ACF10341 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003073169-A1.  
 PD 17-APR-2003.

Query Match  
Best Local Similarity 4.7%; Score 132.8; DB 9; Length 1985;  
RESULT 1443  
ID ACF33793 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1444  
ID ACF44755 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1445  
ID ACD90387 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1446  
ID ACD91000 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1447  
ID ACF30311 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1448  
ID ACD87010 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1449  
ID ACF60064 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1450  
ID ACF46614 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1451  
ID ACF75471 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1452

ID ADA79571 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1453  
ID ACF17131 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1454  
ID ACF22885 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1455  
ID ACF07885 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1456  
ID ACF08192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1457  
ID ACF40496 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1458  
ID ACF53675 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1459  
ID ACD46939 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1460  
ID ACF47842 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1461  
ID ACF47228 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068753-A1.

PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1462  
ID ACF46000 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1463  
ID ACD86089 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1464  
ID ACF52447 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1465  
ID ACF52754 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1466  
ID ACF64747 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1467  
ID ACF76392 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1468  
ID ACF61292 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1469  
ID ACF61599 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1470  
ID ACD30630 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;

RESULT 1471  
ID ACD31551 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1472  
ID ACD32472 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1473  
ID ACF17438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1474  
ID ACF07271 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1475  
ID ACF20429 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1476  
ID ACF21043 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1477  
ID ACF20736 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1478  
ID ACD47553 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1479  
ID ACF47535 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 132.8; DB 9; Length 1985;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1480  
ID ACF53368 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068679-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1481  
ID ACD86703 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1482  
ID ACH04951 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1483  
ID ACF44448 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1484  
ID ADA42393 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1485  
ID ADA81298 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1486  
ID ACD24450 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044920-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1487  
ID ACD24450 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044920-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1488  
ID ACD39653 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1489  
ID ACD39660 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1490  
ID ACF13268 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1491  
ID ACF03070 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1492  
ID ACD23303 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1493  
ID ACF78541 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1494  
ID ACF11262 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1495  
ID ACF50605 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1496  
ID ACF34100 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1497  
ID ACD46325 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1498  
ID ACD48167 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1499  
ID ACF27548 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match 86.9%; Pred. No. 4.2e-10;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;  
RESULT 1500  
ID ACP24420 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 132.8; DB 9; Length 1985;  
Query Match 86.9%; Pred. No. 4.2e-10;  
Best Local Similarity 86.9%; Pred. No. 4.2e-10;



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OM protein - protein search, using sw model  
Run on: May 8, 2005, 15:55:03 ; Search time 77 Seconds  
(without alignments)  
3616.461 Million cell updates/sec

Title: US-10-063-692-38  
Perfect score: 3945  
Sequence: 1 MELGCTWQLGLFLQLLLIS.....LSTAFKVLFFKDWIERNMK 720  
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%

Database : A\_Geneseq\_16Dec04:\*  
Listing first 1500 summaries  
Maximum Match 100%

1: Genesecp1980s:\*  
2: Genesecp1990s:\*  
3: Genesecp2000s:\*  
4: Genesecp2001s:\*  
5: Genesecp2002s:\*  
6: Genesecp2003s:\*  
7: Genesecp2003bs:\*  
8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1  
ID AAY66695 standard; protein; 720 AA.  
DE Membrane-bound protein PRO1344.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 3; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 2  
ID AAU29108 standard; protein; 720 AA.  
DE Human PRO polypeptide sequence #85.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 4; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 3  
ID AAB87544 standard; protein; 720 AA.  
DE Human PRO1344.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 4; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 4  
ID AAB65218 standard; protein; 720 AA.  
DE Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 4; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 5  
ID ABG95869 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 5; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 6  
ID ABUS9484 standard; protein; 720 AA.

DE Human PRO polypeptide #85.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 7  
ID ABUS8032 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 8  
ID ABUS4347 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 9  
ID ABR66221 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 10  
ID ABR65611 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 11  
ID ABUS9551 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 12  
ID ABUS8033 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 13  
ID ABUS9111 standard; protein; 720 AA.  
DE Novel human secreted or transmembrane protein PRO1344.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 14  
ID ABUS2623 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 15  
ID ABUS2790 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 16  
ID ABUS9911 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036147-A1.

PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 17  
ID ABR68160 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 18  
ID ABU60542 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 19  
ID ABU96213 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 20  
ID ABU92644 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 21  
ID ABO08721 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 22  
ID ABO02773 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 23  
ID ABR74927 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 24  
ID ABR94689 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 25  
ID ABU13924 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 26  
ID ABU85662 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036140-A1.  
PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 27  
ID ABU98822 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 28  
ID ABU98037 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 29  
ID ABU91743 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 30  
ID ABU9436 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 31  
ID ABU6277 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 32  
ID ABU67490 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 33  
ID ABU80518 standard; protein; 720 AA.  
DE Human PRO protein #85.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 34  
ID ABU72509 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 35  
ID ABU90894 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 36  
ID ABO33953 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 37  
ID ABR99436 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 38  
ID ABR98826 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 39  
ID ABO16349 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 40  
ID ABR92249 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 41  
ID ABO18890 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 42  
ID ABR78311 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 43  
ID ABU71970 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 44  
ID ABU85047 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 45  
ID ABO00186 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 46  
ID ABO1518 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040060-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 47  
ID ABO02163 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 48  
ID ABU89737 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 49  
ID ABU83432 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 50  
ID ABO06233 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 51  
ID ABR59269 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 52  
ID ABO09331 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 53  
ID ABO19195 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 54  
ID ABO11213 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 55  
ID ABR66831 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 56  
ID ABO16044 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040060-A1.

PD' 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 57  
ID ABO13750 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 58  
ID ABU71524 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 59  
ID ABU65653 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, SEQ ID 170.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 60  
ID ABO07501 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 61  
ID ABO03688 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 62  
ID ABR67136 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 63  
ID ABO15739 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 64  
ID ABU56020 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US200302298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 65  
ID ABU72305 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 66  
ID ABU65348 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032102-A1.

PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 67  
ID ABU95293 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 68  
ID ABU71196 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 69  
ID ABO07806 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 70  
ID ABR70047 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 71  
ID ABR69380 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 72  
ID ABO01521 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 73  
ID ABU81323 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 74  
ID ABR60120 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 75  
ID ABU90978 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 76  
ID ABR67855 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027269-A1.

PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 77  
ID ABR65243 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 78  
ID ABR68465 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 79  
ID ABR71877 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 80  
ID ABUS9258 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 81  
ID ABUS5357 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US200302285-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 82  
ID ABUS9047 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US200302237-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 83  
ID ABUS3127 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 84  
ID ABUS4983 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 85  
ID ABUS90531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 86  
ID ABUS4042 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 87  
ID ABUS3693 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 88  
ID ABO25955 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 89  
ID ABR64938 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 90  
ID ABO27299 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 91  
ID ABR68770 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 92  
ID ABO06586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 93  
ID ABR99131 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 94  
ID ABUS7015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 95  
ID ABUS5967 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003023300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 96  
ID ABUS2254 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 97  
ID ABR66526 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 98  
ID ABR90944 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 99  
ID ABO08111 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 100  
ID ABU92494 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 101  
ID ABU81822 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 102  
ID ABU65986 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 103  
ID ABU81164 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 104  
ID ABR59815 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 105  
ID ABU94003 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 106  
ID ABU99856 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 107  
ID ABR66526 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 108  
ID ABR90944 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 109  
ID ABO53279 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 110  
ID ABUS8964 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 111  
ID ABU94371 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 112  
ID ABU79253 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 113  
ID ABUS6582 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 114  
ID ABUS6587 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 115  
ID ABU94676 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 116  
ID ABO04603 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 117  
ID ABR70352 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 118  
ID ABR92342 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 119  
ID ABR98517 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 120  
ID ABR65916 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 121  
ID ABR64633 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 122  
ID ABR59407 standard; protein; 720 AA.  
DE Novel human secreted or transmembrane protein PRO1109.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 123  
ID ABR79558 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 124  
ID ABR92949 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 125  
ID ABR95908 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 126  
ID ABR91128 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 127  
ID ABR90221 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 128  
ID ABR09636 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 129  
ID ABR010908 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 130  
ID ABR70962 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 131  
ID ABR98281 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 132  
ID ABR87570 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 133  
ID ABR91438 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 134  
ID ABR99286 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 135  
ID ABR84652 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 136  
ID ABR69742 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 137  
ID ABR80119 standard; protein; 720 AA.  
DE Human PRO protein #85.



PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 138  
ID ABU82493 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 139  
ID ABU92173 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 140  
ID ABU93388 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 141  
ID ABO09941 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 142  
ID ABO09026 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 143  
ID ABU96457 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 144  
ID ABU10879 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 145  
ID ABU10594 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein #85.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 146  
ID ABU81631 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 147

ID ABU72127 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 148  
ID ABU95603 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 149  
ID ABU96812 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 150  
ID ABR70657 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 151  
ID ABO05008 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 152  
ID ABO08416 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 153  
ID ABU88570 standard; protein; 720 AA.  
DE Human secreted and transmembrane polypeptide PRO1344.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 154  
ID ABO34084 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 155  
ID ABO05623 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 156  
ID ABR74012 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 157  
ID ABR95604 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 158  
ID ABR80901 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 159  
ID ABR81206 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 160  
ID ABM00902 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 161  
ID ABR88504 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003088743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 162  
ID ABM77325 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 163  
ID ABO28809 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 164  
ID ABO31554 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 165  
ID ABM07971 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 166

ID ABO40451 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 167  
ID ABO35876 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 168  
ID ABO44015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 169  
ID ADA77922 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 170  
ID ABM24810 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 171  
ID ABO03078 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 172  
ID ABR90334 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 173  
ID ABM17248 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 174  
ID ABR94994 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 175  
ID ABR95299 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.



ID ABM29080 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 195  
ID ABM07056 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 196  
ID ABM21150 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 197  
ID ABM09496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 198  
ID ABO41366 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 199  
ID ABO36181 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 200  
ID ABO43710 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 201  
ID ABM76410 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 202  
ID ABM76106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 203  
ID ABM25725 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 204  
ID ABM26030 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 205  
ID ADA21428 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 206  
ID ABO03383 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 207  
ID ABO02468 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 208  
ID ABO44257 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 209  
ID ABR90639 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 210  
ID ABR73707 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 211  
ID ABO16959 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 212  
ID ABR94384 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 213  
ID ABR75891 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 214  
ID ABR71267 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 215  
ID ABR93164 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 216  
ID ABR93469 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 217  
ID ADA10215 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 218  
ID ABR87894 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 219  
ID ABO27894 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 220  
ID ABO30029 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 221  
ID ABO33238 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 222  
ID ABO4926 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 223  
ID ABO8886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 224  
ID ABO36486 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 225  
ID ABO35571 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 226  
ID ABO39536 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 227  
ID ABM10411 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 228  
ID ABM11936 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 229  
ID ABO52082 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 230  
ID ABO52387 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 231  
ID ADA19900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 232  
ID ABO23705 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 233  
ID ADB17283 standard; protein; 720 AA.  
DE Human transmembrane PRO polypeptide (SeqID 38).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 234  
ID ADA17759 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 235  
ID ABR97191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 236  
ID ABR86979 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 237  
ID ABM11021 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 238  
ID ABM28165 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 239  
ID ABO32164 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 240  
ID ABM15291 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 241  
ID ABM06446 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 242  
ID ABM04257 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 243  
ID ABM22370 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 244  
ID ABM07666 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 245  
ID ABO40756 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 246  
ID ABM35403 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 247  
ID ABM33166 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 248  
ID ABO52692 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 249  
ID ABO50252 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 250  
ID ABU99246 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040055-A1.

PD, 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 251  
ID ABO04298 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US20030316164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 252  
ID ABO05928 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 253  
ID ABM18468 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 254  
ID ADA27867 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 255  
ID ABR97496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 256  
ID ABR80596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 257  
ID ABM01207 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 258  
ID ABR88809 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 259  
ID ABM13461 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 260  
ID ABM20845 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 261  
ID ABO41976 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 262  
ID ABO42586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 263  
ID ABM10106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 264  
ID ABO38621 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 265  
ID ABM32861 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 266  
ID ABM22675 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 267  
ID ABM74886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 268  
ID ADA79714 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 269  
ID ABR96276 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 270  
ID ABM02427 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 271  
ID ABR86369 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 272  
ID ABR86674 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 273  
ID ABM16638 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 274  
ID ABM29690 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 275  
ID ABO29114 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 276  
ID ABM23895 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 277  
ID ABM23285 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 278  
ID ABM22065 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 279  
ID ABO37706 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 280  
ID ABM28470 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 281  
ID ABM28775 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 282  
ID ABM66419 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 283  
ID ABM75801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 284  
ID ABM34081 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 285  
ID ABM34386 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 286  
ID ABO20317 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 287  
ID ABO21232 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 288  
ID ABO22147 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054477-A1.  
PD 20-MAR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 289  
ID ADA20072 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003052222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 290  
ID ABO34185 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 291  
ID ABR36581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 292  
ID ADA94447 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 293  
ID ABR85759 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 294  
ID ABR99741 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 295  
ID ABM00597 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 296  
ID ABM00292 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 297  
ID ABO29724 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 298

ID ABM23590 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 299  
ID ABM29385 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 300  
ID ABO38316 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 301  
ID ABO45616 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 302  
ID ABM20540 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 303  
ID ADA81441 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 304  
ID ABO16654 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 305  
ID ABO18280 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 306  
ID ABO22707 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 307  
ID ABO23012 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054461-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 308  
ID ABR92554 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003064446-A1.  
PD 03-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 309  
ID ABR81511 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003049744-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 310  
ID ABR77935 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003049783-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 311  
ID ABR89724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003073171-A1.  
PD 17-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 312  
ID ABM26640 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003032121-A1.  
PD 13-FEB-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 313  
ID ABM13766 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003064458-A1.  
PD 03-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 314  
ID ABO28504 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003064460-A1.  
PD 03-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 315  
ID ABO30334 standard; protein; 720 AA..  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003064464-A1.  
PD 03-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 316  
ID ABM07361 standard; protein; 720 AA..  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003068702-A1.  
PD 10-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 317  
ID ABM03952 standard; protein; 720 AA..  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003068734-A1.  
PD 10-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 318  
ID ABO37096 standard; protein; 720 AA..  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003068719-A1.  
PD 10-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 319  
ID ABO41671 standard; protein; 720 AA..  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003068729-A1.  
PD 10-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 320  
ID ABO35266 standard; protein; 720 AA..  
DE Human PRO polypeptide #85..  
PN US2003068738-A1.  
PD 10-APR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 321  
ID ABM25115 standard; protein; 720 AA..  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170..  
PN US2003104540-A1.  
PD 05-JUN-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 322  
ID ABO47507 standard; protein; 720 AA..  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003049742-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 323  
ID ABO47812 standard; protein; 720 AA..  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003049747-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 324  
ID ABO48422 standard; protein; 720 AA..  
DE Human secreted/transmembrane protein (PRO) #85..  
PN US2003049750-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 325  
ID ABO51472 standard; protein; 720 AA..  
DE Human PRO polypeptide #85..  
PN US2003049766-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 326  
ID ABO51777 standard; protein; 720 AA..  
DE Human PRO polypeptide #85..  
PN US2003049766-A1.  
PD 13-MAR-2003..  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

DE Human PRO polypeptide #85.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 327  
ID ABO50557 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 328  
ID ABR79681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 329  
ID ABM16943 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 330  
ID ABO17975 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 331  
ID ABO20927 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 332  
ID ABR9686 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 333  
ID ADA38672 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 334  
ID ABM12241 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 335  
ID ABM16333 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 336  
ID ABO24200 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 337  
ID ABM14681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 338  
ID ABM04562 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 339  
ID ABM06751 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 340  
ID ABM09191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 341  
ID ABO39231 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 342  
ID ABM75496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 343  
ID ABM25420 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 344  
ID ABM19930 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 345  
ID ABO46836 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.

PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 346  
ID ABO47141 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 347  
ID ADA33239 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 348  
ID ABR71572 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 349  
ID ABR72182 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 350  
ID ABR98521 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US200303129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 351  
ID ABO6891 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 352  
ID ABR94844 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 353  
ID ABR73402 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 354  
ID ABR76496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 355  
ID ABR73097 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 356  
ID ABR18163 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 357  
ID ABO20622 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 358  
ID ABO25365 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 359  
ID ABO25670 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 360  
ID ABR94079 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 361  
ID ADA92793 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 362  
ID ABR79986 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 363  
ID ABR11326 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 364  
ID ABO32933 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 365  
ID ABO32933 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 365  
ID ABO30639 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 366  
ID ABO30944 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 367  
ID ABM27250 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 368  
ID ABM29995 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 369  
ID ABM05531 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 370  
ID ABM15596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 371  
ID ABM08581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 372  
ID ABO42281 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 373  
ID ABO38011 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 374  
ID ABO45921 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 375  
ID ABM66724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 376  
ID ADB20282 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 377  
ID ABM19625 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 378  
ID ABO49337 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 379  
ID ABO49642 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 380  
ID ADA78534 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 381  
ID ABR88199 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 382  
ID ADA00369 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 383  
ID ABM26945 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068739-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 384  
ID ABM03342 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 385  
ID ABO39841 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 386  
ID ABO49947 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 387  
ID ABO50862 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 388  
ID ABO05318 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 389  
ID ABR74622 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 390  
ID ABR77101 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 391  
ID ABM17858 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 392  
ID ABR95909 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 393  
ID ABO21842 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 394  
ID ABO20012 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 395  
ID ABO24315 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 396  
ID ABR86064 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 397  
ID ABM10716 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 398  
ID ABM76715 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 399  
ID ABR89419 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 400  
ID ABM12546 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 401  
ID ABM05836 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 402  
ID ABO34961 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.

PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 403  
ID ABM03037 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068784-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 404  
ID ABM19015 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 405  
ID ABM19320 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 406  
ID ABO46531 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 407  
ID ABO49032 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 408  
ID ABR69075 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 409  
ID ABR89114 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 410  
ID ABR72487 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 411  
ID ABR74317 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 412  
ID ABO18585 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 413  
ID ABR80291 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 414  
ID ABM01512 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 415  
ID ABM02122 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 416  
ID ABR87284 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 417  
ID ABM12851 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 418  
ID ABM30605 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 419  
ID ABM24505 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 420  
ID ABO29419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 421

ID ABO31249 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 422  
ID ABO14376 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 423  
ID ABO09801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 424  
ID ABO38926 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 425  
ID ABO34691 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 426  
ID ABO51167 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 427  
ID ABO03993 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 428  
ID ABO10463 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 429  
ID ABO53170 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 430  
ID ABR77706 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 431  
ID ABR78916 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 432  
ID ABO24010 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 433  
ID ABR93774 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 434  
ID ABO01817 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 435  
ID ABR78240 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 436  
ID ABR90029 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 437  
ID ADA22354 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 438  
ID ABR27555 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 439  
ID ABR13156 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 440  
ID ABO31859 standard; protein; 720 AA.



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DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 20-FEB-2003.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
RESULT 441
ID ABR14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 10-APR-2003.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
RESULT 442
ID ABR08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 10-APR-2003.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
RESULT 443
ID ABO40146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 10-APR-2003.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
RESULT 444
ID ABR74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 22-MAY-2003.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
RESULT 445
ID ABR33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 22-MAY-2003.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
RESULT 446
ID ABR20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 05-JUN-2003.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
RESULT 447
ID ABO48727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 13-MAR-2003.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 448
ID ABO22540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 23-JAN-2003.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 20-FEB-2003.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 450
ID ABO15434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 20-FEB-2003.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 27-FEB-2003.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
RESULT 452
ID ABO15129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 06-MAR-2003.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 453
ID ABO17264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 27-FEB-2003.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
RESULT 454
ID ABR17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 06-MAR-2003.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 455
ID ADA06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 13-MAR-2003.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 456
ID ADA39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 27-MAR-2003.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 13-MAR-2003.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 458
ID ABR77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 20-MAR-2003.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 7; Length 720;
PD 03-APR-2003.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 460
ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 464
ID ABM14986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 469
ID ABM33471 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 478
ID . ABM32435 standard; protein; 720 AA.
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DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 479  
ID ADB68290 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 480  
ID ADB68097 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 481  
ID ABM31520 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 482  
ID ABM30910 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 483  
ID ADB90914 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 484  
ID ADC57711 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 485  
ID ADC55075 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 486  
ID ADC11942 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 487  
ID ADC06994 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA ( GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 488  
ID ADC56364 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 489  
ID ADC17173 standard; protein; 720 AA.  
DE Mammalian PRO polypeptide (seqID 38).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 490  
ID ADC07419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 491  
ID ADC11409 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 492  
ID ADC14871 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 493  
ID ADC52366 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA ( GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 494  
ID ADC14531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 495  
ID ADD08063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 496  
ID ADC81888 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 497  
ID ADD07530 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002193299-A1.  
PD 19-DEC-2002.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 498  
ID ADC82421 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 499  
ID ADD05643 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 500  
ID ADD08601 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 501  
ID ADD06850 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 502  
ID ADC83097 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 503  
ID ADD55204 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 504  
ID ADD36042 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 505  
ID ADD56162 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 506  
ID ADD54600 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002132233-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 507  
ID ADE26754 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 508  
ID ADE26221 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 509  
ID ADF67158 standard; protein; 720 AA.  
DE Human PRO1344 amino acid sequence SEQ ID NO:231.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 510  
ID ADG01043 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 511  
ID ADG08596 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 512  
ID ADG02638 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 513  
ID ADG01345 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 514  
ID ADF95520 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 515  
ID ADF95217 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 516  
ID ADG12335 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;

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Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 517
ID ADH24070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 518
ID ADH34096 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 519
ID ADH29929 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 520
ID ADH3900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 521
ID ADH08995 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 522
ID ADG85304 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 523
ID ADH24580 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 524
ID ADH37436 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 525
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 526
ID ADH37606 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 527
ID ADG85644 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 528
ID ADH24240 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 529
ID ADH38534 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 530
ID ADG83655 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 531
ID ADH29463 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 532
ID ADH27579 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 533
ID ADH37776 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 534
ID ADH37953 standard; protein; 720 AA.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 535
ID ADH02025 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
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ID ADH57373 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 536  
ID ADH53515 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 537  
ID ADH53685 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 538  
ID ADH52021 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 539  
ID ADH49876 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 540  
ID ADI25386 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 541  
ID ADH90179 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 542  
ID ADI25556 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 543  
ID ADH97730 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 544  
ID ADI35412 standard; protein; 720 AA.

DE Human PRO polypeptide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 545  
ID ADI03578 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 546  
ID ADI11935 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 547  
ID ADH90009 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 548  
ID ADH99904 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 549  
ID ADH98410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 550  
ID ADI11085 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 551  
ID ADI11595 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 552  
ID ADH98240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 553  
ID ADH98580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181708-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 554
ID ADH98070 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 555
ID ADI05058 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 556
ID ADI03408 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 557
ID ADI04803 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 558
ID ADH78257 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 559
ID ADI19601 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 560
ID ADH90349 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 561
ID ADI03068 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 562
ID ADH77917 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 563
ID ADH97900 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 564
ID ADI01285 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 565
ID ADI01980 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 566
ID ADI03238 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 567
ID ADI11425 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 568
ID ADI02327 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 569
ID ADI11765 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 570
ID ADI05402 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 571
ID ADH79474 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
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Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 572  
ID ADI19431 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 573  
ID ADI05232 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 574  
ID ADH79644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 575  
ID ADI01470 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 576  
ID ADI01640 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 577  
ID ADI01810 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 578  
ID ADH79814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 579  
ID ADI04632 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 580  
ID ADI02768 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 581  
ID ADH78087 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 582  
ID ADI25726 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 583  
ID ADI25896 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 584  
ID ADK65408 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 585  
ID ADH98750 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 586  
ID ADH79991 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 587  
ID ADL32776 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 588  
ID ADM30310 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 589  
ID ADL93722 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 590



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ID ADC52176 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 591
ID ADE74307 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 592
ID ADE74919 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 593
ID ADF35357 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 594
ID ADG11607 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 595
ID ADF96132 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 596
ID ADG04403 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 597
ID ADG00563 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 598
ID ADH06608 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 599
ID ADH06438 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 600
ID ADG68859 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 601
ID ADH27749 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 602
ID ADH25090 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 603
ID ADH33722 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 604
ID ADG82819 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 605
ID ADH02365 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 606
ID ADH07972 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 607
ID ADG69369 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
RESULT 608
ID ADH39190 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 8; Length 720;
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Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 609  
ID ADH26100 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 610  
ID ADG83930 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 611  
ID ADH19477 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 612  
ID ADG85474 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 613  
ID ADH06268 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 614  
ID ADH30098 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 615  
ID ADH24410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 616  
ID ADH33069 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 617  
ID ADG69539 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 618  
ID ADH07802 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 619  
ID ADG85814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 620  
ID ADH39360 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 621  
ID ADH33552 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 622  
ID ADH33892 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 623  
ID ADH01102 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 624  
ID ADG69709 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 625  
ID ADH20970 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003244358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 626  
ID ADH02195 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 627  
ID ADG69199 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 628  
ID ADG85984 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 629  
ID ADH24920 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 630  
ID ADH39537 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 631  
ID ADH20010 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 632  
ID ADH02535 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 633  
ID ADG69029 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 634  
ID ADH07632 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 635  
ID ADG86154 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 636  
ID ADH24750 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 637  
ID ADH25798 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 638  
ID ADH38364 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 639  
ID ADH57203 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 640  
ID ADH52191 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 641  
ID ADH49557 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 642  
ID ADH90519 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 643  
ID ADI11255 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 644  
ID ADH98920 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 645  
ID ADI02150 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003190699-A1.

PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 646  
 ID ADH90689 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003181701-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 647  
 ID ADJ54808 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2004023321-A1.  
 PD 05-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 648  
 ID ADJ98564 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003187197-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 649  
 ID ADJ98734 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003187228-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 650  
 ID ADH78893 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003181703-A1.  
 PD 25-SEP-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 651  
 ID ADJ99127 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003186408-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 652  
 ID ADJ99297 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003187196-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 653  
 ID ADJ98915 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003187242-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 654  
 ID ADH79063 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003181702-A1.  
 PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 655  
 ID ADK00923 standard; protein; 720 AA.  
 DE Human PRO polypeptide #19.  
 PN US2003186407-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 656  
 ID ADK14444 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2003187229-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 657  
 ID ADJ64579 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2004038337-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 658  
 ID ADM31475 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2004048334-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 659  
 ID ADM36522 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2004053358-A1.  
 PD 18-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 660  
 ID ADM40327 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2004048335-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 661  
 ID ADM80893 standard; protein; 720 AA.  
 DE Human PRO polypeptide #19.  
 PN US2004058411-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 662  
 ID ADN37935 standard; protein; 720 AA.  
 DE Novel human secreted and transmembrane protein PRO1344.  
 PN US2004091959-A1.  
 PD 13-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 3945; DB 8; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
 RESULT 663  
 ID AAB70532 standard; protein; 720 AA.  
 DE Human PRO2 protein sequence SEQ ID NO:4.  
 PN WO200110902-A2.  
 PD 15-FEB-2001.  
 PA (CURA-) CURAGEN CORP.

Query Match 99.8%; Score 3939; DB 4; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 3.1e-204;  
 RESULT 664  
 ID AAU00401 standard; protein; 720 AA.  
 DE Human secreted protein, POLY13.  
 PN WO200119856-A2.  
 PD 22-MAR-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 99.8%; Score 3939; DB 4; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 3.1e-204;  
 RESULT 665  
 ID ADH89028 standard; protein; 720 AA.  
 DE Human polypeptide #13.  
 PN US2003198958-A1.  
 PD 23-OCT-2003.  
 PA (SHIM/) SHIMKETS R A.  
 PA (FERN/) FERNANDES E.  
 PA (HERR/) HERRMANN J L.  
 PA (LIUK/) LIU X.  
 PA (YANG/) YANG M.  
 PA (BOLD/) BOLDOG F L.  
 PA (SMIT/) SMITHSON G.  
 PA (RAST/) RASTELLI L.  
 Query Match 99.8%; Score 3939; DB 8; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 3.1e-204;  
 RESULT 666  
 ID AAB8280 standard; protein; 720 AA.  
 DE Human TANGO 215 protein.  
 PN WO200018904-A2.  
 PD 06-APR-2000.  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 Query Match 99.8%; Score 3936; DB 3; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 4.5e-204;  
 RESULT 667  
 ID AAB85891 standard; protein; 737 AA.  
 DE Human serine protease-like protein (hc-PLACE1009992).  
 PN WO200109349-A1.  
 PD 08-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 99.4%; Score 3921.5; DB 4; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
 RESULT 668  
 ID AAB93670 standard; protein; 737 AA.  
 DE Human protein sequence SEQ ID NO:13202.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 99.4%; Score 3921.5; DB 4; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
 RESULT 669  
 ID ADJ89990 standard; protein; 737 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1796.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 99.4%; Score 3921.5; DB 7; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
 RESULT 670  
 ID ADN04640 standard; protein; 737 AA.  
 DE Antipsoriatic protein sequence #505.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 99.4%; Score 3921.5; DB 8; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
 RESULT 671  
 ID ADS85034 standard; protein; 737 AA.  
 DE Human atopic dermatitis-related protein sequence SeqID36.  
 PN WO2004031386-A1.  
 PD 15-APR-2004.  
 PA (GENO-) GENOX RES INC.  
 PA (UYJU-) UNIV JUNTENDO.

Query Match 99.4%; Score 3921.5; DB 8; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
 RESULT 672  
 ID ADS85022 standard; protein; 737 AA.  
 DE Human atopic dermatitis-related protein sequence SeqID24.  
 PN WO2004031386-A1.  
 PD 15-APR-2004.  
 PA (GENO-) GENOX RES INC.  
 PA (UYJU-) UNIV JUNTENDO.  
 Query Match 99.4%; Score 3921.5; DB 8; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
 RESULT 673  
 ID AAB85893 standard; protein; 762 AA.  
 DE Human serine protease-like protein (hc-PLACE1009992).  
 PN WO200109349-A1.  
 PD 08-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 99.4%; Score 3921.5; DB 4; Length 762;  
 Best Local Similarity 97.6%; Pred. No. 2.9e-203;  
 RESULT 674  
 ID AAB85892 standard; protein; 720 AA.  
 DE Mouse serine protease-like protein (mc-PLACE1009992).  
 PN WO200109349-A1.  
 PD 08-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 91.6%; Score 3612; DB 4; Length 720;  
 Best Local Similarity 90.1%; Pred. No. 1.3e-186;  
 RESULT 675  
 ID AAB09927 standard; protein; 719 AA.  
 DE Murine TANGO 215 protein.  
 PN WO200018904-A2.  
 PD 06-APR-2000.  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 Query Match 91.3%; Score 3602.5; DB 3; Length 719;  
 Best Local Similarity 90.1%; Pred. No. 4.1e-186;  
 RESULT 676  
 ID AAE19180 standard; protein; 649 AA.  
 DE Human protease, PRTS-17 protein.  
 PN WO200208396-A2.  
 PD 31-JAN-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 88.7%; Score 3500.5; DB 5; Length 649;  
 Best Local Similarity 90.0%; Pred. No. 1.2e-180;  
 RESULT 677  
 ID AAB70531 standard; protein; 567 AA.  
 DE Human PRO1 protein sequence SEQ ID NO:2.  
 PN WO200110902-A2.  
 PD 15-FEB-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 78.3%; Score 3089.5; DB 4; Length 567;  
 Best Local Similarity 99.5%; Pred. No. 1.4e-158;  
 RESULT 678  
 ID AAB49533 standard; protein; 570 AA.  
 DE Clone HPPEY75.  
 PN WO200061774-A2.  
 PD 19-OCT-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 74.7%; Score 2946.5; DB 3; Length 570;  
 Best Local Similarity 96.8%; Pred. No. 7.2e-151;  
 RESULT 679  
 ID ADR41485 standard; protein; 551 AA.  
 DE Human CD-like molecule HSXDF41, SEQ ID NO:284.  
 PN WO200226930-A2.  
 PD 04-APR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 74.6%; Score 2944; DB 5; Length 551;  
 Best Local Similarity 99.3%; Pred. No. 9.5e-151;  
 RESULT 680  
 ID AAM41706 standard; protein; 499 AA.  
 DE Human polypeptide SEQ ID NO 6637.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.

Query Match 65.3%; Score 2577.5; DB 4; Length 499;  
Best Local Similarity 96.6%; Pred. No. 4.8e-131;  
RESULT 681  
ID AAE20817 standard; protein; 455 AA.  
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:79.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 61.2%; Score 2413; DB 5; Length 455;  
Best Local Similarity 99.3%; Pred. No. 3.2e-122;  
RESULT 682  
ID ABG64652 standard; protein; 455 AA.  
DE Human albumin fusion protein #1327.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 61.2%; Score 2413; DB 5; Length 455;  
Best Local Similarity 99.3%; Pred. No. 3.2e-122;  
RESULT 683  
ID ADL77919 standard; protein; 455 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 61.2%; Score 2413; DB 8; Length 455;  
Best Local Similarity 99.3%; Pred. No. 3.2e-122;  
RESULT 684  
ID ADL06662 standard; protein; 417 AA.  
DE Human 373 cell conversion promoter FP938.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match 52.2%; Score 2059; DB 7; Length 417;  
Best Local Similarity 95.6%; Pred. No. 3.4e-103;  
RESULT 685  
ID AAM39920 standard; protein; 359 AA.  
DE Human polypeptide SEQ ID NO 3065.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 48.4%; Score 1909; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 3.6e-95;  
RESULT 686  
ID AAM39957 standard; protein; 359 AA.  
DE Human polypeptide SEQ ID NO 3102.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 48.4%; Score 1909; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 3.6e-95;  
RESULT 687  
ID AAE20797 standard; protein; 323 AA.  
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:59.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 43.3%; Score 1708.5; DB 5; Length 323;  
Best Local Similarity 94.1%; Pred. No. 2.1e-84;  
RESULT 688  
ID ABG64653 standard; protein; 323 AA.  
DE Human albumin fusion protein #1328.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 43.3%; Score 1708.5; DB 5; Length 323;  
Best Local Similarity 94.1%; Pred. No. 2.1e-84;  
RESULT 689  
ID ADL77920 standard; protein; 323 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.

PA (HASE/) HASELTINE W A.  
Query Match 43.3%; Score 1708.5; DB 8; Length 323;  
Best Local Similarity 94.1%; Pred. No. 2.1e-84;  
RESULT 690  
ID AAM24485 standard; protein; 234 AA.  
DE Human EST encoded protein SEQ ID NO: 2010.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 29.8%; Score 1175.5; DB 4; Length 234;  
Best Local Similarity 91.4%; Pred. No. 7.8e-56;  
RESULT 691  
ID ABP72332 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO2003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK ) BLOWHITTAKER INC.  
Query Match 17.0%; Score 672; DB 6; Length 1019;  
Best Local Similarity 25.6%; Pred. No. 4.1e-28;  
RESULT 692  
ID AAM43394 standard; protein; 1019 AA.  
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).  
PN SG42456-A1.  
PD 15-AUG-1997.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
RESULT 693  
ID AAY05750 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO9915676-A1.  
PD 01-APR-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
RESULT 694  
ID AAM94302 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C protein #2.  
PN US5858706-A.  
PD 12-JAN-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
RESULT 695  
ID AAY42490 standard; protein; 1019 AA.  
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.  
PN US5985590-A.  
PD 16-NOV-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 3; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
RESULT 696  
ID AAB60935 standard; protein; 1019 AA.  
DE Horseshoe crab recombinant Factor C #2.  
PN WO200127289-A2.  
PD 19-APR-2001.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 4; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
RESULT 697  
ID ABP72334 standard; protein; 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO2003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK ) BLOWHITTAKER INC.  
Query Match 16.9%; Score 665; DB 6; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
RESULT 698  
ID AAM43393 standard; protein; 1083 AA.  
DE Singapore horseshoe crab factor C proenzyme (CrFC 26).  
PN SG42456-A1.  
PD 15-AUG-1997.  
PA (UYSI-) UNIV SINGAPORE NAT.

Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 699  
ID AAY05749 standard; protein; 1083 AA.  
DE Horseshoe crab Factor C.  
PN, WO9915676-A1.  
PD 01-APR-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 700  
ID AAW94301 standard; protein; 1083 AA.  
DE Horseshoe crab Factor C protein #1.  
PN US5858706-A.  
PD 12-JAN-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 701  
ID AAY42489 standard; protein; 1083 AA.  
DE Horseshoe crab recombinant Factor C protein.  
PN US5985590-A.  
PD 16-NOV-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 3; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 702  
ID AAB60934 standard; protein; 1083 AA.  
DE Horseshoe crab recombinant Factor C #1.  
PN WO200127289-A2.  
PD 19-APR-2001.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 4; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 703  
ID ABP72333 standard; protein; 1083 AA.  
DE Horseshoe crab Factor C.  
PN WO2003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK) B10WHITAKER INC.  
Query Match 16.9%; Score 665; DB 6; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 704  
ID AAM41743 standard; protein; 146 AA.  
DE Human polypeptide SEQ ID NO 6674.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 16.8%; Score 662; DB 4; Length 146;  
Best Local Similarity 85.4%; Pred. No. 2.3e-28;  
RESULT 705  
ID AAY11743 standard; protein; 103 AA.  
DE Human 5' EST secreted protein SEQ ID No: 343.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match 14.7%; Score 580; DB 2; Length 103;  
Best Local Similarity 97.1%; Pred. No. 4.3e-24;  
RESULT 706  
ID ADE87459 standard; protein; 699 AA.  
DE Human MBL-associated serine protease-1 protein.  
PN EP1344533-A1.  
PD 17-SEP-2003.  
PA (NATL-) NATIMMUNE AS.  
Query Match 12.1%; Score 476; DB 7; Length 699;  
Best Local Similarity 24.6%; Pred. No. 1e-17;  
RESULT 707  
ID ADL91028 standard; protein; 699 AA.  
DE Human mannose binding lectin amino acid sequence SEQ ID NO:14.  
PN WO2004024925-A2.  
PD 25-MAR-2004.  
PA (NATI-) NATIMMUNE AS.  
Query Match 12.0%; Score 475; DB 8; Length 699;

Best Local Similarity 24.6%; Pred. No. 1.2e-17;  
RESULT 708  
ID ABM83722 standard; protein; 698 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3971.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.0%; Score 474.5; DB 8; Length 698;  
Best Local Similarity 24.4%; Pred. No. 1.2e-17;  
RESULT 709  
ID AAB85060 standard; protein; 728 AA.  
DE Human serine protease MASP-3 polypeptide.  
PN WO200140451-A2.  
PD 07-JUN-2001.  
PA (JENS/) JENSENIUS J C.  
PA (THIE/) THIEL S.  
Query Match 11.9%; Score 471; DB 4; Length 728;  
Best Local Similarity 25.0%; Pred. No. 2e-17;  
RESULT 710  
ID ADE87461 standard; protein; 728 AA.  
DE Human MBL-associated serine protease-4 protein.  
PN EP1344533-A1.  
PD 17-SEP-2003.  
PA (NATI-) NATIMMUNE AS.  
Query Match 11.9%; Score 468; DB 7; Length 728;  
Best Local Similarity 25.0%; Pred. No. 2.9e-17;  
RESULT 711  
ID ADL91027 standard; protein; 728 AA.  
DE Human mannose binding lectin amino acid sequence SEQ ID NO:13.  
PN WO2004024925-A2.  
PD 25-MAR-2004.  
PA (NATI-) NATIMMUNE AS.  
Query Match 11.9%; Score 468; DB 8; Length 728;  
Best Local Similarity 25.0%; Pred. No. 2.9e-17;  
RESULT 712  
ID AAB47559 standard; protein; 728 AA.  
DE Protease PRPS-1.  
PN WO200171004-A2.  
PD 27-SEP-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.7%; Score 461; DB 4; Length 728;  
Best Local Similarity 24.9%; Pred. No. 6.9e-17;  
RESULT 713  
ID AAG80756 standard; protein; 707 AA.  
DE Murine C1r protein.  
PN KR2001077614-A.  
PD 20-AUG-2001.  
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.  
PA (KIMT/) KIM T Y.  
Query Match 10.9%; Score 429; DB 5; Length 707;  
Best Local Similarity 22.3%; Pred. No. 3.6e-15;  
RESULT 714  
ID ABB50288 standard; protein; 705 AA.  
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.  
PN WO200175177-A2.  
PD 11-OCT-2001.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 10.2%; Score 403.5; DB 4; Length 705;  
Best Local Similarity 22.9%; Pred. No. 8.4e-14;  
RESULT 715  
ID AAG80757 standard; protein; 705 AA.  
DE Human C1r protein.  
PN KR2001077614-A.  
PD 20-AUG-2001.  
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.  
PA (KIMT/) KIM T Y.  
Query Match 10.2%; Score 403.5; DB 5; Length 705;  
Best Local Similarity 22.9%; Pred. No. 8.4e-14;  
RESULT 716  
ID ADP65211 standard; protein; 705 AA.  
DE Human complement component 1, r subcomponent.  
PN WO2003072827-A1.  
PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 10.2%; Score 403.5; DB 7; Length 705;  
 Best Local Similarity 22.6%; Pred. No. 8.4e-14;  
 RESULT 717  
 ID ABE31619 standard; protein; 686 AA.  
 DE Human mannan-binding lectin associated serine protease-2 protein.  
 PN US2002082208-A1.  
 PD 27-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Query Match 10.2%; Score 401.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 718  
 ID AAE14564 standard; protein; 686 AA.  
 DE Human MASP-2 protein.  
 PN WO200206460-A2.  
 PD 24-JAN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Query Match 10.2%; Score 401.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 719  
 ID ABG32115 standard; protein; 686 AA.  
 DE Mannan-binding lectin associated serine protease-2 (MASP-2).  
 PN US2002082209-A1.  
 PD 27-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Query Match 10.2%; Score 401.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 720  
 ID ADL91025 standard; protein; 686 AA.  
 DE Human mannose binding lectin amino acid sequence SEQ ID NO:11.  
 PN WO2004024925-A2.  
 PD 25-MAR-2004.  
 PA (NATI-) NATIMUNE AS.  
 Query Match 10.2%; Score 401.5; DB 8; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 721  
 ID AAE14568 standard; protein; 686 AA.  
 DE Human MASP-2 protein, alternative version.  
 PN WO200206460-A2.  
 PD 24-JAN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Query Match 10.2%; Score 400.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;  
 RESULT 722  
 ID ADE87460 standard; protein; 686 AA.  
 DE Human MBL-associated serine protease-2 protein.  
 PN EP1344533-A1.  
 PD 17-SEP-2003.  
 PA (NATI-) NATIMUNE AS.  
 Query Match 10.2%; Score 400.5; DB 7; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;  
 RESULT 723  
 ID ADQ27010 standard; protein; 671 AA.  
 DE Human MASP-2 mature polypeptide.  
 PN WO2004050907-A2.  
 PD 17-JUN-2004.  
 PA (UYAA-) UNIV.AARHUS.  
 PA (AARH) AARHUS AMT.  
 Query Match 10.1%; Score 399.5; DB 8; Length 671;  
 Best Local Similarity 22.8%; Pred. No. 1.3e-13;  
 RESULT 724  
 ID AAE14565 standard; peptide; 671 AA.  
 DE Human mature MASP-2 protein.  
 PN WO200206460-A2.  
 PD 24-JAN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Query Match 10.1%; Score 398.5; DB 5; Length 671;  
 Best Local Similarity 22.8%; Pred. No. 1.5e-13;

RESULT 725  
 ID ADE56422 standard; protein; 694 AA.  
 DE Rat Protein BRA25797, SEQ ID NO 2275.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 694;  
 Best Local Similarity 21.2%; Pred. No. 2e-10;  
 RESULT 726  
 ID ADE83526 standard; protein; 694 AA.  
 DE Rat Protein BRA25797, SEQ ID NO 11123.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 694;  
 Best Local Similarity 21.2%; Pred. No. 2e-10;  
 RESULT 727  
 ID ADE56418 standard; protein; 695 AA.  
 DE Rat Protein D88250, SEQ ID NO 2271.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 695;  
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;  
 RESULT 728  
 ID ADD45338 standard; protein; 695 AA.  
 DE Rat Protein D88250, SEQ ID NO 10771.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 695;  
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;  
 RESULT 729  
 ID AAB43579 standard; protein; 760 AA.  
 DE Human cancer associated protein sequence SEQ ID NO:1024.  
 PN WO200055350-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 8.5%; Score 336; DB 3; Length 760;  
 Best Local Similarity 21.7%; Pred. No. 3.9e-10;  
 RESULT 730  
 ID ADD45340 standard; protein; 688 AA.  
 DE Human Protein Q9UCV3, SEQ ID NO 10773.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 8.5%; Score 334; DB 7; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
 RESULT 731  
 ID ADE56420 standard; protein; 688 AA.  
 DE Human Protein Q9UCV3, SEQ ID NO 2273.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 PA (FARB) BAYER AG.  
 Query Match 8.5%; Score 334; DB 7; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
 RESULT 732  
 ID ADP65315 standard; protein; 688 AA.  
 DE Human complement c1s component precursor (cl esterase).  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 8.5%; Score 334; DB 7; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
 RESULT 733  
 ID ADJ75392 standard; protein; 688 AA.  
 DE Marker gene related amino acid sequence SEQ ID NO:644.



PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 8.5%; Score 334; DB 8; Length 688;  
Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
RESULT 734  
ID ADL91020 standard; protein; 688 AA.  
DE Human mannose binding lectin amino acid sequence SEQ ID NO:6.  
PN WO2004024925-A2.  
PD 25-MAR-2004.  
PA (NATI-) NATIMUNE AS.  
Query Match 8.5%; Score 334; DB 8; Length 688;  
Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
RESULT 735  
ID ABM81337 standard; protein; 688 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 8.5%; Score 334; DB 8; Length 688;  
Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
RESULT 736  
ID ADI16818 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 354.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.4%; Score 332; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 7.1e-10;  
RESULT 737  
ID ADI16818 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 354.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.4%; Score 332; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 7.1e-10;  
RESULT 738  
ID AAE06940 standard; protein; 1019 AA.  
DE Human enterokinase protein.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.4%; Score 331.5; DB 4; Length 1019;  
Best Local Similarity 22.9%; Pred. No. 9e-10;  
RESULT 739  
ID ADA83985 standard; protein; 1019 AA.  
DE Human PRSS7 protein.  
PN WO2002103028-A2.  
PD 27-DEC-2002.  
PA (BIOM-) BIOMEDICAL CENT.  
Query Match 8.4%; Score 331.5; DB 6; Length 1019;  
Best Local Similarity 22.9%; Pred. No. 9e-10;  
RESULT 740  
ID ADI10400 standard; protein; 1019 AA.  
DE Human cell surface protease #16.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.4%; Score 331.5; DB 7; Length 1019;  
Best Local Similarity 22.9%; Pred. No. 9e-10;  
RESULT 741  
ID ADJ46924 standard; protein; 1019 AA.  
DE Human transmembrane serine protease (MTSP)-related polypeptide #6.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.4%; Score 331.5; DB 8; Length 1019;  
Best Local Similarity 22.9%; Pred. No. 9e-10;  
RESULT 742  
ID ADJ70437 standard; protein; 1019 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2243.  
PN WO2003087768-A2.

PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 8.4%; Score 330.5; DB 7; Length 1019;  
Best Local Similarity 22.9%; Pred. No. 1e-09;  
RESULT 743  
ID ADJ70480 standard; protein; 3389 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID2286.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 8.4%; Score 329.5; DB 7; Length 3389;  
Best Local Similarity 20.8%; Pred. No. 3.5e-09;  
RESULT 744  
ID ADH72216 standard; protein; 3567 AA.  
DE Human protein of the invention NOV54b SEQ ID NO:1112.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.4%; Score 329.5; DB 8; Length 3567;  
Best Local Similarity 20.8%; Pred. No. 3.7e-09;  
RESULT 745  
ID AAR13623 standard; protein; 460 AA.  
DE Human Protein C zymogen SC.  
PN EP443875-A.  
PD 28-AUG-1991.  
PA (ELIL) LILLY & CO ELI.  
Query Match 8.3%; Score 329; DB 2; Length 460;  
Best Local Similarity 25.5%; Pred. No. 5.8e-10;  
RESULT 746  
ID ABG76507 standard; protein; 1274 AA.  
DE DNA encoding protein modification and maintenance molecule #11.  
PN WO200260942-A2.  
PD 08-AUG-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 8.3%; Score 328.5; DB 5; Length 1274;  
Best Local Similarity 20.8%; Pred. No. 1.6e-09;  
RESULT 747  
ID AAU11815 standard; protein; 1783 AA.  
DE Cancer and neurogenesis associated gene, variant 5G-3V3.  
PN WO200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEEDS.  
Query Match 8.3%; Score 328.5; DB 5; Length 1783;  
Best Local Similarity 20.8%; Pred. No. 2.2e-09;  
RESULT 748  
ID AAU11813 standard; protein; 1800 AA.  
DE Cancer and neurogenesis associated gene, variant 5G-3V1.  
PN WO200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEEDS.  
Query Match 8.3%; Score 328.5; DB 5; Length 1800;  
Best Local Similarity 20.8%; Pred. No. 2.2e-09;  
RESULT 749  
ID AAU11812 standard; protein; 1826 AA.  
DE Cancer and neurogenesis associated gene.  
PN WO200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEEDS.  
Query Match 8.3%; Score 328.5; DB 5; Length 1826;  
Best Local Similarity 20.8%; Pred. No. 2.2e-09;  
RESULT 750  
ID AAU11814 standard; protein; 2008 AA.  
DE Cancer and neurogenesis associated gene, variant 5G-3V2.  
PN WO200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEEDS.  
Query Match 8.3%; Score 328.5; DB 5; Length 2008;  
Best Local Similarity 20.8%; Pred. No. 2.4e-09;  
RESULT 751  
ID AAU11817 standard; protein; 2306 AA.  
DE Cancer and neurogenesis associated gene, variant 5R23V2.

PN WO200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEEDS.  
Query Match 8.3%; Score 328.5; DB 5; Length 2306;  
Best Local Similarity 20.8%; Pred. No. 2.8e-09;  
RESULT 752  
ID AAU11816 standard; protein; 2352 AA.  
DE Cancer and neurogenesis associated gene, variant 5R-3V2.  
PN WO200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEEDS.  
Query Match 8.3%; Score 328.5; DB 5; Length 2352;  
Best Local Similarity 20.8%; Pred. No. 2.8e-09;  
RESULT 753  
ID AAB19551 standard; protein; 683 AA.  
DE Human matrixase (truncated form).  
PN WO200053232-A1.  
PD 14-SEP-2000.  
PA (GEOU) UNIV GEORGETOWN.  
Query Match 8.3%; Score 328; DB 3; Length 683;  
Best Local Similarity 21.4%; Pred. No. 9.5e-10;  
RESULT 754  
ID AAY90284 standard; protein; 762 AA.  
DE Human peptidase, HPEP-1 protein sequence.  
PN WO200042201-A2.  
PD 20-JUL-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 8.3%; Score 328; DB 3; Length 762;  
Best Local Similarity 21.4%; Pred. No. 1.1e-09;  
RESULT 755  
ID AAM25628 standard; protein; 851 AA.  
DE Human protein sequence SEQ ID NO:1143.  
PN WO200153455-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.3%; Score 328; DB 4; Length 851;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 756  
ID ABB11428 standard; peptide; 851 AA.  
DE Human membrane-type Ser kinase homologue, SEQ ID NO:1798.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.3%; Score 328; DB 4; Length 851;  
Best Local Similarity 21.6%; Pred. No. 1.2e-09;  
RESULT 757  
ID ADO55145 standard; protein; 853 AA.  
DE Protein #47 with increased gene expression in renal cell carcinoma.  
PN WO2004032842-A2.  
PD 22-APR-2004.  
PA (VAND-) VAN ANDEL INST.  
Query Match 8.3%; Score 328; DB 8; Length 853;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 758  
ID AAB19552 standard; protein; 855 AA.  
DE Human matrixase.  
PN WO200053232-A1.  
PD 14-SEP-2000.  
PA (GEOU) UNIV GEORGETOWN.  
Query Match 8.3%; Score 328; DB 3; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 759  
ID AAB35465 standard; protein; 855 AA.  
DE Human membrane-type serine protease MT-SPI.  
PN WO200123524-A2.  
PD 05-APR-2001.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 8.3%; Score 328; DB 4; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 760  
ID ADI16817 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 353.  
PN WO200268649-A2.

PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 328; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 761  
ID ADI16883 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 419.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 328; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 762  
ID ADI16876 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 412.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 328; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 763  
ID ADN39867 standard; protein; 855 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 8.3%; Score 328; DB 7; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 764  
ID ADN04754 standard; protein; 855 AA.  
DE Antipsoxiatic protein sequence #558.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 8.3%; Score 328; DB 8; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 765  
ID ADP23334 standard; protein; 855 AA.  
DE PRO polypeptide SEQ ID NO:428.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 8.3%; Score 328; DB 8; Length 855;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 766  
ID ADR66721 standard; protein; 863 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 8.3%; Score 328; DB 8; Length 863;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 767  
ID ADR66379 standard; protein; 863 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 8.3%; Score 328; DB 8; Length 863;  
Best Local Similarity 21.4%; Pred. No. 1.2e-09;  
RESULT 768  
ID AAB58274 standard; protein; 449 AA.  
DE Lung cancer associated polypeptide sequence SEQ ID 612.  
PN WO200055180-A2.  
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A. 8.3%; Score 327.5; DB 3; Length 449;  
Query Match 23.3%; Pred. No. 6.8e-10;  
Best Local Similarity 23.3%; Pred. No. 6.8e-10;  
RESULT 769  
ID ADL64961 standard; protein; 688 AA.  
DE Human complement component 1 protein, CIS.  
PN US2004033582-A1.  
PD 19-FEB-2004.  
PA (EDMO/) EDMONDS M.  
PA (HUIL/) HUI L.  
PA (PERR/) PERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAMA/) RAMANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERB/) ZERBA K.  
Query Match 8.3%; Score 327; DB 8; Length 688;  
Best Local Similarity 21.7%; Pred. No. 1.1e-09;  
RESULT 770  
ID ADL16508 standard; protein; 757 AA.  
DE Human NOVX protein to treat human pathological conditions SeqID44.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 5; Length 757;  
Best Local Similarity 21.8%; Pred. No. 1.2e-09;  
RESULT 771  
ID AAY06671 standard; protein; 855 AA.  
DE Tumour antigen derived gene-15 (TAGD-15) protein.  
PN WO942120-A1.  
PD 26-AUG-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 8.3%; Score 327; DB 2; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 772  
ID AAB98500 standard; protein; 855 AA.  
DE Human TAGD-15.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 8.3%; Score 327; DB 4; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 773  
ID AAE06930 standard; protein; 855 AA.  
DE Human membrane-type serine protease (MTSP) 1.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 4; Length 855;  
Best Local Similarity 21.8%; Pred. No. 1.3e-09;  
RESULT 774  
ID AAO22929 standard; protein; 855 AA.  
DE Type II transmembrane serine protease 1 protein SEQ ID No 2.  
PN WO200272786-A2.  
PD 19-SEP-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 775  
ID ADL16816 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 352.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 776  
ID ADL16892 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 418.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 8; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 777  
ID ADL16975 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 411.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 778  
ID ABP56619 standard; protein; 855 AA.  
DE Human membrane-type serine protease MTSP1 protein SEQ ID NO:2.  
PN WO200292841-A2.  
PD 21-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 779  
ID AAO30146 standard; protein; 855 AA.  
DE Human membrane-type serine protease MTSP1 protein.  
PN WO2003044179-A2.  
PD 30-MAY-2003.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 780  
ID AAE29820 standard; protein; 855 AA.  
DE Human membrane-type serine protease 1 (MTSP1).  
PN WO200277267-A2.  
PD 03-OCT-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 781  
ID AAE29791 standard; protein; 855 AA.  
DE Human membrane-type serine protease, MTSP1.  
PN WO200277263-A2.  
PD 03-OCT-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 782  
ID ABP72376 standard; protein; 855 AA.  
DE Transmembrane serine protease 1 (MTSP1).  
PN WO2003004681-A2.  
PD 16-JAN-2003.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 783  
ID ADB97551 standard; protein; 855 AA.  
DE Human MTSP1, SEQ ID NO:2.  
PN WO2003031585-A2.  
PD 17-APR-2003.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 7; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 784  
ID ADI10371 standard; protein; 855 AA.  
DE Human cell surface protease #1.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 7; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 785  
ID ADG65326 standard; protein; 855 AA.  
DE Human MTSP1.  
PN WO2003104394-A2.  
PD 18-DEC-2003.  
PA (DEND-) DENDREON SAN DIEGO LLC.  
Query Match 8.3%; Score 327; DB 8; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 786  
ID AD128861 standard; protein; 855 AA.  
DE Human matrixcase ( MTSP1) serine protease.  
PN WO2004005471-A2.  
PD 15-JAN-2004.  
PA (DEND-) DENDREON SAN DIEGO LLC.  
Query Match 8.3%; Score 327; DB 8; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 787  
ID ADJ46895 standard; protein; 855 AA.  
DE Human transmembrane serine protease (MTSP) polypeptide #1.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 8; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 788  
ID AAE20788 standard; protein; 3095 AA.  
DE Rat C3b/C4b complement receptor like protein.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.2%; Score 324; DB 5; Length 3095;  
Best Local Similarity 20.1%; Pred. No. 6.4e-09;  
RESULT 789  
ID ADN42162 standard; protein; 757 AA.  
DE Human novel protein NOV 8.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R A.  
PA (LILL/) LI L.  
PA (GANG/) GANGOLLI E A.  
PA (PADL/) PADIGARU M.  
PA (ANDE/) ANDERSON D W.  
PA (RAST/) RASTELLI L.  
PA (MILL/) MILLER C E.  
PA (GERL/) GERLACH V.  
PA (TAUP/) TAUPIER R J.  
PA (GUSE/) GUSEV V Y.  
PA (COLM/) COLMAN S D.  
PA (WOLE/) WOLENC A R.  
PA (PENA/) PENNA C E A.  
PA (FURT/) FURTAK K.  
PA (GROS/) GROSSE W M.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C B.  
Query Match 8.2%; Score 323; DB 8; Length 757;  
Best Local Similarity 21.6%; Pred. No. 1.9e-09;  
RESULT 790  
ID ADH71146 standard; protein; 3130 AA.  
DE Human protein of the invention NOV4f SEQ ID NO:42.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 321; DB 8; Length 3130;  
Best Local Similarity 22.6%; Pred. No. 9.4e-09;  
RESULT 791  
ID ADH71144 standard; protein; 3483 AA.  
DE Human protein of the invention NOV4e SEQ ID NO:40.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 321; DB 8; Length 3483;  
Best Local Similarity 22.6%; Pred. No. 1e-08;  
RESULT 792  
ID ADH71136 standard; protein; 3546 AA.

DE Human protein of the invention NOV4a SEQ ID NO:32.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 321; DB 8; Length 3546;  
Best Local Similarity 22.6%; Pred. No. 1.1e-08;  
RESULT 793  
ID AAE20787 standard; protein; 3069 AA.  
DE Human C3b/C4b complement receptor like protein #1.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.1%; Score 320.5; DB 5; Length 3069;  
Best Local Similarity 20.7%; Pred. No. 9.8e-09;  
RESULT 794  
ID AAE20789 standard; protein; 3100 AA.  
DE Human C3b/C4b complement receptor like protein #2.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.1%; Score 320.5; DB 5; Length 3100;  
Best Local Similarity 20.7%; Pred. No. 9.9e-09;  
RESULT 795  
ID AAU99088 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant G383N/G385T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.1%; Score 319.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 1.7e-09;  
RESULT 796  
ID AAU99080 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L349N/D351T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.1%; Score 319.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 1.7e-09;  
RESULT 797  
ID ADG83836 standard; protein; 455 AA.  
DE Rough scale snake venom protease.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU) UNIV QUEENSLAND.  
Query Match 8.1%; Score 319.5; DB 8; Length 455;  
Best Local Similarity 23.4%; Pred. No. 1.9e-09;  
RESULT 798  
ID AAU99078 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant I348N/G350T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.1%; Score 318.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2e-09;  
RESULT 799  
ID ADH71142 standard; protein; 2612 AA.  
DE Human protein of the invention NOV4d SEQ ID NO:38.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 2612;  
Best Local Similarity 22.6%; Pred. No. 1.2e-08;  
RESULT 800  
ID ABG79169 standard; protein; 2669 AA.  
DE Human cub and sushi domain containing protein #2.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 5; Length 2669;  
Best Local Similarity 22.6%; Pred. No. 1.2e-08;

RESULT 801  
ID ADH71140 standard; protein; 2669 AA.  
DE Human protein of the invention NOV4c SEQ ID NO:36.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 2669;  
Best Local Similarity 22.6%; Pred. No. 1.2e-08;  
RESULT 802  
ID ABG79168 standard; protein; 3104 AA.  
DE Human cub and sushi domain containing protein #1.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 5; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 803  
ID ADH71168 standard; protein; 3104 AA.  
DE Human protein of the invention NOV4p SEQ ID NO:64.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 804  
ID ADH71166 standard; protein; 3104 AA.  
DE Human protein of the invention NOV4p SEQ ID NO:62.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 805  
ID ADH71138 standard; protein; 3104 AA.  
DE Human protein of the invention NOV4b SEQ ID NO:34.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 806  
ID AAU99006 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D189N/K191T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 317.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 2.2e-09;  
RESULT 807  
ID AAU99066 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T315N/V317T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 317.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.2e-09;  
RESULT 808  
ID AAR57283 standard; protein; 798 AA.  
DE Bovine enterokinase.  
PN WO9416083-A1.  
PD 21-JUL-1994.  
PA (GEMY) GENETICS INST INC.  
Query Match 8.0%; Score 317.5; DB 2; Length 798;  
Best Local Similarity 24.6%; Pred. No. 4e-09;  
RESULT 809  
ID AAE20900 standard; protein; 3069 AA.  
DE Human C3b/C4b complement receptor like protein #1, alternative version.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.0%; Score 317.5; DB 5; Length 3069;

Best Local Similarity 20.7%; Pred. No. 1.4e-08;  
RESULT 810  
ID AAE20901 standard; protein; 3100 AA.  
DE Human C3b/C4b complement receptor like protein #2, alternative version.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.0%; Score 317.5; DB 5; Length 3100;  
Best Local Similarity 20.7%; Pred. No. 1.4e-08;  
RESULT 811  
ID AAU99076 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant W338N/S340T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 316.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2.5e-09;  
RESULT 812  
ID AAU99022 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K217N/L219T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 316.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.5e-09;  
RESULT 813  
ID AAU99026 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L220N/R222T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;  
RESULT 814  
ID AAU99081 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D351N/Q353S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2.8e-09;  
RESULT 815  
ID AAU99071 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S336N/M338S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2.8e-09;  
RESULT 816  
ID AAU99087 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant G383N/G385S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;  
RESULT 817  
ID AAU99079 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L349N/D351S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;  
RESULT 818  
ID AAU99081 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D351N/Q353S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;

ID AAR62653 standard; protein; 461 AA.  
 DE Human protein C.  
 PN US5358932-A.  
 PD 25-OCT-1994.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 8.0%; Score 315.5; DB 2; Length 461;  
 Best Local Similarity 24.3%; Pred. No. 3.1e-09;  
 RESULT 819  
 ID AAR35760 standard; protein; 419 AA.  
 DE Protein C (PC).  
 PN WO9309804-A1.  
 PD 27-MAY-1993.  
 PA (SCRI ) SCRIPPS RES INST.  
 Query Match 8.0%; Score 314.5; DB 2; Length 419;  
 Best Local Similarity 23.3%; Pred. No. 3.2e-09;  
 RESULT 820  
 ID AAU99053 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant R306N/K308S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 8.0%; Score 314.5; DB 5; Length 419;  
 Best Local Similarity 24.7%; Pred. No. 3.2e-09;  
 RESULT 821  
 ID AAU99007 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant S190N/K192S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 8.0%; Score 314.5; DB 5; Length 419;  
 Best Local Similarity 24.4%; Pred. No. 3.2e-09;  
 RESULT 822  
 ID AAU99077 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant I348N/G350S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 8.0%; Score 314.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 3.2e-09;  
 RESULT 823  
 ID AAU99043 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant L296N.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 8.0%; Score 314.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 3.2e-09;  
 RESULT 824  
 ID ADG83832 standard; protein; 454 AA.  
 DE Red belly black snake venom protease.  
 PN WO2003082914-A1.  
 PD 09-OCT-2003.  
 PA (UYQU ) UNIV QUEENSLAND.  
 Query Match 8.0%; Score 314.5; DB 8; Length 454;  
 Best Local Similarity 23.0%; Pred. No. 3.5e-09;  
 RESULT 825  
 ID ADM77504 standard; protein; 461 AA.  
 DE Human protein C variant #2 amino acid sequence.  
 PN WO2003106666-A2.  
 PD 24-DEC-2003.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 8.0%; Score 314.5; DB 8; Length 461;  
 Best Local Similarity 24.5%; Pred. No. 3.5e-09;  
 RESULT 826  
 ID AAE23083 standard; protein; 855 AA.  
 DE Epithin protein.  
 PN WO200203787-A2.  
 PD 17-JAN-2002.

PA (DELT-) DELTAGEN INC.  
 Query Match 8.0%; Score 314; DB 5; Length 855;  
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;  
 RESULT 827  
 ID ADI16819 standard; protein; 855 AA.  
 DE Murine NOVX protein homologue SeqID 355.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 8.0%; Score 314; DB 5; Length 855;  
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;  
 RESULT 828  
 ID ADI16877 standard; protein; 855 AA.  
 DE Murine NOVX protein homologue SeqID 413.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 8.0%; Score 314; DB 5; Length 855;  
 Best Local Similarity 21.4%; Pred. No. 6.7e-09;  
 RESULT 829  
 ID AAW72753 standard; protein; 419 AA.  
 DE Primary structure of activated human protein C.  
 PN EP875563-A2.  
 PD 04-NOV-1998.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.9%; Score 313.5; DB 2; Length 419;  
 Best Local Similarity 23.3%; Pred. No. 3.6e-09;  
 RESULT 830  
 ID AAU99005 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant D189N/K191S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.9%; Score 313.5; DB 5; Length 419;  
 Best Local Similarity 24.2%; Pred. No. 3.6e-09;  
 RESULT 831  
 ID AAU99025 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant L220N/R222S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.9%; Score 313.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 3.6e-09;  
 RESULT 832  
 ID AAU99065 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant T315N/V317S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.9%; Score 313.5; DB 5; Length 419;  
 Best Local Similarity 24.3%; Pred. No. 3.6e-09;  
 RESULT 833  
 ID AAU99016 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant D214N/S216T.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.9%; Score 313.5; DB 5; Length 419;  
 Best Local Similarity 24.7%; Pred. No. 3.6e-09;  
 RESULT 834  
 ID AAU99023 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant K218N/L220S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.9%; Score 313.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 3.6e-09;  
 RESULT 835

ID AAR13083 standard; protein; 509 AA.  
DE PAP-I-protein C fusion construct.  
PN WO9109533-A.  
PD 11-JUL-1991.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.9%; Score 313; DB 2; Length 509;  
Best Local Similarity 23.5%; Pred. No. 4.6e-09;  
RESULT 836  
ID ADI16820 standard; protein; 855 AA.  
DE Rat NOVX protein homologue SeqID 356.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.9%; Score 313; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 7.5e-09;  
RESULT 837  
ID ADI16881 standard; protein; 855 AA.  
DE Rat NOVX protein homologue SeqID 417.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.9%; Score 313; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 7.5e-09;  
RESULT 838  
ID ADI16878 standard; protein; 855 AA.  
DE Rat NOVX protein homologue SeqID 414.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.9%; Score 313; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 7.5e-09;  
RESULT 839  
ID AAU99072 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S336N/M338T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 840  
ID AAU99097 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant DI89N/K191N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.1e-09;  
RESULT 841  
ID AAU99009 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K191N/K193S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.1e-09;  
RESULT 842  
ID AAU99064 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R312N/R314T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.1e-09;  
RESULT 843  
ID AAU99069 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V334N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 844  
ID AAU99082 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D351N/Q353T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 845  
ID AAU99096 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant M338A.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 846  
ID AAU99091 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L387N/N389S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 847  
ID AAU99024 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K218N/L220T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 848  
ID AAU99048 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H303N/S305T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.3%; Pred. No. 4.1e-09;  
RESULT 849  
ID AAU99067 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant F316N/L318S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 850  
ID AAU99075 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant M338N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 851  
ID AAU99092 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L387N/N389T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 852  
ID AAU99011 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K192N/L194S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 853  
ID AAU99032 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S250N/S252T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 854  
ID ADM77507 standard; protein; 461 AA.  
DE Human protein C variant #5 amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 8; Length 461;  
Best Local Similarity 24.3%; Pred. No. 4.5e-09;  
RESULT 855  
ID ADM77505 standard; protein; 461 AA.  
DE Human protein C variant #3 amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 4.5e-09;  
RESULT 856  
ID AAB82677 standard; protein; 419 AA.  
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 312; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.4e-09;  
RESULT 857  
ID AAR13537 standard; protein; 460 AA.  
DE Human Protein C zymogen N.  
PN EP443875-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 312; DB 2; Length 460;  
Best Local Similarity 24.7%; Pred. No. 4.8e-09;  
RESULT 858  
ID ADG83830 standard; protein; 467 AA.  
DE Coastal taipan venom protease.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU ) UNIV QUEENSLAND.  
Query Match 7.9%; Score 312; DB 8; Length 467;  
Best Local Similarity 23.0%; Pred. No. 4.9e-09;  
RESULT 859  
ID ABP60993 standard; protein; 1031 AA.  
DE Novel human protein. SEQ ID 80.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 7.9%; Score 312; DB 5; Length 1031;  
Best Local Similarity 22.6%; Pred. No. 1e-08;  
RESULT 860

ID AAU99008 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S190N/K192T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.7e-09;  
RESULT 861  
ID AAU99039 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T254N/N256S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 862  
ID AAU99047 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H303N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.3%; Pred. No. 4.7e-09;  
RESULT 863  
ID AAU99070 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V334N/S336T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 864  
ID AAU99017 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant E215N/K217S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 865  
ID AAU99044 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L296N/T298S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 866  
ID AAU99014 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K193N/A195T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 867  
ID AAU99031 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S250N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.7e-09;  
RESULT 868  
ID AAU99057 standard; protein; 419 AA.



DE Human Protein C zymogen protein mutant K308N/A310S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 869  
ID AAU99054 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R306N/K308T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 870  
ID AAU99095 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D214A.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 871  
ID AAU99015 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D214N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 872  
ID AAP81205 standard; protein; 461 AA.  
DE Human protein C.  
PN EP266190-A.  
PD 04-MAY-1988.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 7.9%; Score 311.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 873  
ID AAR13539 standard; protein; 461 AA.  
DE Human Protein C zymogen LIN.  
PN EP43875-A.  
PD 28-AUG-1991.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 311.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 874  
ID AAR13997 standard; protein; 461 AA.  
DE Human protein C zymogen Q329.  
PN EP43874-A.  
PD 28-AUG-1991.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 311.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 875  
ID ADM77503 standard; protein; 461 AA.  
DE Human protein C variant #1 amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 876  
ID AAB82678 standard; protein; 419 AA.  
DE Human protein C derivative (HI0Q/Q32E/N33D/L194S/T254S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.

Query Match 7.9%; Score 311; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5e-09;  
RESULT 877  
ID AAB82675 standard; protein; 419 AA.  
DE Human protein C derivative (SIIG/Q32E/N33D/L194S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 311; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5e-09;  
RESULT 878  
ID ADC40013 standard; protein; 409 AA.  
DE Human activated protein C-related protein #2.  
PN WO2003075834-A2.  
PD 18-SEP-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 7; Length 409;  
Best Local Similarity 24.5%; Pred. No. 5.2e-09;  
RESULT 879  
ID ADC40012 standard; protein; 410 AA.  
DE Human activated protein C-related protein #1.  
PN WO2003075834-A2.  
PD 18-SEP-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 7; Length 410;  
Best Local Similarity 24.5%; Pred. No. 5.2e-09;  
RESULT 880  
ID AAI56803 standard; protein; 415 AA.  
DE Truncated human protein C polypeptide.  
PN WO9963070-A1.  
PD 09-DEC-1999.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 3; Length 415;  
Best Local Similarity 24.5%; Pred. No. 5.2e-09;  
RESULT 881  
ID AAB82673 standard; protein; 419 AA.  
DE Wild-type human protein C.  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 882  
ID AAB36896 standard; protein; 419 AA.  
DE Human protein C derivative 3.  
PN WO200066754-A1.  
PD 09-NOV-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 883  
ID AAB36894 standard; protein; 419 AA.  
DE Human protein C derivative 1.  
PN WO200066754-A1.  
PD 09-NOV-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 884  
ID AAE08625 standard; protein; 419 AA.  
DE Human mature wild type protein C.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 885  
ID AAU99063 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R312N/R314S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.

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Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 886
ID AAU99012 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K192N/L194T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 887
ID AAU99050 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S304N/R306T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 888
ID AAU99010 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant K191N/K193T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 889
ID AAU99040 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant T254N/N256T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 890
ID AAU99060 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 891
ID AAU99055 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 892
ID AAU99056 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E307N/E309T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 893
ID AAU99059 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant E309N/K311S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 894
ID AAU99002 standard; protein; 419 AA.
DE Human Protein C zymogen protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 895
ID AAU99051 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307S.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 896
ID AAU99052 standard; protein; 419 AA.
DE Human Protein C zymogen protein mutant S305N/E307T.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 897
ID ABR55547 standard; protein; 419 AA.
DE Amino acid sequence of mature human protein C (PC).
PN FR2831170-A1.
PD 25-APR-2003.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 5; Length 419;
RESULT 898
ID ADC40014 standard; protein; 419 AA.
DE Human activated protein C-related protein #3.
PN WO2003075834-A2.
PD 18-SEP-2003.
PA (ELLIL ) LILLY & CO ELI.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 7; Length 419;
RESULT 899
ID ADO18786 standard; protein; 419 AA.
DE Mature human zymogen-like protein C.
PN WO2004044130-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 419;
RESULT 900
ID ADG83834 standard; protein; 453 AA.
DE Mainland tiger snake venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU ) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 8; Length 453;
RESULT 901
ID AAP81104 standard; protein; 460 AA.
DE Sequence of human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH ) HOECHST JAPAN LTD.
Query Match
Best Local Similarity 7.9%; Score 310.5; DB 1; Length 460;
RESULT 902
ID AAW25086 standard; protein; 460 AA.
DE Human protein C.
PN WO9720043-A1.

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ID 05-JUN-1997.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 7.9%; Score 310.5; DB 2; Length 460;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 903  
ID AAP60001 standard; protein; 461 AA.  
DE Sequence of polypeptide with human protein C activity.  
PN EP191606-A.  
PD 20-AUG-1986.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 904  
ID AAP70855 standard; protein; 461 AA.  
DE Human Protein C.  
PN EP215548-A.  
PD 25-MAR-1987.  
PA (ZYMO) ZYMOGENETICS INC.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 7.9%; Score 310.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 905  
ID AAP90401 standard; protein; 461 AA.  
DE Zymogen form of human protein C.  
PN EP323149-A.  
PD 05-JUL-1989.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 906  
ID AAR13622 standard; protein; 461 AA.  
DE Human protein C.  
PN WO9112320-A.  
PD 22-AUG-1991.  
PA (ZYMO) ZYMOGENETICS INC.  
PA (TEIJ) TEIJIN LTD.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 907  
ID AAR13081 standard; protein; 461 AA.  
DE Human protein C.  
PN WO9109953-A.  
PD 11-JUL-1991.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 908  
ID AAR13074 standard; protein; 461 AA.  
DE Protein C precursor.  
PN WO9109951-A.  
PD 11-JUL-1991.  
PA (ZYMO) ZYMOGENETICS INC.  
PA (TEIJ) TEIJIN LTD.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 909  
ID AAR34295 standard; protein; 461 AA.  
DE Protein C.  
PN JP05064588-A.  
PD 19-MAR-1993.  
PA (TEIJ) TEIJIN LTD.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 910  
ID AAW02600 standard; protein; 461 AA.  
DE Human protein C.  
PN US5316550-A.  
PD 14-MAY-1996.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 911

ID AAY49561 standard; protein; 461 AA.  
DE Human lecithin cholesterol acyltransferase protein sequence.  
PN WO950454-A2.  
PD 07-OCT-1999.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 912  
ID AAB82674 standard; protein; 461 AA.  
DE Wild-type human protein C.  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 913  
ID AAB36895 standard; protein; 461 AA.  
DE Human protein C derivative 2.  
PN WO200066754-A1.  
PD 09-NOV-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 914  
ID AAE08626 standard; protein; 461 AA.  
DE Human wild type protein C.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 915  
ID AAU99001 standard; protein; 461 AA.  
DE Human Protein C precursor protein.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 916  
ID ADM77502 standard; protein; 461 AA.  
DE Human protein C wild-type amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 917  
ID ADO18787 standard; protein; 461 AA.  
DE Human zymogen-like protein C.  
PN WO2004044190-A2.  
PD 27-MAY-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 918  
ID AAB82676 standard; protein; 419 AA.  
DE Human protein C derivative (S11G/Q32E/N33D/L194S/T354S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.6e-09;  
RESULT 919  
ID AAE08630 standard; protein; 419 AA.  
DE Human protein C derivative #4.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310; DB 4; Length 419;

Best Local Similarity 24.5%; Pred. No. 5.6e-09;  
 RESULT 920  
 ID AAR13538 standard; protein; 460 AA.  
 DE Human Protein C zymogen FN.  
 PN EP443875-A.  
 PD 28-AUG-1991.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.9%; Score 310; DB 2; Length 460;  
 Best Local Similarity 24.7%; Pred. No. 6.1e-09;  
 RESULT 921  
 ID AAB36897 standard; protein; 419 AA.  
 DE Human protein C derivative 4.  
 PN WO200066754-A1.  
 PD 09-NOV-2000.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.8%; Score 309.5; DB 4; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 922  
 ID AAB36898 standard; protein; 419 AA.  
 DE Human protein C derivative 5.  
 PN WO200066754-A1.  
 PD 09-NOV-2000.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.8%; Score 309.5; DB 4; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 923  
 ID AAU99018 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant E215N/K217T.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.4%; Pred. No. 6e-09;  
 RESULT 924  
 ID AAU99033 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant K251N.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 925  
 ID AAU99013 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant K193N/A195S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.2%; Pred. No. 6e-09;  
 RESULT 926  
 ID AAU99068 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant F316N/L318T.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.4%; Pred. No. 6e-09;  
 RESULT 927  
 ID AAU99062 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant A310N/R312T.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.8%; Pred. No. 6e-09;  
 RESULT 928  
 ID AAU99020 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant S216N/K218T.

PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.4%; Pred. No. 6e-09;  
 RESULT 929  
 ID AAU99035 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant S252N.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 930  
 ID AAU99085 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant E357N/D359S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 931  
 ID AAU99058 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant K308N/A310T.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 932  
 ID AAU99019 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant S216N/K218S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.5%; Pred. No. 6e-09;  
 RESULT 933  
 ID AAU99094 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant H388N/Y390T.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.7%; Pred. No. 6e-09;  
 RESULT 934  
 ID AAU99089 standard; protein; 419 AA.  
 DE Human Protein C zymogen protein mutant L386N/H388S.  
 PN WO200232461-A2.  
 PD 25-APR-2002.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.8%; Score 309.5; DB 5; Length 419;  
 Best Local Similarity 24.8%; Pred. No. 6e-09;  
 RESULT 935  
 ID AAP90070 standard; protein; 461 AA.  
 DE Human protein C.  
 PN EP319312-A.  
 PD 07-JUN-1989.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.8%; Score 309.5; DB 1; Length 461;  
 Best Local Similarity 24.5%; Pred. No. 6.5e-09;  
 RESULT 936  
 ID AAR13540 standard; protein; 461 AA.  
 DE Human Protein C zymogen FLIN.  
 PN EP443875-A.  
 PD 28-AUG-1991.

PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 6.5e-09;  
RESULT 937  
ID ADI16874 standard; protein; 799 AA.  
DE Murine NOVX protein homologue SeqID 410.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 309.5; DB 5; Length 799;  
Best Local Similarity 21.6%; Pred. No. 1.1e-08;  
RESULT 938  
ID ADI16880 standard; protein; 799 AA.  
DE Murine NOVX protein homologue SeqID 416.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 309.5; DB 5; Length 799;  
Best Local Similarity 21.6%; Pred. No. 1.1e-08;  
RESULT 939  
ID AAE08627 standard; protein; 419 AA.  
DE Human protein C derivative #1.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.4e-09;  
RESULT 940  
ID AAE08629 standard; protein; 419 AA.  
DE Human protein C derivative #3.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.4e-09;  
RESULT 941  
ID RAU99049 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S304N/R306S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 942  
ID RAU99061 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant A310N/R312S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.1%; Pred. No. 6.8e-09;  
RESULT 943  
ID RAU99090 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L386N/H388T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 944  
ID RAU99086 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant E357N/D359T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 945  
ID RAU99036 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant S252N/T254S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 946  
ID AAU99045 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant Y302N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 947  
ID AAU99034 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K251N/T253S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 948  
ID ADM77506 standard; protein; 461 AA.  
DE Human protein C variant #4 amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 7.4e-09;  
RESULT 949  
ID AAE08628 standard; protein; 419 AA.  
DE Human protein C derivative #2.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 308; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 7.2e-09;  
RESULT 950  
ID RAU99084 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R352N/D354T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.6%; Pred. No. 7.7e-09;  
RESULT 951  
ID AAU99021 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K317N/L219S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 7.7e-09;  
RESULT 952  
ID RAU99046 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant Y302N/S304T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 7.7e-09;  
RESULT 953  
ID AAU99093 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H388N/Y390S.  
PN WO200232461-A2.

PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 7.7e-09;  
RESULT 954  
ID AAU99083 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R352N/D354S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 306.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 8.7e-09;  
RESULT 955  
ID AAU99074 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V339T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 306.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 8.7e-09;  
RESULT 956  
ID AAU99003 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D172N/K174S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 306.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 8.7e-09;  
RESULT 957  
ID AAU99027 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V243N/V245S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 301.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 1.6e-08;  
RESULT 958  
ID AAR13585 standard; protein; 461 AA.  
DE Human Protein C zymogen Q313.  
PN EP443874-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 306.5; DB 2; Length 461;  
Best Local Similarity 24.1%; Pred. No. 9.5e-09;  
RESULT 959  
ID ABM83654 standard; protein; 495 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3903.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.8%; Score 306.5; DB 8; Length 495;  
Best Local Similarity 24.8%; Pred. No. 1e-08;  
RESULT 960  
ID AAU99004 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D172N/K174T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 305.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 9.8e-09;  
RESULT 961  
ID AAU99073 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V339S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 305.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 9.8e-09;  
RESULT 962  
ID AAR13584 standard; protein; 461 AA.  
DE Human protein C zymogen Q097.  
PN EP443874-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.7%; Score 304.5; DB 2; Length 461;

Best Local Similarity 24.4%; Pred. No. 1.2e-08;  
RESULT 962  
ID AAR13584 standard; protein; 461 AA.  
DE Human protein C zymogen Q248.  
PN EP443874-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.7%; Score 304.5; DB 2; Length 461;  
Best Local Similarity 24.4%; Pred. No. 1.2e-08;  
RESULT 963  
ID AAU99037 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T253N/D255S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 302.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 1.4e-08;  
RESULT 964  
ID AAU99028 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V243N/V245T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 302.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 1.4e-08;  
RESULT 965  
ID AAU99027 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V243N/V245S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 301.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 1.6e-08;  
RESULT 966  
ID AAU99038 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T253N/D255T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 301.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 1.6e-08;  
RESULT 967  
ID AAP93714 standard; protein; 461 AA.  
DE Hybrid protein of protein-C and Factor-X.  
PN EP296413-A.  
PD 28-DEC-1988.  
PA (FARH ) HORCHST JAPAN LTD.  
Query Match 7.6%; Score 301.5; DB 1; Length 461;  
Best Local Similarity 24.7%; Pred. No. 1.8e-08;  
RESULT 968  
ID AAU99041 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D255N/D257S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 299.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 2.1e-08;  
RESULT 969  
ID AAU99029 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V245N/P247S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 298.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 2.3e-08;  
RESULT 970  
ID AAU99030 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant V245N/P247T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.6%; Score 298.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 2.3e-08;  
RESULT 971  
ID. AAU99042 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D255N/D257T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.6%; Score 298.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 2.3e-08;  
RESULT 972  
ID ADB65750 standard; protein; 397 AA.  
DE Human protein encoded by clone UTERU20087070.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.6%; Score 298; DB 7; Length 397;  
Best Local Similarity 24.1%; Pred. No. 2.4e-08;  
RESULT 973  
ID ADI17268 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 804.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.5%; Score 296; DB 5; Length 230;  
Best Local Similarity 32.3%; Pred. No. 1.8e-08;  
RESULT 974  
ID ADI17276 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 812.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.5%; Score 296; DB 5; Length 230;  
Best Local Similarity 32.3%; Pred. No. 1.8e-08;  
RESULT 975  
ID ADJ83075 standard; protein; 230 AA.  
DE Trypsin-like serine protease protein - SEQ ID 66.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHS/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERR/) ZERRHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match 7.5%; Score 296; DB 7; Length 230;

Best Local Similarity 32.3%; Pred. No. 1.8e-08;  
RESULT 976  
ID ABG21442 standard; protein; 932 AA.  
DE Novel human diagnostic protein #21433.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.5%; Score 296; DB 4; Length 932;  
Best Local Similarity 21.0%; Pred. No. 6.7e-08;  
RESULT 977  
ID AAR09290 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue GF6 (Leu 66, Asp 67, Thr 68, Gln 117).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.5%; Score 294; DB 2; Length 562;  
Best Local Similarity 23.3%; Pred. No. 5.4e-08;  
RESULT 978  
ID ABU12065 standard; protein; 986 AA.  
DE Human NOV12a CG92293-01 protein SEQ ID 50.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.4%; Score 293; DB 6; Length 986;  
Best Local Similarity 23.1%; Pred. No. 1e-07;  
RESULT 979  
ID AAR70903 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A432,A434).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.4%; Score 292; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 6.5e-08;  
RESULT 980  
ID AAR70895 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A331,A332).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.4%; Score 292; DB 2; Length 527;  
Best Local Similarity 23.5%; Pred. No. 6.5e-08;  
RESULT 981  
ID ADN03787 standard; protein; 516 AA.  
DE Antipsoriatic protein sequence #90.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.4%; Score 291.5; DB 8; Length 516;  
Best Local Similarity 23.1%; Pred. No. 6.8e-08;  
RESULT 982  
ID ABM80985 standard; protein; 516 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.4%; Score 291.5; DB 8; Length 516;  
Best Local Similarity 23.1%; Pred. No. 6.8e-08;  
RESULT 983  
ID ADQ39246 standard; protein; 516 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.4%; Score 291.5; DB 8; Length 516;  
Best Local Similarity 23.1%; Pred. No. 6.8e-08;  
RESULT 984  
ID AAR13921 standard; protein; 522 AA.  
DE Delta (466-470) tPA variant with H432A and R434A substns.  
PN WO9113149-A.  
PD 05-SEP-1991.  
PA (GETH ) GENENTECH INC.  
Query Match 7.4%; Score 291.5; DB 2; Length 522;

Best Local Similarity 22.7%; Pred. No. 6.8e-08;  
 RESULT 985  
 ID AAR70475 standard; protein; 564 AA.  
 DE Sequence of tissue plasminogen (TPA) analogue.  
 PN WO8703906-A.  
 PD 02-JUL-1987.  
 PA (UPJO ) UPJOHN CO.  
 PA (MARO/) MAROTTI K R.  
 Query Match 7.4%; Score 291.5; DB 1; Length 564;  
 Best Local Similarity 22.9%; Pred. No. 7.4e-08;  
 RESULT 986  
 ID ADG83838 standard; protein; 376 AA.  
 DE Rough scale snake venom prothrombin activator, trocarin.  
 PN WO2003082914-A1.  
 PD 09-OCT-2003.  
 PA (UYQU ) UNIV QUEENSLAND.  
 Query Match 7.4%; Score 291; DB 8; Length 376;  
 Best Local Similarity 22.2%; Pred. No. 5.4e-08;  
 RESULT 987  
 ID AAP60614 standard; protein; 516 AA.  
 DE Plasmid pDAP3 encoded sequence.  
 PN JP61139386-A.  
 PD 26-JUN-1986.  
 PA (TOXJ ) TOYO SODA MFG CO LTD.  
 PA (SAGA ) SAGAMI CHEM RES CENTRE.  
 PA (CENG ) CENTRAL GLASS CO LTD.  
 PA (HODO ) HODOGAYA CHEM IND CO LTD.  
 Query Match 7.4%; Score 290.5; DB 1; Length 516;  
 Best Local Similarity 23.1%; Pred. No. 7.7e-08;  
 RESULT 988  
 ID AAP70257 standard; protein; 516 AA.  
 DE Sequence of human tissue plasminogen activator (TPA) and leader.  
 PN EP231883-A.  
 PD 12-AUG-1987.  
 PA (SAGA ) SAGAMI CHEM RES CENTRE.  
 PA (NIPS ) NIPPON SODA CO.  
 PA (CENG ) CENTRAL GLASS CO LTD.  
 PA (TOXJ ) TOYO SODA MFG CO LTD.  
 PA (NISC ) NISSAN CHEM IND LTD.  
 PA (NISC ) NISSAN CHEMICAL INDS KK.  
 Query Match 7.4%; Score 290.5; DB 1; Length 516;  
 Best Local Similarity 23.1%; Pred. No. 7.7e-08;  
 RESULT 989  
 ID AAR70878 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,D184,E275).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.4%; Score 290; DB 2; Length 483;  
 Best Local Similarity 23.3%; Pred. No. 7.7e-08;  
 RESULT 990  
 ID AAR70885 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,D184,E275,I277).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.4%; Score 290; DB 2; Length 483;  
 Best Local Similarity 23.3%; Pred. No. 7.7e-08;  
 RESULT 991  
 ID AAR70894 standard; protein; 527 AA.  
 DE Human t-PA variant (N103,A303,A304).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.4%; Score 290; DB 2; Length 527;  
 Best Local Similarity 24.0%; Pred. No. 8.3e-08;  
 RESULT 992  
 ID ADL00357 standard; protein; 520 AA.  
 DE Human tissue type plasminogen activator (h-tPA) mutant polypeptide.  
 PN CN1397564-A.  
 PD 19-FEB-2003.  
 PA (LIBB/) LI B.  
 Query Match 7.3%; Score 289.5; DB 7; Length 520;

Best Local Similarity 23.2%; Pred. No. 8.7e-08;  
 RESULT 993  
 ID AAR12340 standard; protein; 559 AA.  
 DE T-PA variant contg. fibronectin for thrombosis lysis (1).  
 PN JP03061482-A.  
 PD 18-MAR-1991.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Query Match 7.3%; Score 289.5; DB 2; Length 559;  
 Best Local Similarity 22.2%; Pred. No. 9.4e-08;  
 RESULT 994  
 ID AAR22664 standard; protein; 564 AA.  
 DE tPA analogue KK2A.  
 PN US5106741-A.  
 PD 21-APR-1992.  
 PA (UPJO ) UPJOHN CO.  
 Query Match 7.3%; Score 289.5; DB 2; Length 564;  
 Best Local Similarity 23.4%; Pred. No. 9.4e-08;  
 RESULT 995  
 ID AAB06934 standard; protein; 658 AA.  
 DE Human membrane-type serine protease (MTSP) 4-S splice variant.  
 PN WO200157194-A2.  
 PD 09-AUG-2001.  
 PA (CORV-) CORVAS INT INC.  
 Query Match 7.3%; Score 289.5; DB 4; Length 658;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-07;  
 RESULT 996  
 ID ADI10379 standard; protein; 658 AA.  
 DE Human cell surface protease #5.  
 PN WO200295007-A2.  
 PD 28-NOV-2002.  
 PA (CORV-) CORVAS INT INC.  
 Query Match 7.3%; Score 289.5; DB 7; Length 658;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-07;  
 RESULT 997  
 ID ADJ46903 standard; protein; 658 AA.  
 DE Human transmembrane serine protease (MTSP) polypeptide #5.  
 PN US2004001801-A1.  
 PD 01-JAN-2004.  
 PA (CORV-) CORVAS INT INC.  
 Query Match 7.3%; Score 289.5; DB 8; Length 658;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-07;  
 RESULT 998  
 ID AAB06933 standard; protein; 802 AA.  
 DE Human membrane-type serine protease (MTSP) 4-L splice variant.  
 PN WO200157194-A2.  
 PD 09-AUG-2001.  
 PA (CORV-) CORVAS INT INC.  
 Query Match 7.3%; Score 289.5; DB 4; Length 802;  
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;  
 RESULT 999  
 ID ADI10377 standard; protein; 802 AA.  
 DE Human cell surface protease #4.  
 PN WO200295007-A2.  
 PD 28-NOV-2002.  
 PA (CORV-) CORVAS INT INC.  
 Query Match 7.3%; Score 289.5; DB 7; Length 802;  
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;  
 RESULT 1000  
 ID ADJ46901 standard; protein; 802 AA.  
 DE Human transmembrane serine protease (MTSP) polypeptide #4.  
 PN US2004001801-A1.  
 PD 01-JAN-2004.  
 PA (CORV-) CORVAS INT INC.  
 Query Match 7.3%; Score 289.5; DB 8; Length 802;  
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;  
 RESULT 1001  
 ID AAR21598 standard; protein; 527 AA.  
 DE tPA variant - T103N, D236A, D238A, K240A.  
 PN WO20202612-A.  
 PD 20-FEB-1992.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 289; DB 2; Length 527;  
 Best Local Similarity 23.4%; Pred. No. 9.4e-08;



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RESULT 1002
ID AAR09217 standard; protein; 529 AA.
DE t-PA insertion variant I304 HH.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 289; DB 2; Length 529;
Best Local Similarity 23.4%; Pred. No. 9.5e-08;
RESULT 1003
ID AAB85076 standard; peptide; 296 AA.
DE Amino acid sequence of MASP-1 polypeptide.
PN WO200140451-A2.
PD 07-JUN-2001.
PA (JENS/) JENSENIUS J C.
PA (THIE/) THIEL S.
Query Match 7.3%; Score 288.5; DB 4; Length 296;
Best Local Similarity 29.3%; Pred. No. 5.9e-08;
RESULT 1004
ID AAY41710 standard; protein; 802 AA.
DE Human PRO618 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 2; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1005
ID AAB44266 standard; protein; 802 AA.
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1006
ID AAB24052 standard; protein; 802 AA.
DE Human PRO618 protein sequence SEQ ID NO:24.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 3; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1007
ID RAU82755 standard; protein; 802 AA.
DE Amino acid sequence of novel human protease #54.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUG-) SUGEN INC.
Query Match 7.3%; Score 288.5; DB 5; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1008
ID ABO25212 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1009
ID ABU72218 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1010
ID ABU84898 standard; protein; 802 AA.
DE Human secreted and transmembrane polypeptide PRO618.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1011
ID ABU61096 standard; protein; 802 AA.
DE Human PRO618 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1012
ID ABU80365 standard; protein; 802 AA.
DE Human secreted/transmembrane protein PRO618.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1013
ID ADA24708 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1014
ID ABO19667 standard; protein; 802 AA.
DE Novel human secreted and transmembrane protein PRO618.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1015
ID ADA12369 standard; protein; 802 AA.
DE Human secreted/transmembrane polypeptide PRO618.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1016
ID ABO19558 standard; protein; 802 AA.
DE Novel human secreted and transmembrane polypeptide #26.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 6; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1017
ID ADB73675 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003045482-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1018
ID ADB76391 standard; protein; 802 AA.
DE Human PRO polypeptide #26.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1019
ID ADC43817 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1020
ID ADC61577 standard; protein; 802 AA.
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DE Human secreted/transmembrane protein, PRO618.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1021  
ID ADC63541 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1022  
ID ADC66641 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1023  
ID ADC68765 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1024  
ID ADC62825 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1025  
ID ADC67890 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003089178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1026  
ID ADC41210 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1027  
ID ADC67265 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1028  
ID ADC62201 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1029  
ID ADC41834 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.

PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1030  
ID ADE49203 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1031  
ID ADE35257 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1032  
ID ADE16371 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1033  
ID ADD72986 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1034  
ID ADD72344 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1035  
ID ADE16995 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1036  
ID ADF47009 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1037  
ID ADG52766 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1038  
ID ADG60086 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003206915-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1039  
ID ADI60846 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 7; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1040  
ID ADE48503 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1041  
ID ADE89604 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1042  
ID ADF61244 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1043  
ID ADF39936 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1044  
ID ADF45732 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.

PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1045  
ID ADF24128 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1046  
ID ADF40560 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1047  
ID ADF23504 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1048  
ID ADF33487 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1049  
ID ADF26954 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1050  
ID ADF27590 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1051  
ID ADF41184 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1052  
ID ADF32863 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
Query Match 22.7%; Pred. No. 1.5e-07;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1053  
ID ADF25229 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003211092-A1.

PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1054  
 ID ADF26330 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003199674-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1055  
 ID ADF34119 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003194410-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1056  
 ID ADF46356 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003195344-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1057  
 ID ADG50342 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003207803-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1058  
 ID ADG49718 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003215905-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1059  
 ID ADG51590 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003215908-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1060  
 ID ADG49094 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003216305-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1061  
 ID ADG48470 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2003216560-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1062  
 ID ADG50966 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.

PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1063  
 ID ADG58910 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2004005657-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1064  
 ID ADG62366 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2004006219-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1065  
 ID ADH25391 standard; protein; 802 AA.  
 DE Human neurotrophin homologue related protein sequence SEQ ID NO:169.  
 PN EP1386931-A1.  
 PD 04-FEB-2004.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1066  
 ID ADH17168 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2004048332-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1067  
 ID ADL07002 standard; protein; 802 AA.  
 DE Human secreted/transmembrane protein, PRO618.  
 PN US2004063921-A1.  
 PD 01-APR-2004.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1068  
 ID ADT91615 standard; protein; 802 AA.  
 DE Human PRO618 protein sequence.  
 PN AU2002317529-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC. 7.3%; Score 288.5; DB 8; Length 802;  
 Query Match  
 Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
 RESULT 1069  
 ID AAB98507 standard; protein; 902 AA.  
 DE Murine epithin.  
 PN WO200129056-A1.  
 PD 26-APR-2001.  
 PA (UYAR-) UNIV ARKANSAS.  
 Query Match  
 Best Local Similarity 21.4%; Pred. No. 1.7e-07;  
 RESULT 1070  
 ID AAU80517 standard; protein; 902 AA.  
 DE Mouse epithilin-like serine protease.  
 PN WO200196378-A2.  
 PD 20-DEC-2001.  
 PA (FARB ) BAYER AG.  
 Query Match  
 Best Local Similarity 21.4%; Pred. No. 1.7e-07;  
 RESULT 1071  
 ID AAU77549 standard; protein; 902 AA.  
 DE Murine type II membrane serine protease, epithin.  
 PN WO20022461-A2.  
 PD 14-FEB-2002.  
 PA (FARB ) BAYER AG.

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Query Match
Best Local Similarity 7.3%; Score 288.5; DB 5; Length 902;
RESULT 1072
ID AAR05489 standard; protein; 527 AA.
DE tPA024 precursor protein.
PN EP373896-A.
PD 20-JUN-1990.
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
PA (YAMA ) NIPPON STEEL CORP.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
DE tPA variant - N117Q, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR21599 standard; protein; 527 AA.
DE tPA variant - N117Q, D236A, D238A, K240A.
PN WO9202612-A.
PD 20-FEB-1992.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR20220 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-012.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR20219 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-011.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR20217 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-009.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR20218 standard; protein; 527 AA.
DE t-PA analogue expressed by pCDM8-010.
PN JP03285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR70901 standard; protein; 527 AA.
DE Human t-PA variant (N103,A416,A417,A418) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAR70904 standard; protein; 527 AA.
DE Human t-PA variant (N103,A440) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 288; DB 2; Length 527;
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHEE ) WHITEHEAD INST BIOMEDICAL RES.

Query Match
Best Local Similarity 7.3%; Score 287.5; DB 2; Length 356;
RESULT 1081
ID AAM52187 standard; protein; 406 AA.
DE Human FVII mutant K143N/N145T/R315N/V317T.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 4; Length 406;
ID ADJ56078 standard; protein; 406 AA.
DE Human factor VII polypeptide mutant K143N/ N145T/ R290N/ A292T.
PN WO2004000366-A1.
PD 31-DEC-2003.
PA (NOVO ) NOVO NORDISK AS.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 8; Length 406;
ID AAR13918 standard; protein; 522 AA.
DE Delta (466-470) tPA variant with K416A, H417A and E418A substns.
PN WO9113149-A.
PD 05-SEP-1991.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 2; Length 522;
ID ABP43952 standard; protein; 795 AA.
DE Human PRO618.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.3%; Score 287.5; DB 5; Length 795;
ID ADG83828 standard; protein; 467 AA.
DE Coastal taipan venom protease.
PN WO2003082914-A1.
PD 09-OCT-2003.
PA (UYQU ) UNIV QUEENSLAND.
Query Match
Best Local Similarity 7.3%; Score 287; DB 8; Length 467;
ID AAR70879 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,S184,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
ID AAR70883 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,K210,E275) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
ID AAR70884 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
ID AAR70886 standard; protein; 483 AA.
DE Human tissue PA variant (deltal-44,N103,S184,E275,I277) .
PN US5385732-A.
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 287; DB 2; Length 483;
ID AAY49558 standard; protein; 356 AA.
DE Human protein C protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHEE ) WHITEHEAD INST BIOMEDICAL RES.
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Best Local Similarity 23.4%; Score 287; DB 2; Length 483;  
 RESULT 1090  
 ID AAR70877 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,E275).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1091  
 ID AAR70887 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,K213,E275,I277).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1092  
 ID AAR70881 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1093  
 ID AAR70882 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,R252,E275).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1094  
 ID AAR70889 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,R252,E275,O277).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1095  
 ID AAR70888 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275,I277).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.1%; Pred. No. 1.1e-07;  
 RESULT 1096  
 ID AAR70890 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,K210,E275,I277).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1097  
 ID AAR70880 standard; protein; 483 AA.  
 DE Human tissue PA variant (deltal-44,N103,K213,E275).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 483;  
 Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
 RESULT 1098  
 ID AAR70907 standard; protein; 527 AA.  
 DE Human t-PA variant (N103,A460,A462).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 527;  
 Best Local Similarity 23.4%; Pred. No. 1.2e-07;

RESULT 1099  
 ID AAR70874 standard; protein; 527 AA.  
 DE Human t-PA variant (N67,N103).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 527;  
 Best Local Similarity 23.4%; Pred. No. 1.2e-07;  
 RESULT 1100  
 ID AAR70892 standard; protein; 527 AA.  
 DE Human t-PA variant (N103,A283,A287).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 287; DB 2; Length 527;  
 Best Local Similarity 23.4%; Pred. No. 1.2e-07;  
 RESULT 1101  
 ID AAM52182 standard; protein; 406 AA.  
 DE Human FVII mutant K143N/N145T.  
 PN WO200158935-A2.  
 PD 16-AUG-2001.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.3%; Score 286.5; DB 4; Length 406;  
 Best Local Similarity 23.0%; Pred. No. 1e-07;  
 RESULT 1102  
 ID ADJ56073 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant K143N/ N145T.  
 PN WO2004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.3%; Score 286.5; DB 8; Length 406;  
 Best Local Similarity 23.0%; Pred. No. 1e-07;  
 RESULT 1103  
 ID ADO10589 standard; protein; 406 AA.  
 DE Human factor VII/VIIa protein mutant #25.  
 PN WO2004029091-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.3%; Score 286.5; DB 8; Length 406;  
 Best Local Similarity 23.0%; Pred. No. 1e-07;  
 RESULT 1104  
 ID ADG83826 standard; protein; 467 AA.  
 DE Brown snake venom protease.  
 PN WO2003082914-A1.  
 PD 09-OCT-2003.  
 PA (UYQU ) UNIV QUEENSLAND.  
 Query Match 7.3%; Score 286.5; DB 8; Length 467;  
 Best Local Similarity 22.2%; Pred. No. 1.1e-07;  
 RESULT 1105  
 ID AAR14486 standard; protein; 522 AA.  
 DE Delta (466-470) tPA variant with Y67N substitution.  
 PN WO9113149-A.  
 PD 05-SEP-1991.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.3%; Score 286.5; DB 2; Length 522;  
 Best Local Similarity 22.7%; Pred. No. 1.3e-07;  
 RESULT 1106  
 ID AAR44816 standard; protein; 527 AA.  
 DE Human tPA variant (N67,N103).  
 PN US5270198-A.  
 PD 14-DEC-1993.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.2%; Score 286; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 1.4e-07;  
 RESULT 1107  
 ID AAR44812 standard; protein; 527 AA.  
 DE Human tPA variant N103.  
 PN US5270198-A.  
 PD 14-DEC-1993.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.2%; Score 286; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 1.4e-07;

RESULT 1108  
ID AAR70868 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A432,A434).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.4e-07;  
RESULT 1109  
ID AAR70860 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A331,A332).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.4e-07;  
RESULT 1110  
ID AAR70900 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A410).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 1.4e-07;  
RESULT 1111  
ID AAR09220 standard; protein; 529 AA.  
DE t-PA insertion variant 1304H, 1305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 529;  
Best Local Similarity 23.2%; Pred. No. 1.4e-07;  
RESULT 1112  
ID AAP70449 standard; protein; 530 AA.  
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).  
PN WO8705934-A.  
PD 08-OCT-1987.  
PA (CREA/) CREA R.  
Query Match 7.2%; Score 286; DB 1; Length 530;  
Best Local Similarity 22.9%; Pred. No. 1.4e-07;  
RESULT 1113  
ID AAR12342 standard; protein; 561 AA.  
DE T-PA with -ve charged finger and/or kringle domain (1).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.2%; Score 286; DB 2; Length 561;  
Best Local Similarity 22.1%; Pred. No. 1.4e-07;  
RESULT 1114  
ID AAR09289 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BENT12 (Asp 67, Thr 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.2%; Score 286; DB 2; Length 562;  
Best Local Similarity 23.3%; Pred. No. 1.5e-07;  
RESULT 1115  
ID AAP70880 standard; protein; 527 AA.  
DE Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GEMY ) GENETICS INST INC.  
PA (LARS/) LARSEN G R.  
Query Match 7.2%; Score 285.5; DB 1; Length 527;  
Best Local Similarity 23.1%; Pred. No. 1.5e-07;  
RESULT 1116  
ID AAP91683 standard; protein; 527 AA.  
DE Sequence of tissue plasminogen activator (tPA).  
PN WO8911531-A.  
PD 30-NOV-1989.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 1; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.5e-07;  
RESULT 1117  
ID AAR09270 standard; protein; 527 AA.  
DE t-PA variant H331A, H332A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.5e-07;  
RESULT 1118  
ID AAR09278 standard; protein; 527 AA.  
DE t-PA variant H432A, R434A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 1.5e-07;  
RESULT 1119  
ID AAP71449 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EF238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 1; Length 528;  
Best Local Similarity 23.4%; Pred. No. 1.6e-07;  
RESULT 1120  
ID AAR13148 standard; protein; 556 AA.  
DE T-PA variant contg. fibronectin for thrombosis lysis (2).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.2%; Score 285; DB 2; Length 556;  
Best Local Similarity 21.9%; Pred. No. 1.6e-07;  
RESULT 1121  
ID AAB11710 standard; protein; 264 AA.  
DE Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 7.2%; Score 284.5; DB 3; Length 264;  
Best Local Similarity 28.0%; Pred. No. 8.6e-08;  
RESULT 1122  
ID AAP91961 standard; protein; 518 AA.  
DE Sequence of des 1-44E275 t-PA mutant.  
PN WO8909266-A.  
PD 05-OCT-1989.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284.5; DB 1; Length 518;  
Best Local Similarity 22.9%; Pred. No. 1.6e-07;  
RESULT 1123  
ID ABM84749 standard; protein; 629 AA.  
DE Human diagnostic and therapeutic pproteic protein SEQ ID NO:4998.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.2%; Score 284.5; DB 8; Length 629;  
Best Local Similarity 19.5%; Pred. No. 1.9e-07;  
RESULT 1124  
ID ABM82817 standard; protein; 629 AA.  
DE Human diagnostic and therapeutic pproteic protein SEQ ID NO:3066.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.2%; Score 284.5; DB 8; Length 629;  
Best Local Similarity 19.5%; Pred. No. 1.9e-07;  
RESULT 1125  
ID AAR70851 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.

Query Match 7.2%; Score 284; DB 2; Length 483;  
Best Local Similarity 23.1%; Pred. No. 1.8e-07;  
RESULT 1126  
ID AAR70844 standard; protein; 483 AA.  
DE Human tissue PA variant (delcal-44,N67,D184,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 483;  
Best Local Similarity 23.1%; Pred. No. 1.6e-07;  
RESULT 1127  
ID AAR44809 standard; protein; 527 AA.  
DE Human tPA variant (N65, S67).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 1.8e-07;  
RESULT 1128  
ID AAR70908 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A477).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.8e-07;  
RESULT 1129  
ID AAR70859 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A303,A304).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.8%; Pred. No. 1.8e-07;  
RESULT 1130  
ID AAR70893 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A296,A297,A298,A299).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.5%; Pred. No. 1.8e-07;  
RESULT 1131  
ID AAR70891 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A267).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.7%; Pred. No. 1.8e-07;  
RESULT 1132  
ID AAP70474 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen (TPA) analogue.  
PN WO8703906-A.  
PD 02-JUL-1987.  
PA (UPJO ) UPJOHN CO.  
PA (MARO/) MAROTTI K R.  
Query Match 7.2%; Score 284; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 1.9e-07;  
RESULT 1133  
ID AAR09286 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.2%; Score 284; DB 2; Length 562;  
Best Local Similarity 23.1%; Pred. No. 1.9e-07;  
RESULT 1134  
ID AAR23807 standard; protein; 562 AA.  
DE t-PA (Tyr 297) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.

Query Match 7.2%; Score 284; DB 2; Length 562;  
Best Local Similarity 23.2%; Pred. No. 1.9e-07;  
RESULT 1135  
ID ABB80068 standard; protein; 406 AA.  
DE Human coagulation factor VII mutant L305V/M306D/D309S.  
PN WO200183725-A1.  
PD 08-NOV-2001.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.2%; Score 283.5; DB 5; Length 406;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1136  
ID ABG73125 standard; protein; 406 AA.  
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.  
PN WO200277218-A1.  
PD 03-OCT-2002.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.2%; Score 283.5; DB 6; Length 406;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1137  
ID ADJ55852 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ M306D/ D309S.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.2%; Score 283.5; DB 8; Length 406;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1138  
ID ADE83543 standard; protein; 482 AA.  
DE Rat Protein NP 058839, SEQ ID NO 11161.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.2%; Score 283.5; DB 7; Length 482;  
Best Local Similarity 22.8%; Pred. No. 1.7e-07;  
RESULT 1139  
ID AAR3917 standard; peptide; 522 AA.  
DE Delta (466-470) tPA variant with K296A, H297A, R298A and R299A  
DE substitutions.  
PN WO9113149-A.  
PD 05-SEP-1991.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283.5; DB 2; Length 522;  
Best Local Similarity 22.8%; Pred. No. 1.8e-07;  
RESULT 1140  
ID AAP90169 standard; peptide; 571 AA.  
DE Tissue plasminogen activator mutant 2G.  
PN WO8907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Query Match 7.2%; Score 283.5; DB 1; Length 571;  
Best Local Similarity 22.4%; Pred. No. 2e-07;  
RESULT 1141  
ID AAR09257 standard; protein; 483 AA.  
DE t-PA variant d1-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 1.8e-07;  
RESULT 1142  
ID AAR09269 standard; protein; 527 AA.  
DE t-PA variant E303A, R304A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 527;  
Best Local Similarity 23.7%; Pred. No. 2e-07;  
RESULT 1143  
ID AAR44810 standard; protein; 527 AA.  
DE Human tPA variant (N65, T67).  
PN US5270198-A.  
PD 14-DEC-1993.



PA (GETH ) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.1%; Pred. No. 2e-07;  
RESULT 1144  
ID AAR44817 standard; protein; 527 AA.  
DE Human tPA variant (N67,A296,A297,A298,A299).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.4%; Pred. No. 2e-07;  
RESULT 1145  
ID AAR44814 standard; protein; 527 AA.  
DE Human tPA variant (N105, T107).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.6%; Pred. No. 2e-07;  
RESULT 1146  
ID AAR70899 standard; protein; 527 AA.  
DE Human tPA variant (N103,A408).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC. 7.2%; Score 283; DB 2; Length 527;  
Query Match  
Best Local Similarity 22.9%; Pred. No. 2e-07;  
RESULT 1147  
ID AAR12341 standard; protein; 560 AA.  
DE T-PA variant contg. fibronectin for thrombosis lysis (3).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Query Match  
Best Local Similarity 7.2%; Score 283; DB 2; Length 560;  
RESULT 1148  
ID RAR12367 standard; protein; 561 AA.  
DE T-PA with -ve charged finger and/or kringle domain (7).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Query Match  
Best Local Similarity 7.2%; Score 283; DB 2; Length 561;  
RESULT 1149  
ID AAR09231 standard; protein; 524 AA.  
DE t-PA deletion variant d297-299.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. 7.2%; Score 282.5; DB 2; Length 524;  
Query Match  
Best Local Similarity 22.8%; Pred. No. 2.1e-07;  
RESULT 1150  
ID AAR09246 standard; protein; 483 AA.  
DE t-PA variant dl-44, N184D, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 483;  
Query Match  
Best Local Similarity 23.0%; Pred. No. 2.1e-07;  
RESULT 1151  
ID AAR09254 standard; protein; 483 AA.  
DE t-PA variant dl-44, I210R, G211H, K212Q, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 483;  
Query Match  
Best Local Similarity 22.8%; Pred. No. 2.1e-07;  
RESULT 1152  
ID AAR09230 standard; protein; 525 AA.  
DE t-PA deletion variant d297-298.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 7.1%; Score 282; DB 2; Length 525;  
RESULT 1153  
ID AAR09255 standard; protein; 527 AA.  
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;  
Query Match  
Best Local Similarity 22.8%; Pred. No. 2.2e-07;  
RESULT 1154  
ID AAR21600 standard; protein; 527 AA.  
DE tPA variant - E94A, D95A, T103N.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 2.2e-07;  
RESULT 1155  
ID AAR70866 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A416,A417,A418).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.4%; Pred. No. 2.2e-07;  
RESULT 1156  
ID AAR70902 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A426,A427,A429,A430).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.4%; Pred. No. 2.2e-07;  
RESULT 1157  
ID AAR70869 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A440).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC. 7.1%; Score 282; DB 2; Length 527;  
Query Match  
Best Local Similarity 23.2%; Pred. No. 2.2e-07;  
RESULT 1158  
ID AAR2582 standard; protein; 562 AA.  
DE Tissue plasminogen activator with S-119 substd for M and QG196-98 substd  
DE for NGT.  
PN JP63230083-A.  
PD 26-SEP-1988.  
PA (EISA ) EISAI CO LTD.  
Query Match  
Best Local Similarity 7.1%; Score 282; DB 1; Length 562;  
RESULT 1159  
ID AAR09287 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match  
Best Local Similarity 7.1%; Score 282; DB 2; Length 562;  
RESULT 1160  
ID AAR23808 standard; protein; 562 AA.  
DE t-PA (Glu 298) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match  
Best Local Similarity 7.1%; Score 282; DB 2; Length 562;  
RESULT 1161  
ID AAR23810 standard; protein; 562 AA.  
DE t-PA (Gly 301) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.



RESULT 1180  
ID ADO10585 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #21.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.8%; Pred. No. 1.9e-07;  
RESULT 1181  
ID ADO10626 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #62.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 1.9e-07;  
RESULT 1182  
ID ADS12886 standard; protein; 406 AA.  
DE Human factor VII G237L mutant.  
PN WO2004083361-A2.  
PD 30-SEP-2004.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 1.9e-07;  
RESULT 1183  
ID AAR09233 standard; protein; 522 AA.  
DE t-PA deletion variant d297-301.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281.5; DB 2; Length 522;  
Best Local Similarity 23.4%; Pred. No. 2.4e-07;  
RESULT 1184  
ID AAR13919 standard; protein; 522 AA.  
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A  
DE substitutions.  
PN WO9113149-A.  
PD 05-SEP-1991.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281.5; DB 2; Length 522;  
Best Local Similarity 22.7%; Pred. No. 2.4e-07;  
RESULT 1185  
ID AAR09239 standard; protein; 524 AA.  
DE t-PA deletion variant d300-302.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281.5; DB 2; Length 524;  
Best Local Similarity 23.2%; Pred. No. 2.4e-07;  
RESULT 1186  
ID AAR12366 standard; protein; 562 AA.  
DE T-PA with -ve charged finger and/or kringle domain (5).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 281.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 2.5e-07;  
RESULT 1187  
ID AAR09249 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.3%; Pred. No. 2.3e-07;  
RESULT 1188  
ID AAR70855 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,K210,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.

PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1189  
ID AAR70845 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,S184,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1190  
ID AAR70848 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,R252,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1191  
ID AAR70849 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,K210,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1192  
ID AAR70854 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,R252,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1193  
ID AAR70843 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1194  
ID AAR70846 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,K213,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1195  
ID AAR79144 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,S184,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1196  
ID AAR70850 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1197  
ID AAR70852 standard; protein; 483 AA.  
DE Human tissue PA variant (deltal-44,N67,K213,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;

Query Match 7.1%; Score 281; DB 2; Length 483;  
 Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
 RESULT 1198  
 ID AAR70847 standard; protein; 483 AA.  
 DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 483;  
 Best Local Similarity 23.0%; Pred. No. 2.3e-07;  
 RESULT 1199  
 ID AAR70853 standard; protein; 483 AA.  
 DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,I277).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 483;  
 Best Local Similarity 23.0%; Pred. No. 2.3e-07;  
 RESULT 1200  
 ID AAR70858 standard; protein; 487 AA.  
 DE Cattle Factor-Xa.  
 PN WO9418227-A2.  
 PD 18-AUG-1994.  
 PA (DENZ-) DENZYME APS.  
 Query Match 7.1%; Score 281; DB 2; Length 487;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1201  
 ID AAW76216 standard; protein; 488 AA.  
 DE Human Factor X protein.  
 PN WO9838317-A1.  
 PD 03-SEP-1998.  
 PA (IMMO ) IMMUNO AG.  
 Query Match 7.1%; Score 281; DB 2; Length 488;  
 Best Local Similarity 24.0%; Pred. No. 2.4e-07;  
 RESULT 1202  
 ID AAW76217 standard; protein; 488 AA.  
 DE Human Factor X protein analogue.  
 PN WO9838317-A1.  
 PD 03-SEP-1998.  
 PA (IMMO ) IMMUNO AG.  
 Query Match 7.1%; Score 281; DB 2; Length 488;  
 Best Local Similarity 22.6%; Pred. No. 2.4e-07;  
 RESULT 1203  
 ID AAW76218 standard; protein; 488 AA.  
 DE Human Factor X protein.  
 PN WO9838318-A1.  
 PD 03-SEP-1998.  
 PA (IMMO ) IMMUNO AG.  
 Query Match 7.1%; Score 281; DB 2; Length 489;  
 Best Local Similarity 24.0%; Pred. No. 2.4e-07;  
 RESULT 1204  
 ID AAB70411 standard; protein; 488 AA.  
 DE Human factor X protein sequence SEQ ID NO:2.  
 PN WO200110896-A2.  
 PD 15-FEB-2001.  
 PA (BAXT ) BAXTER AG.  
 Query Match 7.1%; Score 281; DB 4; Length 489;  
 Best Local Similarity 24.0%; Pred. No. 2.4e-07;  
 RESULT 1205  
 ID AAR60502 standard; protein; 492 AA.  
 DE Serine protease for fusion protein cleavage.  
 PN WO9418227-A2.  
 PD 18-AUG-1994.  
 PA (DENZ-) DENZYME APS.  
 Query Match 7.1%; Score 281; DB 2; Length 492;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1206  
 ID AAR09238 standard; protein; 525 AA.  
 DE t-PA deletion variant d300-301.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 525;

Best Local Similarity 22.8%; Pred. No. 2.5e-07;  
 RESULT 1207  
 ID AAR09276 standard; protein; 527 AA.  
 DE t-PA variant K416A, H417A, E418A.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 RESULT 1208  
 ID AAR09279 standard; protein; 527 AA.  
 DE t-PA variant R440A.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.5e-07;  
 RESULT 1209  
 ID AAR70875 standard; protein; 527 AA.  
 DE Human t-PA variant (N60,N103).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 RESULT 1210  
 ID AAR70876 standard; protein; 527 AA.  
 DE Human t-PA variant (N60,N67,N103).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 RESULT 1211  
 ID AAR70857 standard; protein; 527 AA.  
 DE Human t-PA variant (N67,A283,A287).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 RESULT 1212  
 ID AAR70898 standard; protein; 527 AA.  
 DE Human t-PA variant (N103,A364,A365,A366).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 RESULT 1213  
 ID AAR70906 standard; protein; 527 AA.  
 DE Human t-PA variant (N103,A449,A453).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.5e-07;  
 RESULT 1214  
 ID AAR70872 standard; protein; 527 AA.  
 DE Human t-PA variant (N67,A460,A462).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
 RESULT 1215  
 ID AAR70842 standard; protein; 527 AA.  
 DE Wild type tissue plasminogen activator protein.  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 281; DB 2; Length 527;  
 Best Local Similarity 23.2%; Pred. No. 2.5e-07;

RESULT 1216  
ID AAR13150 standard; protein; 558 AA.  
DE T-PA with -ve charged finger and/or kringle domain (3).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 281; DB 2; Length 558;  
Best Local Similarity 23.0%; Pred. No. 2.7e-07;  
RESULT 1217  
ID AAR13152 standard; protein; 559 AA.  
DE T-PA with -ve charged finger and/or kringle domain (6).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 281; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 2.7e-07;  
RESULT 1218  
ID AAP80691 standard; protein; 1087 AA.  
DE Hybrid plasminogen/t-PA compound 1.  
PN EP292328-A.  
PD 23-NOV-1988.  
PA (BEECH) BEECHAM GROUP PLC.  
Query Match 7.1%; Score 281; DB 1; Length 1087;  
Best Local Similarity 22.3%; Pred. No. 5e-07;  
RESULT 1219  
ID ABM81778 standard; protein; 264 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GENTH) GENENTECH INC.  
Query Match 7.1%; Score 280.5; DB 8; Length 264;  
Best Local Similarity 27.2%; Pred. No. 1.4e-07;  
RESULT 1220  
ID ABM84054 standard; protein; 279 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4303.  
PN WO20040231973-A2.  
PD 25-MAR-2004.  
PA (INCY) INCYTE CORP.  
Query Match 7.1%; Score 280.5; DB 8; Length 279;  
Best Local Similarity 27.2%; Pred. No. 1.5e-07;  
RESULT 1221  
ID AAO30575 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158D/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1222  
ID AAO30604 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1223  
ID AAO30577 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1224  
ID AAO30594 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1225  
ID AAO30596 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158D/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;

ID AAO30569 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1226  
ID AAO30606 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/V158D/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1227  
ID AAO30613 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1228  
ID AAO30621 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1229  
ID AAO30619 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1230  
ID ADJ55876 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant / M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1231  
ID ADJ55937 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1232  
ID ADJ56047 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1233  
ID ADJ55949 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1234  
ID ADJ55965 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1235  
ID ADJ55965 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;

DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1235  
ID ADJ55948 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1236  
ID ADJ56057 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y V158T M298Q L305V S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1237  
ID ADJ55885 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1238  
ID ADJ55921 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1239  
ID ADJ55958 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1240  
ID ADJ55963 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1241  
ID ADJ56016 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1242  
ID ADJ56046 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1243  
ID ADJ55919 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.

PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1244  
ID ADJ56056 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1245  
ID ADJ55887 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1246  
ID ADJ55914 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1247  
ID ADJ56004 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305VK337A/ M298Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1248  
ID ADO10616 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #52.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.1e-07;  
RESULT 1249  
ID ADO10607 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #43.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.1e-07;  
RESULT 1250  
ID AAR09221 standard; protein; 526 AA.  
DE t-PA deletion variant d297.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280.5; DB 2; Length 526;  
Best Local Similarity 23.1%; Pred. No. 2.7e-07;  
RESULT 1251  
ID AAP70020 standard; protein; 561 AA.  
DE Sequence of tissue plasminogen activator (tPA).  
PN EF242836-A.  
PD 28-OCT-1987.  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
Query Match 7.1%; Score 280.5; DB 1; Length 561;  
Best Local Similarity 21.7%; Pred. No. 2.9e-07;  
RESULT 1252  
ID ABR62449 standard; protein; 583 AA.

DE Bovine recombinant prothrombin, expressed in Escherichia coli.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.1%; Score 280.5; DB 7; Length 583;  
Best Local Similarity 21.9%; Pred. No. 3e-07;  
RESULT 1253  
ID ABR62451 standard; protein; 635 AA.  
DE Bovine recombinant prothrombin, expressed in CHO cells.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.1%; Score 280.5; DB 7; Length 635;  
Best Local Similarity 21.9%; Pred. No. 3.2e-07;  
RESULT 1254  
ID AAR37402 standard; protein; 448 AA.  
DE Factor X.  
PN WO9309803-A1.  
PD 27-MAY-1993.  
PA (SCHN/) SCHAFFER S C.  
PA (SCRI ) SCRIPPS RES INST.  
Query Match 7.1%; Score 280; DB 2; Length 448;  
Best Local Similarity 24.0%; Pred. No. 2.5e-07;  
RESULT 1255  
ID AAW66092 standard; peptide; 448 AA.  
DE Human factor X variant.  
PN WO9839456-A1.  
PD 11-SEP-1998.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 7.1%; Score 280; DB 2; Length 448;  
Best Local Similarity 24.0%; Pred. No. 2.5e-07;  
RESULT 1256  
ID AAR09245 standard; protein; 525 AA.  
DE t-PA deletion variant d297, d305.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 525;  
Best Local Similarity 23.1%; Pred. No. 2.9e-07;  
RESULT 1257  
ID AAR05488 standard; protein; 527 AA.  
DE t-PA024 precursor protein.  
PN EP373896-A.  
PD 20-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
PA (YAWA ) NIPPON STEEL CORP.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1258  
ID AAR09267 standard; protein; 527 AA.  
DE t-PA variant D283A, H287A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1259  
ID AAR09282 standard; protein; 527 AA.  
DE t-PA variant D460A, R462A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1260  
ID AAR13911 standard; protein; 527 AA.  
DE t-PA deriv. (II).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1261  
ID AAR13914 standard; protein; 527 AA.  
DE T-PA deriv. (V).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1262  
ID AAR13912 standard; protein; 527 AA.  
DE T-PA deriv. (III).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1263  
ID AAR13910 standard; protein; 527 AA.  
DE T-PA deriv. (I).  
PN EP445464-A.  
PD 11-SEP-1991.  
PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1264  
ID AAR21594 standard; protein; 527 AA.  
DE t-PA variant - D95A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1265  
ID AAR21593 standard; protein; 527 AA.  
DE t-PA variant - E94A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 2.9e-07;  
RESULT 1266  
ID AAR20221 standard; protein; 527 AA.  
DE t-PA analogue expressed by pCDM8-013.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1267  
ID AAR20215 standard; protein; 527 AA.  
DE R462E t-PA analogue.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1268  
ID AAR20216 standard; protein; 527 AA.  
DE R462G t-PA analogue.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1269  
ID AAR20222 standard; protein; 527 AA.  
DE t-PA analogue expressed by pCDM8-014.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1270  
ID AAR20223 standard; protein; 527 AA.

DE t-PA analogue expressed by pCDM8-018.  
PN JF03285680-A.  
PD 16-DEC-1991.  
PA (SUMU) SUMITOMO SEIVAKU KK.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1271  
ID AAR44811 standard; protein; 527 AA.  
DE Human tPA variant N67.  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1272  
ID AAR70865 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A410).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 22.9%; Pred. No. 2.9e-07;  
RESULT 1273  
ID RAM57778 standard; protein; 527 AA.  
DE R275E,H417D human tissue-type plasminogen activator protein mutant.  
PN WO9821320-A2.  
PD 22-MAY-1998.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1274  
ID AAM45907 standard; peptide; 527 AA.  
DE Single chain form of the intact t-PA molecule.  
PN WO9802454-A2.  
PD 22-JAN-1998.  
PA (ADPR-) ADPROTECH PLC.  
Query Match 7.1%; Score 280; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1275  
ID AAE24190 standard; protein; 527 AA.  
DE Human tissue plasminogen activator (tPA) protein.  
PN WO200240695-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Query Match 7.1%; Score 280; DB 5; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1276  
ID AAG79362 standard; protein; 527 AA.  
DE Human tissue plasminogen activator.  
PN WO200243747-A2.  
PD 06-JUN-2002.  
PA (ISIS-) ISIS INNOVATION LTD.  
Query Match 7.1%; Score 280; DB 5; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1277  
ID AAE25044 standard; protein; 527 AA.  
DE Human tissue plasminogen activator (tPA) protein.  
PN WO200240650-A2.  
PD 23-MAY-2002.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Query Match 7.1%; Score 280; DB 5; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1278  
ID ADL92126 standard; protein; 527 AA.  
DE Alteplase protein sequence.  
PN WO200309862-A1.  
PD 04-DEC-2003.  
PA (NANO-) APPLIED NANOSYSTEMS BV.  
Query Match 7.1%; Score 280; DB 8; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
RESULT 1279  
ID ABM82630 standard; protein; 534 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2879.

PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.1%; Score 280; DB 8; Length 534;  
Best Local Similarity 22.7%; Pred. No. 2.9e-07;  
RESULT 1280  
ID ABM82821 standard; protein; 534 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3070.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.1%; Score 280; DB 8; Length 534;  
Best Local Similarity 22.7%; Pred. No. 2.9e-07;  
RESULT 1281  
ID AAR13020 standard; protein; 557 AA.  
DE T-PA variant contg. fibronectin for thrombosis lysis (4).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 280; DB 2; Length 557;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1282  
ID AAR13149 standard; protein; 557 AA.  
DE T-PA variant contg. fibronectin for thrombosis lysis (4).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 280; DB 2; Length 557;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1283  
ID AAP50219 standard; protein; 561 AA.  
DE Tissue plasminogen activator encoded by cDNA clone.  
PN EP143081-A.  
PD 29-MAY-1985.  
PA (CIBA) CIBA GEIGY AG.  
Query Match 7.1%; Score 280; DB 1; Length 561;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1284  
ID AAP60790 standard; protein; 562 AA.  
DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).  
PN GB2173804-A.  
PD 22-OCT-1986.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1285  
ID AAP60810 standard; protein; 562 AA.  
DE Sequence of modified human tissue plasminogen activator (t-PA).  
PN FR2581652-A.  
PD 14-NOV-1986.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1286  
ID AAP60214 standard; protein; 562 AA.  
DE Sequence of active human uterine tissue plasminogen activator (UTPA).  
PN EP178105-A.  
PD 16-APR-1986.  
PA (INTE-) INTEG GENETICS INC.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1287  
ID AAP81913 standard; protein; 562 AA.  
DE Tissue plasminogen activator encoded by pEmpl-tPA.  
PN WO8800242-A.  
PD 14-JAN-1988.  
PA (DAMO-) DAMON BIOTECH INC.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1288  
ID AAP80655 standard; protein; 562 AA.  
DE Tissue plasminogen activator analogue.  
PN EP293934-A.



PD 07-DEC-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (NOVO ) NOVO IND AS.  
PA (EISA ) EISA CO LTD.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1289  
ID AAP94406 standard; protein; 562 AA.  
DE Sequence encoded by native tPA of plasmid pST112.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1290  
ID AAP93716 standard; protein; 562 AA.  
DE Human melanoma t-PA encoded by plasmid pKG12.  
PN EP297066-A.  
PD 28-DEC-1988.  
PA (KABI ) KABIGEN AB.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1291  
ID AAP90916 standard; protein; 562 AA.  
DE Human tissue plasminogen activator.  
PN JP01174388-A.  
PD 10-JUL-1989.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 280; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1292  
ID AAR09288 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1293  
ID AAR06237 standard; protein; 562 AA.  
DE Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1294  
ID AAR04700 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1295  
ID AAR04701 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1296  
ID AAR04699 standard; protein; 562 AA.  
DE Native tissue plasminogen activator (t-PA).  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.

PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1297  
ID AAR13727 standard; protein; 562 AA.  
DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.  
PN US5041376-A.  
PD 20-AUG-1991.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1298  
ID AAR12847 standard; protein; 562 AA.  
DE T-PA Ktingle 1 domain substitution mutant.  
PN JP03127987-A.  
PD 31-MAY-1991.  
PA (KANF ) KANEGAFUCHI CHEM KK.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1299  
ID AAR3811 standard; protein; 562 AA.  
DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.5%; Pred. No. 3.1e-07;  
RESULT 1300  
ID AAR23806 standard; protein; 562 AA.  
DE t-PA (Glu 296) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1301  
ID AAR23804 standard; protein; 562 AA.  
DE t-PA (Glu 304) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1302  
ID AAR34426 standard; protein; 562 AA.  
DE Sequence of human pre-pro tissue plasminogen activator (t-PA).  
PN US5200340-A.  
PD 06-APR-1993.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1303  
ID AAR96220 standard; protein; 562 AA.  
DE Full-length tissue plasminogen activator.  
PN US5504001-A.  
PD 02-APR-1996.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.1%; Score 280; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1304  
ID AAY50868 standard; protein; 562 AA.  
DE Human tissue plasminogen activator protein fragment.  
PN WO957251-A2.  
PD 11-NOV-1999.  
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
Query Match 7.1%; Score 280; DB 3; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1305  
ID AAY43397 standard; protein; 562 AA.  
DE Human tissue plasminogen activator protein sequence.  
PN US5985607-A.  
PD 16-NOV-1999.

PA (CANG-) CANGENE CORP.  
Query Match 7.1%; Score 280; DB 3; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1306  
ID AAY99590 standard; protein; 562 AA.  
DE Human tissue-type plasminogen activator t-PA.  
PN WO200032759-A1.  
PD 08-JUN-2000.  
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
Query Match 7.1%; Score 280; DB 3; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1307  
ID RAU97700 standard; protein; 562 AA.  
DE Human tissue plasminogen activator (t-PA) protein sequence.  
PN WO200232446-A2.  
PD 25-APR-2002.  
PA (PFIZ) PFIZER LTD.  
PA (PFIZ) PFIZER INC.  
Query Match 7.1%; Score 280; DB 5; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1308  
ID AAE37130 standard; protein; 562 AA.  
DE Human tissue-type plasminogen activator (t-PA) protein.  
PN WO2003033009-A2.  
PD 24-APR-2003.  
PA (OMNI-) OMNIO AB.  
Query Match 7.1%; Score 280; DB 6; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1309  
ID ABR55851 standard; protein; 562 AA.  
DE Human tissue-type plasminogen activator (TPA).  
PN WO2003031464-A2.  
PD 17-APR-2003.  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
Query Match 7.1%; Score 280; DB 6; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1310  
ID ABUS7646 standard; protein; 562 AA.  
DE Differentially expressed breast cancer associated protein #33.  
PN US2002156263-A1.  
PD 24-OCT-2002.  
PA (CHEN/) CHEN H.  
Query Match 7.1%; Score 280; DB 6; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1311  
ID ADN95624 standard; protein; 562 AA.  
DE Human BSC/LEC-related protein sequence SeqID547.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 7.1%; Score 280; DB 7; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1312  
ID ADNA9698 standard; protein; 562 AA.  
DE Human tissue type plasminogen activator TPA protein SeqID 26.  
PN WO2004033651-A2.  
PD 22-APR-2004.  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
Query Match 7.1%; Score 280; DB 8; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1313  
ID ADO28679 standard; protein; 562 AA.  
DE Human tPA protein SEQ ID NO:108.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 8; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1314  
ID ABM80983 standard; protein; 562 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.  
PN WO2004030615-A2.

PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 280; DB 8; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1315  
ID ADO39248 standard; protein; 562 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.1%; Score 280; DB 8; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1316  
ID AAO30591 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1317  
ID AAO30599 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1318  
ID AAO30597 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/V158D/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1319  
ID ADJ55873 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1320  
ID ADJ55985 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1321  
ID ADJ55941 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316H.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1322  
ID ADJ55943 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1323  
ID ADJ56009 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ M298Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.

PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1324  
ID ADJ55879 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1325  
ID ADJ56014 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158T/ M298Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1326  
ID ADJ55881 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1327  
ID ADJ55936 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1328  
ID ADO10619 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #55.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.4e-07;  
RESULT 1329  
ID AAR74689 standard; protein; 520 AA.  
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).  
PN CN1082111-A.  
PD 16-FEB-1994.  
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
Query Match 7.1%; Score 279.5; DB 2; Length 520;  
Best Local Similarity 23.3%; Pred. No. 3e-07;  
RESULT 1330  
ID AAR09229 standard; protein; 526 AA.  
DE t-PA deletion variant d305.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279.5; DB 2; Length 526;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1331  
ID AAR09228 standard; protein; 526 AA.  
DE t-PA deletion variant d304.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279.5; DB 2; Length 526;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1332  
ID AAR09218 standard; protein; 528 AA.  
DE t-PA insertion variant i305 H, T, N, K, R, Q.  
PN WO9002798-A.  
PD 22-MAR-1990.

PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279.5; DB 2; Length 528;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1333  
ID ABG96427 standard; protein; 782 AA.  
DE Human ovarian cancer marker OV82.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.1%; Score 279.5; DB 5; Length 782;  
Best Local Similarity 20.8%; Pred. No. 4.4e-07;  
RESULT 1334  
ID AAB84871 standard; protein; 401 AA.  
DE Mutant blood coagulant factor VII (FVII-39).  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
Query Match 7.1%; Score 279; DB 4; Length 401;  
Best Local Similarity 22.8%; Pred. No. 2.5e-07;  
RESULT 1335  
ID AAR09250 standard; protein; 483 AA.  
DE t-PA variant d1-44, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1336  
ID AAR09248 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211A, K212R, V213R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 22.8%; Pred. No. 3e-07;  
RESULT 1337  
ID AAR09247 standard; protein; 483 AA.  
DE t-PA variant d1-44, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1338  
ID AAR09251 standard; protein; 483 AA.  
DE t-PA variant d1-44, T252R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1339  
ID AAR09263 standard; protein; 483 AA.  
DE t-PA variant Y67N, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1340  
ID AAR09252 standard; protein; 483 AA.  
DE t-PA variant d1-44, V213K, T252R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1341  
ID AAR09253 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.

Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3.e-07;  
RESULT 1342  
ID AAR09243 standard; protein; 525 AA.  
DE t-PA deletion variant d304-305.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 525;  
Best Local Similarity 23.0%; Pred. No. 3.2e-07;  
RESULT 1343  
ID AAR04186 standard; protein; 527 AA.  
DE Plasminogen activator.  
PN EP35468-A.  
PD 25-APR-1990.  
PA (CIBA ) CIBA GEIGY AG.  
PA (UCPG-) UCP GEN-PHARMA AG.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 3.3e-07;  
RESULT 1344  
ID AAR06236 standard; protein; 527 AA.  
DE Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJII ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.3e-07;  
RESULT 1345  
ID AAR09256 standard; protein; 527 AA.  
DE t-PA variant I210R, G211A, K212R, V213R, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 22.8%; Pred. No. 3.3e-07;  
RESULT 1346  
ID AAR09275 standard; protein; 527 AA.  
DE t-PA variant E410A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1347  
ID AAR09215 standard; protein; 527 AA.  
DE t-PA variant F305 H, T, N, K, R, Q.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1348  
ID AAR09262 standard; protein; 527 AA.  
DE t-PA variant Y67N, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1349  
ID AAR21596 standard; protein; 527 AA.  
DE tPA variant - E94A, D95A, N117Q.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1350  
ID AAR21595 standard; protein; 527 AA.  
DE tPA variant - D95G.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.

Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1351  
ID AAR21597 standard; protein; 527 AA.  
DE tPA variant - E94A, D95A, D236A, D238A, K240A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.3e-07;  
RESULT 1352  
ID AAR44813 standard; protein; 527 AA.  
DE Human tPA variant (N105, S107).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 3.3e-07;  
RESULT 1353  
ID AAR70905 standard; protein; 527 AA.  
DE Human t-PA variant (N103, A445, A449).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1354  
ID AAW57779 standard; protein; 527 AA.  
DE R275E-H417E human tissue-type plasminogen activator protein mutant.  
PN WO9821320-A2.  
PD 22-MAY-1998.  
PA (SCRI ) SCRIPPS RES INST.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1355  
ID AAR25435 standard; protein; 528 AA.  
DE t-PA variant R299D.  
PN WO9211377-A1.  
PD 09-JUL-1992.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 528;  
Best Local Similarity 23.5%; Pred. No. 3.3e-07;  
RESULT 1356  
ID AAR09219 standard; protein; 529 AA.  
DE t-PA insertion variant I305 HH.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 529;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1357  
ID AAP70882 standard; protein; 530 AA.  
DE Thrombolytic protein 1-19-1-21 having t-PA activity, deleted or replaced  
DE R275 is and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC.  
PA (LARS ) LARSEN G R.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1358  
ID AAP71659 standard; protein; 530 AA.  
DE Thrombolytic protein with t-PA activity where R275 is deleted or replaced  
DE and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC.  
PA (LARS ) LARSEN G R.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1359  
ID AAP70879 standard; protein; 530 AA.  
DE Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted

DE or replaced.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GEMV ) GENETICS INST INC.  
PA (LARS/) LARSEN G R.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1360  
ID AAP22277 standard; protein; 530 AA.  
DE Sequence of modified tPA-type thrombolytic proteins.  
PN WO8810119-A.  
PD 29-DEC-1988.  
PA (GEMV ) GENETICS INST INC.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1361  
ID AAP30001 standard; protein; 562 AA.  
DE Sequence of full length tissue plasminogen activator (t-Pa).  
PN EP93619-A.  
PD 09-NOV-1983.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 1; Length 562;  
Best Local Similarity 22.9%; Pred. No. 3.5e-07;  
RESULT 1362  
ID AAP94238 standard; protein; 562 AA.  
DE Human tissue plasminogen activator (t-Pa) gene.  
PN WO8900197-A.  
PD 12-JAN-1989.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1363  
ID AAR23803 standard; protein; 562 AA.  
DE t-PA (Ser 304) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1364  
ID AAR23801 standard; protein; 562 AA.  
DE Zymogen-like t-PA (His 305).  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1365  
ID AAW47536 standard; protein; 562 AA.  
DE Tissue plasminogen activator variant R275E.  
PN US5714372-A.  
PD 03-FEB-1998.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1366  
ID AAW47537 standard; protein; 562 AA.  
DE Tissue plasminogen activator variant I276P.  
PN US5714372-A.  
PD 03-FEB-1998.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1367  
ID AAW47535 standard; protein; 562 AA.  
DE Tissue plasminogen activator variant R275G.  
PN US5714372-A.  
PD 03-FEB-1998.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1368  
ID AAM48426 standard; protein; 562 AA.

DE Tissue type plasminogen activator, tPA.  
PN KR141262-B1.  
PD 15-JUN-1998.  
PA (GLDS ) LG CHEM LTD.  
Query Match 7.1%; Score 279; DB 3; Length 562;  
Best Local Similarity 22.9%; Pred. No. 3.5e-07;  
RESULT 1369  
ID ADR43718 standard; protein; 932 AA.  
DE Human protease PRIS-6, SEQ ID 6.  
PN WO20020736-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.1%; Score 279; DB 5; Length 932;  
Best Local Similarity 23.4%; Pred. No. 5.5e-07;  
RESULT 1370  
ID AAU82743 standard; protein; 970 AA.  
DE Amino acid sequence of novel human protease #42.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 7.1%; Score 279; DB 5; Length 970;  
Best Local Similarity 23.4%; Pred. No. 5.8e-07;  
RESULT 1371  
ID ABR39439 standard; protein; 264 AA.  
DE Human GENSET polypeptide clone name vCTRL-1.  
PN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GEST ) GENSET SA.  
Query Match 7.1%; Score 278.5; DB 6; Length 264;  
Best Local Similarity 27.2%; Pred. No. 1.8e-07;  
RESULT 1372  
ID AAB84867 standard; protein; 406 AA.  
DE Mutant blood coagulant factor VII (FVII-5).  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
Query Match 7.1%; Score 278.5; DB 4; Length 406;  
Best Local Similarity 23.0%; Pred. No. 2.7e-07;  
RESULT 1373  
ID AAM52183 standard; protein; 406 AA.  
DE Human FVII mutant V253N.  
PN WO200158935-A2.  
PD 16-AUG-2001.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 278.5; DB 4; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1374  
ID AAO30631 standard; protein; 406 AA.  
DE Human factor VII variant (K316Q/L305V/V158T/E296V/M298Q/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1375  
ID AAO30610 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1376  
ID AAO30615 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/K337A/V158T).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1377  
ID AAO30587 standard; protein; 406 AA.  
DE Human factor VII variant (S314E/L305V/V158T/E296V/M298Q/K337A).

PN WO2003037932-A2.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1378  
ID AAO30571 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158T).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1379  
ID AAO30630 standard; protein; 406 AA.  
DE Human factor VII variant (K316Q/L305V/V158D/E296V/M298Q/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1380  
ID AAO30574 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158D).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1381  
ID AAO30618 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/K337A/V158D).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1382  
ID AAO30586 standard; protein; 406 AA.  
DE Human factor VII variant (S314E/L305V/V158D/E296V/M298Q/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1383  
ID AAO30566 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1384  
ID ADJ55962 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1385  
ID ADJ56051 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158T/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1386  
ID ADJ55918 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.

PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1387  
ID ADJ56069 standard; protein; 406 AA.  
DE Human factor VII mutein F374Y/ V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1388  
ID ADJ55917 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1389  
ID ADJ55931 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1390  
ID ADJ55972 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1391  
ID ADJ56005 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1392  
ID ADJ56039 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158DK337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1393  
ID ADJ56041 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158D/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1394  
ID ADJ55928 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1395  
ID ADJ56064 standard; protein; 406 AA.  
DE Human factor VII mutein F374Y/ V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.

PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1396  
ID ADJ56074 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V253N.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1397  
ID ADJ55961 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1398  
ID ADJ56017 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ M298Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 2.7e-07;  
RESULT 1399  
ID ADJ55954 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1400  
ID ADJ55910 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1401  
ID ADJ55975 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1402  
ID ADJ56050 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1403  
ID ADO10592 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #28.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1404  
ID ADO10602 standard; protein; 406 AA.  
DE Human factor VII/VIIa protein mutant #38.  
PN WO2004029091-A2.  
PD 08-APR-2004.

PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1405  
ID AAP60056 standard; protein; 466 AA.  
DE Factor VII peptide encoded by cDNA clone lambda VII2463.  
PN EP200421-A.  
PD 10-DEC-1986.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.1%; Score 278.5; DB 1; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1406  
ID AAR52562 standard; protein; 466 AA.  
DE Factor VIII.  
PN WO9323074-A1.  
PD 25-NOV-1993.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
Query Match 7.1%; Score 278.5; DB 2; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1407  
ID AAM69606 standard; protein; 466 AA.  
DE Human Factor VIIa.  
PN WO9831394-A2.  
PD 23-JUL-1998.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 278.5; DB 2; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1408  
ID ADB36327 standard; protein; 466 AA.  
DE Human factor VII (F7) protein reference sequence.  
PN US2003087244-A1.  
PD 08-MAY-2003.  
PA (VITI-) VITIVITY INC.  
Query Match 7.1%; Score 278.5; DB 7; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1409  
ID AAR74682 standard; protein; 521 AA.  
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHSTVQT).  
PN CN1082111-A.  
PD 16-FEB-1994.  
PA (BIOB-) BIOENGINEERING INST ACAD MILITARY.  
Query Match 7.1%; Score 278.5; DB 2; Length 521;  
Best Local Similarity 22.9%; Pred. No. 3.4e-07;  
RESULT 1410  
ID AAR09222 standard; protein; 526 AA.  
DE t-PA deletion variant d298.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.3%; Pred. No. 3.5e-07;  
RESULT 1411  
ID AAR09224 standard; protein; 526 AA.  
DE t-PA deletion variant d300.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.3%; Pred. No. 3.5e-07;  
RESULT 1412  
ID AAR09223 standard; protein; 526 AA.  
DE t-PA deletion variant d299.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.3%; Pred. No. 3.5e-07;  
RESULT 1413  
ID AAR09225 standard; protein; 526 AA.  
DE t-PA deletion variant d301.  
PN WO9002798-A.  
PD 22-MAR-1990.

PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.1%; Pred. No. 3.5e-07;  
RESULT 1414  
ID AAR09227 standard; protein; 526 AA.  
DE t-PA deletion variant d303.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1415  
ID AAR12343 standard; protein; 562 AA.  
DE t-PA with -ve charged finger and/or kringle domain (2).  
PN JF03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 278.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 3.7e-07;  
RESULT 1416  
ID AAR12423 standard; protein; 562 AA.  
DE T-PA variant having Lys416 substitution (1).  
PN JF03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 278.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 3.7e-07;  
RESULT 1417  
ID AAR12424 standard; protein; 562 AA.  
DE T-PA variant having Lys416 substitution (3).  
PN JF03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 278.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 3.7e-07;  
RESULT 1418  
ID ADJ57511 standard; protein; 701 AA.  
DE Human FVII-IgG1 Fc domain fusion protein.  
PN WO2004006962-A2.  
PD 22-JAN-2004.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 701;  
Best Local Similarity 22.0%; Pred. No. 4.5e-07;  
RESULT 1419  
ID ABB71752 standard; protein; 408 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42048.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.0%; Score 278; DB 4; Length 408;  
Best Local Similarity 25.2%; Pred. No. 2.9e-07;  
RESULT 1420  
ID AAR35762 standard; protein; 448 AA.  
DE Factor X (X).  
PN WO9309804-A1.  
PD 27-MAY-1993.  
PA (SCRI ) SCRIPPS RES INST.  
Query Match 7.0%; Score 278; DB 2; Length 448;  
Best Local Similarity 24.0%; Pred. No. 3.2e-07;  
RESULT 1421  
ID AAR22511 standard; protein; 488 AA.  
DE Human Factor Xa1.  
PN WO9204378-A.  
PD 19-MAR-1992.  
PA (CORT-) COR THERAPEUTICS INC.  
Query Match 7.0%; Score 278; DB 2; Length 488;  
Best Local Similarity 24.0%; Pred. No. 3.4e-07;  
RESULT 1422  
ID ADQ17444 standard; protein; 488 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 261.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 7.0%; Score 278; DB 8; Length 488;  
Best Local Similarity 24.0%; Pred. No. 3.4e-07;  
RESULT 1423  
ID AAR09232 standard; protein; 523 AA.  
DE t-PA deletion variant d297-300.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 523;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1424  
ID AAR09244 standard; protein; 525 AA.  
DE t-PA deletion variant d297, d300.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 525;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1425  
ID AAR05806 standard; protein; 527 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.  
PN JF02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1426  
ID AAR22621 standard; protein; 527 AA.  
DE Mutated recombinant tPA.  
PN JF04094684-A.  
PD 26-MAR-1992.  
PA (KANF ) KANEKA CORP.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 3.7e-07;  
RESULT 1427  
ID AAR70896 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A339,A342).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1428  
ID AAR70858 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A296,A297,A298,A299).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.3%; Pred. No. 3.7e-07;  
RESULT 1429  
ID AAR70897 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A347,A348,A349,A351).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1430  
ID AAR70856 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A267).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.5%; Pred. No. 3.7e-07;  
RESULT 1431  
ID AAR70873 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A477).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.



Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1432  
ID AAP71450 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 1; Length 528;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1433  
ID AAR07033 standard; protein; 528 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen  
DE activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 528;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1434  
ID AAP70881 standard; protein; 530 AA.  
DE Thrombolytic protein 1-12-1-18 having t-PA activity, deleted or replaced  
DE R275 is and containing a modified N-linked glycosylation site.  
PN W08704722-A.  
PD 13-AUG-1987.  
PA (GEMY ) GENETICS INST INC.  
PA (LARS ) LARSEN G R.  
Query Match 7.0%; Score 278; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.7e-07;  
RESULT 1435  
ID AAR07034 standard; protein; 531 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen  
DE activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 531;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1436  
ID AAR13153 standard; protein; 558 AA.  
DE T-PA with -ve charged finger and/or kringle domain (8) .  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 558;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1437  
ID AAR13151 standard; protein; 559 AA.  
DE T-PA with -ve charged finger and/or kringle domain (4) .  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1438  
ID AAR13155 standard; protein; 559 AA.  
DE T-PA variant having Lys416 substitution (4) .  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1439  
ID AAR13154 standard; protein; 559 AA.  
DE T-PA variant having Lys416 substitution (2) .  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1440  
ID AAP81359 standard; protein; 562 AA.  
DE Pre-pro tissue plasminogen activator.

PN EP293934-A.  
PD 07-DEC-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (NOVO ) NOVO IND AS.  
PA (EISA ) EISA CO LTD.  
Query Match 7.0%; Score 278; DB 1; Length 562;  
Best Local Similarity 23.2%; Pred. No. 3.9e-07;  
RESULT 1441  
ID AAR07079 standard; protein; 562 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen  
DE activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 562;  
Best Local Similarity 22.9%; Pred. No. 3.9e-07;  
RESULT 1442  
ID AAR04702 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S; K419S  
DE with altered residues 87 and 419.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.0%; Score 278; DB 2; Length 562;  
Best Local Similarity 22.7%; Pred. No. 3.9e-07;  
RESULT 1443  
ID AAR3809 standard; protein; 562 AA.  
DE t-PA (Glu 299) mutant.  
PN W09206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.0%; Score 278; DB 2; Length 562;  
Best Local Similarity 23.5%; Pred. No. 3.9e-07;  
RESULT 1444  
ID ADI27177 standard; protein; 1113 AA.  
DE Mouse LRP binding family protein #17.  
PN W02003106657-A2.  
PD 24-DEC-2003.  
PA (STOW ) STOWERS INST MEDICAL RES.  
Query Match 7.0%; Score 278; DB 8; Length 1113;  
Best Local Similarity 20.7%; Pred. No. 7.4e-07;  
RESULT 1445  
ID ADR29372 standard; protein; 1113 AA.  
DE Murine Lrp4 dopaminergic neuronal marker SEQ ID NO:3.  
PN W02004085599-A1.  
PD 05-AUG-2004.  
PA (EISA ) EISAI CO LTD.  
Query Match 7.0%; Score 278; DB 8; Length 1113;  
Best Local Similarity 20.7%; Pred. No. 7.4e-07;  
RESULT 1446  
ID AAO30596 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158D) .  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1447  
ID AAO30549 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/K337A) .  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1448  
ID AAO30561 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/K337A) .  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;

Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1449  
ID AAO30570 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158T).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1450  
ID AAO30588 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1451  
ID AAO30623 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1452  
ID AAO30611 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158D).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1453  
ID AAO30567 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158D).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1454  
ID AAO30529 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/K316Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1455  
ID AAO30548 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1456  
ID AAO30564 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1457  
ID AAO30609 standard; protein; 406 AA.  
DE Human factor VII variant (K316H/L305V/V158T/E296V/M298Q/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;

RESULT 1458  
ID AAO30579 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1459  
ID AAO30581 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1460  
ID AAO30593 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158T).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1461  
ID AAO30624 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158D/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1462  
ID AAO30632 standard; protein; 406 AA.  
DE Human factor VII variant (L305V/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1463  
ID AAO30552 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1464  
ID AAO30580 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1465  
ID AAO30614 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1466  
ID AAO30608 standard; protein; 406 AA.  
DE Human factor VII variant (K316H/L305V/V158D/E296V/M298Q/K337A).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1467

ID AAO30625 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1468  
ID AAO30560 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1469  
ID ADJ55906 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1470  
ID ADJ56001 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ M298Q/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1471  
ID ADJ56022 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158D.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1472  
ID ADJ56024 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1473  
ID ADJ55878 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1474  
ID ADJ55983 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1475  
ID ADJ56019 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1476  
ID ADJ56037 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant F374Y/ S314E/ E296V/ M298Q/ L305V.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1477  
ID ADJ55909 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1478  
ID ADJ55953 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1479  
ID ADJ55955 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1480  
ID ADJ55893 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1481  
ID ADJ55932 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1482  
ID ADJ55897 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1483  
ID ADJ55956 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1484  
ID ADJ56036 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ E296V/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1485  
ID ADJ55875 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K337A.

PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1486  
ID ADJ55912 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1487  
ID ADJ55940 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1488  
ID ADJ56029 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298QV158T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1489  
ID ADJ56059 standard; protein; 406 AA.  
DE Human factor VII protein mutant F374Y/ V158D/ E296V/ M298Q/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.1%; Pred. No. 3.1e-07;  
RESULT 1490  
ID ADJ55891 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant S314E/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1491  
ID ADJ55923 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant E296V/ M298Q/ L305V/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1492  
ID ADJ55925 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1493  
ID ADJ55939 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1494  
ID ADJ55968 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ E296V/ M298Q/ L305V/ K316Q.  
PN WO2004000366-A1.

PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1495  
ID ADJ55969 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1496  
ID ADJ56010 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1497  
ID ADJ56026 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158D.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1498  
ID ADJ55861 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1499  
ID ADJ55950 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1500  
ID ADJ56020 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158D.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 8, 2005, 15:31:03 ; Search time 77 Seconds  
(without alignments)  
4788.273 Million cell updates/sec

Title: US-10-063-692-38  
Perfect score: 3945  
Sequence: 1 MBLCGWTQLGLFLQLLLIS.....LSTAFKVLPPKDWIERNMK 720

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	720	2 Q6UXH9	Q6uxh9 homo sapien
2	3936	99.8	720	2 Q6N062	Q6n062 homo sapien
3	3921.5	99.4	737	2 Q96JW2	Q96jw2 homo sapien
4	3612	91.6	720	2 Q8BU25	Q8bu25 m mus muscu
5	3612	91.6	720	2 Q8K2B8	Q8k2b8 mus musculus
6	2823	71.6	722	2 Q6DIV5	Q6div5 xenopus tro
7	2059	52.2	417	2 Q7IRE9	Q7ire9 homo sapien
8	949	24.1	181	2 Q9Y432	Q9y432 homo sapien
9	678	17.2	1019	2 Q8T9S1	Q8t9s1 tachypleus
10	672	17.0	1019	1 LFC TACTR	P28175 tachypleus
11	665	16.9	1019	1 LFC CARRO	Q26422 carcinoscor
12	665	16.9	1083	2 Q26423	Q26423 carcinoscor
13	608.5	15.4	680	2 Q868H7	Q868h7 branchiosto
14	604	15.3	680	2 Q868H5	Q868h5 branchiosto
15	597	15.1	688	2 Q868H6	Q868h6 branchiosto
16	576.5	14.6	688	2 Q868H4	Q868h4 branchiosto
17	507.5	12.9	698	2 Q6GPF9	Q6gpf9 xenopus lae
18	490.5	12.4	730	2 Q6Q1Q8	Q6q1q8 gallus gall
19	489.5	12.4	698	2 Q9PU71	Q9pu71 xenopus lae
20	483	12.2	701	2 Q9JJS9	Q9jjs9 rattus norv
21	482.5	12.2	703	2 Q8CHN8	Q8chn8 rattus norv
22	482	12.2	717	2 Q8AXR1	Q8axr1 xenopus lae
23	478	12.1	699	1 CRAR HUMAN	P48740 h complemen
24	475	12.0	704	1 CRAR_MOUSE	P98064 mus musculus
25	468	11.9	728	2 Q9GRS4	Q9grs4 homo sapien
26	467	11.8	697	2 Q8CG43	Q8cg43 rattus norv
27	466	11.8	717	2 Q8AXR0	Q8axr0 xenopus lae
28	459	11.6	733	2 Q8CD27	Q8cd27 mus musculus
29	457	11.6	719	2 Q9PVY2	Q9pyv2 triakis scy
30	452	11.5	733	2 Q920S0	Q920s0 mus musculus
31	448	11.4	745	2 Q9PVY3	Q9pyv3 cyprinus ca

32	447	11.3	686	2 Q6Q1Q9	Q6q1q9 gallus gall
33	436.5	11.1	681	2 Q7ZT70	Q7zt70 lampetra ja
34	428	10.8	707	1 C1R_MOUSE	Q8cg16 mus musculus
35	424	10.7	678	2 Q9JJS8	Q9jjs8 rattus norv
36	421.5	10.7	688	2 Q9PVY4	Q9pyv4 xenopus lae
37	420	10.6	643	2 Q9QX84	Q9qx84 rattus norv
38	417	10.6	685	2 Q9IWP0	Q9iwp0 mus musculus
39	416.5	10.6	706	2 Q8CFG9	Q8cfg9 mus musculus
40	412	10.4	685	2 Q9Z338	Q9z338 mus musculus
41	403.5	10.2	705	1 C1R_HUMAN	P00736 homo sapien
42	401.5	10.2	496	2 Q8CHP7	Q8chp7 cavia porce
43	401.5	10.2	746	2 Q8IAD8	Q8iad8 halocynthia
44	400.5	10.2	686	1 MAS2_HUMAN	P00187 homo sapien
45	398.5	10.2	746	2 O01654	O01654 halocynthia
46	395	10.1	721	2 Q7ZT69	Q7zt69 lampetra ja
47	395	10.0	721	2 Q7ZT69	Q7zt69 lampetra ja
48	384	9.7	688	2 Q8CFG8	Q8cfg8 mus musculus
49	382.5	9.7	752	2 O01655	O01655 halocynthia
50	382	9.7	722	2 Q8AW90	Q8aw90 lampetra ja
51	381	9.7	722	2 Q9PSZ5	Q9psz5 lampetra ja
52	380.5	9.6	687	2 Q69DK8	Q69dk8 sus scrofa
53	378.5	9.6	695	1 CASP_MESAU	P15156 mesocricetu
54	376	9.5	623	2 Q9JJF3	Q9jjf3 rattus norv
55	372.5	9.4	752	2 Q8IAD7	Q8iad7 halocynthia
56	371.5	9.4	541	2 Q9QX90	Q9qx90 rattus norv
57	370	9.4	688	2 Q8CG14	Q8cg14 mus musculus
58	369	9.4	694	2 Q8BJC4	Q8bjc4 mus musculus
59	368	9.3	685	2 Q9DGC1	Q9dgc1 cyprinus ca
60	366	9.3	685	2 Q9DGC0	Q9dgc0 cyprinus ca
61	364	9.2	688	2 Q8CH28	Q8ch28 mus musculus
62	364	9.2	694	2 Q8VBY4	Q8vby4 mus musculus
63	357	9.0	676	2 Q6DUJ6	Q6duj6 cyprinus ca
64	354	9.0	1524	2 Q91674	Q91674 xenopus lae
65	342	8.7	694	2 Q8R099	Q8r099 mus musculus
66	340.5	8.6	694	2 Q70542	Q70542 rattus norv
67	340.5	8.6	694	2 Q6P6T1	Q6p6t1 rattus norv
68	339.5	8.6	707	2 Q70W31	Q70w31 oncorhynch
69	335	8.5	645	2 Q7PY92	Q7py92 anopheles g
70	335	8.5	666	2 Q69BL0	Q69bl0 manduca sex
71	334	8.5	503	2 Q8AYE4	Q8aye4 brachydanio
72	334	8.5	688	1 C1S_HUMAN	P09871 homo sapien
73	331.5	8.4	1019	1 ENTK_HUMAN	P98073 homo sapien
74	329.5	8.4	1034	1 ENTK_PIG	P98074 sus scrofa
75	329.5	8.4	3565	1 CSM1_HUMAN	Q96p27 homo sapien
76	329	8.3	3564	1 CSM1_MOUSE	Q92313 mus musculus
77	328	8.3	855	1 ST14_HUMAN	Q9y5v6 homo sapien
78	318	8.1	3487	1 CSM2_HUMAN	Q7z408 homo sapien
79	317.5	8.0	1035	1 ENTK_BOVIN	P98072 bos taurus
80	316.5	8.0	460	1 PRTC_MOUSE	P33587 mus musculus
81	315	8.0	444	1 FA7_RABIT	P98139 oryctolagus
82	314.5	8.0	475	1 FA10_CHICK	P25155 gallus gall
83	314	8.0	855	1 ST14_MOUSE	P56677 mus musculus
84	313	7.9	855	2 Q9JJJ7	Q9jjj7 rattus norv
85	311	7.9	446	1 FA7_RAT	Q8k3u6 rattus norv
86	310.5	7.9	434	2 Q7T3B6	Q7t3b6 brachydanio
87	310.5	7.9	461	1 PRTC_HUMAN	P04070 homo sapien
88	309.5	7.8	799	2 Q6PF94	Q6pf94 mus musculus
89	309.5	7.8	811	1 TMS6_MOUSE	Q9dbi0 mus musculus
90	305	7.7	456	1 PRTC_CANFA	Q28278 canis famil
91	304	7.7	1069	1 ENTK_MOUSE	P97435 mus musculus
92	302.5	7.7	446	1 FA7_MOUSE	P70375 mus musculus
93	301.5	7.6	433	2 Q8JHD0	Q8jhd0 brachydanio
94	300.5	7.6	463	2 Q6IT10	Q6it10 pseudonaja
95	299.5	7.6	467	2 Q6IT09	Q6it09 pseudonaja
96	299	7.6	1111	2 Q80YN4	Q80yn4 rattus norv
97	298.5	7.6	433	2 Q90IK1	Q90yk1 brachydanio
98	298.5	7.6	553	2 Q6P719	Q6p719 xenopus lae
99	297.5	7.5	543	2 Q8BU99	Q8bu99 homo sapien
100	297.5	7.5	777	2 Q8CAN9	Q8can9 mus musculus
101	297	7.5	459	1 PRTC_PIG	Q9g1p2 sus scrofa
102	296	7.5	458	1 PRTC_RABIT	Q28661 oryctolagus
103	295.5	7.5	336	2 Q8CIR9	Q8cir9 mus musculus
104	295.5	7.5	441	2 Q804X2	Q804x2 fugu rubrip

105	295	7.5	425	2	Q804X7	Q804x7 gallus gall	178	263	6.7	653	2	Q8VCS4	Q8vcs4 mus musculus
106	294	7.5	461	2	Q68FY8	Q68fy8 rattus norv	179	262.5	6.7	300	2	Q819P4	Q819p4 aurelia aur
107	293.5	7.4	407	1	FA7_BOVIN	P22457 bos taurus	180	262.5	6.7	461	1	FA9_HUMAN	P00740 homo sapien
108	293	7.4	430	2	Q804X0	Q804x0 fugu rubrip	181	262.5	6.7	461	1	FA9_PANTR	Q95nd7 pan troglod
109	292	7.4	461	1	PRTC_RAT	P31394 rattus norv	182	262.5	6.7	1042	1	CORI_HUMAN	Q9ysq5 homo sapien
110	291.5	7.4	390	2	Q69DL3	Q69dl3 sus scrofa	183	262	6.6	477	1	URT2_DESRO	P15638 desmodus ro
111	291	7.4	376	1	FA10_TROCA	P81428 tropidechis	184	261.5	6.6	284	2	Q8AXQ8	Q8axq8 xenopus lae
112	291	7.4	475	2	Q804W9	Q804w9 fugu rubrip	185	261.5	6.6	442	1	UROK_PIG	P04185 sus scrofa
113	289.5	7.3	466	2	Q6SA95	Q6sa95 felis silve	186	261.5	6.6	561	2	Q7QDT9	Q7qdt9 anopheles g
114	288.5	7.3	802	2	Q6UXD8	Q6uxd8 homo sapien	187	261	6.6	431	1	UROK_HUMAN	P00749 homo sapien
115	287.5	7.3	811	1	TMS6_HUMAN	Q8iu80 homo sapien	188	260.5	6.6	433	1	UROK_BOVIN	Q05589 bos taurus
116	285.5	7.2	300	2	Q7PZ02	P7p202 anopheles g	189	260.5	6.6	264	2	Q9EQZ8	Q9eqz8 rattus norv
117	285.5	7.2	452	1	FA9_CANPA	P19540 canis famil	190	260.5	6.6	456	2	Q7TT43	Q7tt43 mus musculus
118	285	7.2	504	2	Q6PGW7	Q6pgw7 brachydanio	191	260.5	6.6	462	2	Q6PAG2	Q6pag2 xenopus lae
119	284	7.2	432	2	Q6GNA2	Q6гна2 xenopus lae	192	259	6.6	245	1	CTRB_GADMO	P80546 gadus morhu
120	284	7.2	974	2	Q90WD8	Q90wd8 bufo japoni	193	259	6.6	416	1	FA9_BOVIN	P00741 bos taurus
121	283.5	7.2	482	1	FA10_RAT	Q63207 rattus norv	194	259	6.6	474	2	Q8JHC8	Q8jhc8 brachydanio
122	283.5	7.2	589	2	Q6RJAS	Q6rja5 homo sapien	195	259	6.6	581	2	Q9XZM7	Q9xzm7 strongyloce
123	283	7.2	376	1	FA10_HOPST	P83370 hoptcephal	196	258.5	6.6	683	2	Q8MRH5	Q8mrh5 drosophila
124	282.5	7.2	320	2	Q8CIR7	Q8cir7 rattus norv	197	258.5	6.6	786	1	STUB_DROME	Q05319 drosophila
125	282	7.1	456	1	PRTC_BOVIN	P00745 bos taurus	198	258.5	6.6	787	2	Q9VEY6	Q9vey6 drosophila
126	282	7.1	1466	2	Q9GMD9	Q9gmd9 ornithorhyn	199	258	6.5	263	2	Q9FWQ6	P9pwq6 gadus morhu
127	282	7.1	469	2	Q7ZZ41	Q7zz41 brachydanio	200	258	6.5	433	1	UROK_PAPCY	P16227 papio cynoc
128	281.5	7.1	476	2	Q6GLK4	Q6glk4 xenopus lae	201	258	6.5	545	2	Q7QKS0	Q7qks0 anopheles g
129	281.5	7.1	558	2	Q6L711	Q6l711 rattus norv	202	258	6.5	612	2	Q804W7	Q804w7 fugu rubrip
130	281	7.1	481	1	FA10_MOUSE	Q88947 mus musculus	203	257.5	6.5	1004	2	P79953	P79953 xenopus lae
131	281	7.1	492	1	FA10_BOVIN	P00743 bos taurus	204	257	6.5	568	2	Q7Q8L2	Q7q8l2 anopheles g
132	280.5	7.1	264	1	CTRL_HUMAN	P40313 homo sapien	205	256.5	6.5	264	2	Q9D7P8	Q9d7p8 mus musculus
133	280.5	7.1	269	2	Q8IUW0	Q8iuw0 homo sapien	206	256.5	6.5	264	2	Q9ER05	Q9er05 mus musculus
134	280	7.1	562	1	TPA_HUMAN	P00750 homo sapien	207	255.5	6.5	268	2	Q642S8	Q642s8 xenopus tro
135	278.5	7.1	466	1	FA7_HUMAN	P08709 homo sapien	208	255.5	6.5	763	2	Q31430	Q31430 lampetra ja
136	278.5	7.1	824	2	Q6ICC2	Q6icc2 homo sapien	209	255	6.5	325	2	O15944	O15944 sarcophaga
137	278	7.0	408	2	Q9VW19	Q9vwc19 drosophila	210	255	6.5	845	2	Q6GR54	Q6gr54 xenopus lae
138	278	7.0	433	2	Q804X5	Q804x5 gallus gall	211	254.5	6.5	315	2	Q7TT44	Q7tt44 mus musculus
139	278	7.0	488	1	FA10_HUMAN	P00742 homo sapien	212	254.5	6.5	374	2	Q7QCS5	Q7qcs5 anopheles g
140	278	7.0	1113	1	CORI_MOUSE	Q92319 mus musculus	213	254.5	6.5	461	2	Q95ND6	Q95nd6 pan troglod
141	277	7.0	559	1	TPA_RAT	P19637 rattus norv	214	254	6.4	314	2	Q9VR15	Q9vr15 drosophila
142	276.5	7.0	655	1	HGFA_HUMAN	Q04756 homo sapien	215	254	6.4	617	1	THRB_RAT	P18292 rattus norv
143	276.5	7.0	679	2	Q96PQ8	Q96pq8 homo sapien	216	253.5	6.4	487	2	Q9NZP8	Q9nzp8 homo sapien
144	276	7.0	559	2	Q6P7U0	Q6p7u0 mus musculus	217	253.5	6.4	615	2	Q6GNK4	Q6gnk4 xenopus lae
145	275.5	7.0	1134	2	THRY7	Q7rt77 homo sapien	218	253.5	6.4	628	2	Q9VER6	Q9ver6 drosophila
146	274.5	7.0	625	1	THRB_BOVIN	P00735 bos taurus	219	253	6.4	471	2	Q804X6	Q804x6 gallus gall
147	274.5	7.0	654	2	Q6QNF4	Q6qnf4 canis famil	220	253	6.4	616	2	Q97507	Q97507 sus scrofa
148	274.5	7.0	1235	2	Q659T9	Q659t9 ciona intes	221	253	6.4	1070	2	P91972	P91972 aplysia cal
149	274.5	7.0	3670	1	CSM3_HUMAN	Q72407 homo sapien	222	252	6.4	260	2	Q6P2V9	Q6p2v9 xenopus tro
150	273.5	6.9	443	2	Q8JHC9	Q8jhc9 brachydanio	223	252	6.4	261	2	Q66HW9	Q66hw9 brachydanio
151	273.5	6.9	517	2	Q8K0D2	Q8k0d2 mus musculus	224	252	6.4	607	2	Q6DFJ5	Q6dfj5 xenopus lae
152	273.5	6.9	566	1	TPA_BOVIN	Q28198 bos taurus	225	251.5	6.4	261	2	Q7FC94	Q7fc94 anopheles g
153	273	6.9	366	2	Q9QX85	Q9qx85 rattus norv	226	251	6.4	295	2	Q8CIP7	Q8cip7 rattus norv
154	273	6.9	560	2	Q14520	Q14520 homo sapien	227	251	6.4	537	2	Q804W8	Q804w8 fugu rubrip
155	273	6.9	2796	1	CSM3_MOUSE	Q80t79 mus musculus	228	250.5	6.3	347	1	HPT_RABIT	P19007 oryctolagus
156	272.5	6.9	321	2	Q6MZL2	Q6mzl2 homo sapien	229	250	6.3	306	1	BS84_MOUSE	Q9er10 mus musculus
157	271.5	6.9	244	1	KLK6_HUMAN	Q92876 homo sapien	230	250	6.3	562	2	Q8SQZ3	Q8sqz3 sus scrofa
158	271.5	6.9	461	2	Q6I864	Q6ie64 rattus norv	231	250	6.3	845	2	Q63ZQ6	Q63zq6 xenopus lae
159	271	6.9	433	2	Q8MHY7	Q8mhy7 oryctolagus	232	250	6.3	1379	2	Q9V4N6	Q9v4n6 drosophila
160	271	6.9	433	2	Q8MIL0	Q8mil0 oryctolagus	233	250	6.3	1397	2	Q7KQO9	Q7kqo9 drosophila
161	271	6.9	559	1	TPA_MOUSE	P12114 mus musculus	234	249.5	6.3	400	2	Q27081	Q27081 tachypyleus
162	270	6.8	477	1	URT1_DESRO	P98119 desmodus ro	235	249.5	6.3	875	1	NETR_HUMAN	P56730 homo sapien
163	270	6.8	490	1	FA10_RABIT	O19045 oryctolagus	236	249	6.3	263	2	Q6GPI1	Q6gpi1 homo sapien
164	269	6.8	261	2	Q6DHD9	O19045 desmodus ro	237	249	6.3	263	2	Q9CR35	Q9cr35 m mus muscu
165	269	6.8	643	2	Q97506	Q6dh9 brachydanio	238	248.5	6.3	459	1	FA9_MOUSE	P16294 mus musculus
166	269	6.8	833	2	Q96442	Q96442 strongyloce	239	248.5	6.3	645	2	Q7PWE4	Q7pwe4 anopheles g
167	267.5	6.8	268	2	Q6GQE9	Q6gqe9 xenopus lae	240	248	6.3	1335	2	Q7Q137	Q7q137 anopheles g
168	267	6.8	339	2	Q9QX91	Q9qx91 rattus norv	241	248	6.3	259	2	Q6AZC2	Q6azc2 brachydanio
169	267	6.8	455	2	Q7SY86	Q7sy86 xenopus lae	242	248	6.3	261	2	Q9W7Q4	Q9w7q4 paralichthy
170	267	6.8	868	2	Q9Y1V3	Q9ylv3 polyanthroca	243	248	6.3	263	1	CTRB_HUMAN	P17538 homo sapien
171	266	6.7	352	2	Q7KVN3	Q7kvm3 drosophila	244	248	6.3	540	2	Q800Y7	Q800y7 meleagris g
172	265.5	6.7	250	2	Q9V514	Q9v514 drosophila	245	248	6.3	638	1	KAL_HUMAN	P03952 homo sapien
173	264.5	6.7	431	1	URTB_DESRO	P98121 desmodus ro	246	248	6.3	764	1	CFAB_PANTR	Q864w0 pan troglod
174	264.5	6.7	613	1	THRB_MOUSE	P19221 mus musculus	247	248	6.3	775	2	Q6P550	Q6p550 mus musculus
175	264	6.7	653	1	HGFA_MOUSE	Q9r098 mus musculus	248	248	6.3	991	2	Q6NZM2	Q6nzm2 mus musculus
176	263.5	6.7	263	2	Q7SX97	Q7sx97 brachydanio	249	247.5	6.3	307	2	Q7TML0	Q7tml0 mus musculus
177	263	6.7	270	2	Q7Q144	Q7qi44 anopheles g	250	247.5	6.3	311	2	Q9W2C2	Q9w2c2 drosophila

251	247.5	6.3	991	1	BMP1_MOUSE	P98063	mus musculus	324	237.5	6.0	415	2	Q7PY21	Q7py21 anopheles g
252	247	6.3	235	2	Q28731	Q28731 oryctolagus	325	237.5	6.0	735	2	O57381	O57381 xenopus lae	
253	247	6.3	270	2	Q7PK67	Q7pk67 anopheles g	326	237.5	6.0	735	2	O66K13	O66K13 xenopus lae	
254	247	6.3	275	1	TRYT_CANFA	P15944 canis famil	327	237.5	6.0	810	1	PLAN_BRIEU	Q29485 erinaceus e	
255	247	6.3	364	2	Q917V4	Q917v4 drosophila	328	237	6.0	237	2	Q91515	Q91515 fugu rubrip	
256	247	6.3	386	2	Q81924	Q81924 bombyx mori	329	237	6.0	263	1	CTRB_RAT	P07338 rattus norv	
257	247	6.3	764	1	CFAB_HUMAN	P00751 homo sapien	330	237	6.0	263	2	Q6PGS4	Q6pgs4 xenopus lae	
258	247	6.3	986	1	BMP1_HUMAN	P13497 homo sapien	331	236.5	6.0	251	2	Q7Q9W2	Q7q9w2 anopheles g	
259	246.5	6.2	235	2	Q90387	Q90387 cynops pyrr	332	236.5	6.0	274	1	MCT6_RAT	P50343 rattus norv	
260	246.5	6.2	264	2	Q9D960	Q9d960 mus musculus	333	236.5	6.0	707	1	BMP1_XENLA	P98070 xenopus lae	
261	246.5	6.2	297	2	Q88781	Q88781 rattus ratt	334	236.5	6.0	761	2	Q99JC8	Q99jc8 rattus norv	
262	246.5	6.2	333	2	Q960G4	Q960G4 homo sapien	335	236.5	6.0	1013	2	Q62381	Q62381 mus musculus	
263	246.5	6.2	347	1	HPT_ATEGE	P50417 ateles geof	336	236	6.0	239	2	Q7Q057	Q7q057 anopheles g	
264	246.5	6.2	622	1	THRB_HUMAN	P00734 homo sapien	337	236	6.0	812	1	PLMN_MOUSE	P20918 mus musculus	
265	246.5	6.2	622	2	Q7Z7F3	Q7z7f3 homo sapien	338	235.5	6.0	260	2	Q9W7Q3	Q9w7q3 paralichthy	
266	246	6.2	243	2	Q7PK66	Q7pk66 anopheles g	339	235.5	6.0	369	2	Q6AXZ6	Q6axz6 rattus norv	
267	246	6.2	263	2	Q9D8X8	Q9d8x8 mus musculus	340	235.5	6.0	453	2	Q812A6	Q812a6 mus musculus	
268	246	6.2	764	1	CFAB_GORGO	Q864v9 gorilla gor	341	235	6.0	270	1	TRYT_MERUN	P50342 meriones un	
269	246	6.2	812	1	PLMN_BOVIN	P06868 bos taurus	342	235	6.0	336	2	Q7RTY5	Q7rtY5 homo sapien	
270	245.5	6.2	265	2	Q804G1	Q804g1 brachydanio	343	235	6.0	345	2	Q28800	Q28800 pan troglod	
271	245.5	6.2	369	2	Q7QKL1	Q7qkl1 anopheles g	344	235	6.0	524	2	Q7SXH8	Q7sxh8 brachydanio	
272	245.5	6.2	467	2	Q967X8	Q967x8 panulirus a	345	235	6.0	812	1	PLMN_RAT	Q01177 rattus norv	
273	245	6.2	248	2	Q7PK68	Q7pk68 anopheles g	346	235	6.0	1420	1	APOA_MACMU	P14417 macaca mula	
274	245	6.2	263	2	Q6GNF7	Q6gnf7 xenopus lae	347	234.5	5.9	395	2	Q9BZW1	Q9bzW1 homo sapien	
275	245	6.2	638	2	Q8R0P5	Q8r0p5 mus musculus	348	234.5	5.9	418	2	Q6NP02	Q6np02 drosophila	
276	245	6.2	639	1	BMPH_STRPU	P98069 strongyloce	349	234.5	5.9	453	1	TMS3_MOUSE	Q8k1t0 mus musculus	
277	244.5	6.2	608	2	Q9PTW7	Q9ptw7 struthio ca	350	234.5	5.9	489	2	Q7Q432	Q7q432 anopheles g	
278	244	6.2	263	2	Q9DC86	Q9dc86 mus musculus	351	234.5	5.9	624	2	Q9DAT3	Q9dat3 mus musculus	
279	244	6.2	322	2	Q920S2	Q920s2 mus musculus	352	234	5.9	575	2	Q81RB8	Q81rb8 drosophila	
280	244	6.2	638	1	KAL_MOUSE	P26262 mus musculus	353	233.5	5.9	263	1	CTRA_GADMO	P47796 gadus morhu	
281	243.5	6.2	245	2	Q7PQ00	Q7pq00 anopheles g	354	233.5	5.9	267	2	Q7SZ51	Q7sz51 brachydanio	
282	243.5	6.2	285	2	Q8CG42	Q8cg42 rattus norv	355	233.5	5.9	420	2	Q90504	Q90504 eptaretus	
283	243.5	6.2	435	1	SNAK_DROME	P05049 drosophila	356	233	5.9	273	2	Q9XSM1	Q9xsm1 ovis aries	
284	243.5	6.2	764	1	CFAB_PONPY	Q864w1 pongo pygma	357	233	5.9	445	2	Q8CJ17	Q8cj17 rattus norv	
285	243	6.2	273	1	TRYT_SHEEP	Q9xsm2 ovis aries	358	232.5	5.9	936	2	Q81FX2	Q81fx2 crassostrea	
286	243	6.2	282	2	Q9DAI3	Q9daI3 mus musculus	359	232.5	5.9	1013	2	Q43897	Q43897 homo sapien	
287	243	6.2	412	2	Q804X1	Q804x1 fugu rubrip	360	232.5	5.9	1013	2	Q9NQS4	Q9nq4 homo sapien	
288	242.5	6.1	564	2	Q8MKB1	Q8mb1 oryctolagus	361	232	5.9	283	2	Q7Q056	Q7q056 anopheles g	
289	242.5	6.1	574	2	Q86RL8	Q86rl8 ilyanassa o	362	232	5.9	416	1	HEFS_RAT	Q05511 rattus norv	
290	242.5	6.1	691	2	O57658	Q57658 gallus gall	363	232	5.9	638	1	KAL_RAT	P14272 rattus norv	
291	242.5	6.1	1019	2	O57382	Q57382 xenopus lae	364	231.5	5.9	269	1	EL2_BOVIN	Q29461 bos taurus	
292	242	6.1	247	2	Q7PK69	Q7pk69 anopheles g	365	231.5	5.9	270	2	Q91039	Q91039 gadus morhu	
293	241.5	6.1	279	2	Q99MS4	Q99ms4 mus musculus	366	231.5	5.9	371	2	Q8CJ16	Q8cj16 rattus norv	
294	241.5	6.1	314	2	Q7QLC2	Q7qlc2 anopheles g	367	231.5	5.9	483	2	Q8T8X4	Q8t8x4 drosophila	
295	241.5	6.1	416	2	Q86T26	Q86t26 homo sapien	368	231.5	5.9	483	2	Q9VK10	Q9vk10 drosophila	
296	241	6.1	306	2	Q7Q058	Q7q058 anopheles g	369	231.5	5.9	624	2	Q9SME7	Q9sme7 oryctolagus	
297	241	6.1	346	1	HPT_MESAU	Q35086 mesocricetu	370	231.5	5.9	666	2	Q6VPU8	Q6vpU8 drosophila	
298	241	6.1	818	2	Q6PEA6	Q6pba6 brachydanio	371	231	5.9	242	2	Q93266	Q93266 pseudopleur	
299	241	6.1	1415	2	Q8MJ16	Q8mj16 bos taurus	372	231	5.9	1008	2	Q9DER7	Q9der7 gallus gall	
300	240.5	6.1	238	2	Q9W7Q6	Q9w7q6 paralichthy	373	231	5.9	1012	2	Q9WVM6	Q9wvm6 mus musculus	
301	240.5	6.1	422	2	Q8WVC1	Q8wvc1 homo sapien	374	230.5	5.8	259	2	Q69EZ7	Q69ez7 homo sapien	
302	240.5	6.1	441	2	Q7QKH8	Q7qkh8 anopheles g	375	230.5	5.8	295	2	Q69EZ8	Q69ez8 homo sapien	
303	240	6.1	242	2	Q92099	Q92099 paranotothe	376	230	5.8	244	2	Q8QGM3	Q8qgm3 anguilla ja	
304	240	6.1	1059	2	Q7Z411	Q7z411 homo sapien	377	230	5.8	265	2	Q9VVT3	Q9vt3 drosophila	
305	239.5	6.1	240	2	Q98TH0	Q98th0 engraulis j	378	230	5.8	318	2	Q7RTY9	Q7rtY9 homo sapien	
306	239.5	6.1	406	1	HPT_HUMAN	P00738 homo sapien	379	230	5.8	372	2	Q9Y1K6	Q9y1k6 anopheles g	
307	239.5	6.1	1015	2	Q9Y6L7	Q9y6l7 homo sapien	380	230	5.8	607	2	Q91001	Q91001 gallus gall	
308	239.5	6.1	1078	2	Q9UQ00	Q9uq00 homo sapien	381	229.5	5.8	329	1	HPT_CANFA	P19006 canis famil	
309	239.5	6.1	3567	2	Q9ES77	Q9es77 mus musculus	382	229.5	5.8	374	2	Q9VTG2	Q9vtg2 drosophila	
310	239	6.1	245	1	CTRA_BOVIN	P00766 bos taurus	383	229.5	5.8	624	1	FALL_MOUSE	Q91477 mus musculus	
311	239	6.1	314	2	Q7PZ03	Q7pz03 anopheles g	384	229	5.8	267	2	Q9BK47	Q9bk47 luidia foli	
312	239	6.1	436	1	HEPS_MOUSE	Q35453 mus musculus	385	229	5.8	274	2	Q924N9	Q924n9 mus musculus	
313	239	6.1	456	2	Q7QC30	Q7qc30 anopheles g	386	229	5.8	722	2	Q6NUF5	Q6nuf5 xenopus lae	
314	239	6.1	977	2	Q91925	Q91925 xenopus lae	387	229	5.8	733	2	Q9VXT9	Q9vxt9 drosophila	
315	238.5	6.0	268	2	Q46151	Q46151 pacifastacu	388	229	5.8	845	2	Q9DGR1	Q9dgr1 xenopus lae	
316	238.5	6.0	578	2	Q6Q017	Q6q0i7 bos taurus	389	228.5	5.8	347	2	Q63927	Q63927 mus sp. hap	
317	238	6.0	237	1	TRYP_ASTFL	P00765 astacus flu	390	228.5	5.8	352	2	Q6UWB4	Q6uwb4 homo sapien	
318	238	6.0	263	1	CTR2_CANFA	P04813 canis famil	391	228.5	5.8	513	2	Q7PKB9	Q7pkb9 anopheles g	
319	238	6.0	275	1	TRYT_PIG	P912d1 sus scrofa	392	228.5	5.8	600	2	O17490	O17490 anopheles g	
320	238	6.0	375	1	PCE_TACTR	P21902 tachypleus	393	228.5	5.8	600	2	Q7PV58	Q7pv58 anopheles g	
321	238	6.0	435	2	Q9NFF2	Q9nfy2 anopheles g	394	228.5	5.8	1084	2	Q9BP40	Q9bp40 halocynthia	
322	238	6.0	767	2	Q9DGR2	Q9dgr2 xenopus lae	395	228.5	5.8	2516	2	Q7TQ52	Q7td52 mus musculus	
323	237.5	6.0	288	2	Q7QAX5	Q7qax5 anopheles g	396	228.5	5.8	2526	2	Q7TQ51	Q7td51 mus musculus	



397	228.5	5.8	2531	1	NTCL_MOUSE	Q01705 mus musculus	470	223	5.7	529	2	Q7Q299	Q7q299 anopheles g
398	228.5	5.8	2531	2	Q8K428	Q8k428 mus musculus	471	222.5	5.6	411	2	Q7VUF0	Q7vuf0 drosophila
399	228.5	5.8	2531	2	Q7TQ50	Q7td50 mus musculus	472	222.5	5.6	417	1	HEPS_HUMAN	P05981 homo sapien
400	228	5.8	3687	2	Q9W332	Q9w332 drosophila	473	222.5	5.6	434	1	UROK_CHICK	P15120 gallus gall
401	227.5	5.8	235	2	Q91004	Q91004 gekko gekko	474	222.5	5.6	455	1	TMS_MOUSE	Q9er04 mus musculus
402	227.5	5.8	242	1	TRY1_SALSA	P35031 salmo salar	475	222.5	5.6	790	1	PLMN_PIG	P06867 sus scrofa
403	227.5	5.8	251	1	KLKE_HUMAN	Q9p033 homo sapien	476	222.5	5.6	957	2	Q75UQ6	Q75uq6 achaeaxanea
404	227.5	5.8	251	1	Q6B089	Q6b089 homo sapien	477	222	5.6	267	2	Q9V942	Q9v942 drosophila
405	227.5	5.8	349	2	Q28802	Q28802 pan troglod	478	222	5.6	269	1	EL2_PIG	P08419 sus scrofa
406	227.5	5.8	385	2	Q92659	Q92659 homo sapien	479	222	5.6	273	2	Q92IN4	Q92in4 mus musculus
407	227.5	5.8	418	2	Q6IE15	Q6ie15 rattus norv	480	222	5.6	275	1	TRB2_HUMAN	P20331 homo sapien
408	227.5	5.8	714	2	Q7PWE5	Q7pwe5 anopheles g	481	222	5.6	275	1	TRYA_HUMAN	P15157 homo sapien
409	227	5.8	242	2	Q6RI79	Q6ri79 tautogolabr	482	222	5.6	275	2	Q86TM8	Q86tm8 homo sapien
410	227	5.8	263	2	Q7SY84	Q7sy84 xenopus lae	483	222	5.6	276	2	Q86UA5	Q86ua5 homo sapien
411	227	5.8	275	2	Q7YS62	Q7ys62 equus cabal	484	222	5.6	282	2	Q6NZY1	Q6nzy1 homo sapien
412	227	5.8	324	1	TEST_MOUSE	Q9yhj7 mus musculus	485	222	5.6	422	1	DES1_HUMAN	Q9u152 homo sapien
413	227	5.8	336	2	Q80YD8	Q80yd8 mus musculus	486	222	5.6	423	2	Q6UW31	Q6uw31 homo sapien
414	227	5.8	317	2	Q8B210	Q8bz10 mus musculus	487	222	5.6	561	2	Q7PN97	Q7pn97 anopheles g
415	227	5.8	488	2	Q9TYH4	Q9tyh4 schistosoma	488	222	5.6	860	2	Q7QAH1	Q7qah1 anopheles g
416	227	5.8	1464	2	Q23395	Q23395 drosophila	489	221.5	5.6	271	2	Q803Z4	Q803z4 brachydanio
417	227	5.8	1464	2	Q24132	Q24132 drosophila	490	221.5	5.6	453	2	Q6ZMC3	Q6zmc3 homo sapien
418	227	5.8	1464	2	Q9VC47	Q9vc47 drosophila	491	221.5	5.6	2531	1	NTCL_RAT	Q7t008 rattus norv
419	226.5	5.7	238	1	TRY3_SALSA	P35033 salmo salar	492	221.5	5.6	3620	2	Q9TU53	Q9tu53 canis famil
420	226.5	5.7	257	2	Q8B204	Q8bz04 mus musculus	493	221	5.6	227	2	Q7PHB4	Q7phb4 anopheles g
421	226.5	5.7	371	2	Q8MS52	Q8ms52 drosophila	494	221	5.6	231	1	TRY2_SALSA	P35032 salmo salar
422	226.5	5.7	761	1	NETR_MOUSE	Q08762 mus musculus	495	221	5.6	258	2	Q97359	Q97359 phaeton coc
423	226.5	5.7	855	2	Q7Z410	Q7z410 homo sapien	496	221	5.6	268	1	CLCR_RAT	P55091 rattus norv
424	226.5	5.7	1429	1	ATRN_HUMAN	Q75882 homo sapien	497	221	5.6	273	2	MCT7_RAT	P27435 rattus norv
425	226	5.7	394	1	URTQ DESRO	P49150 desmodus ro	498	221	5.6	273	2	Q6PEW8	Q6pew8 rattus norv
426	226	5.7	432	2	Q6UX37	Q6ux37 homo sapien	499	221	5.6	314	2	Q6RUT2	Q6rut2 mus musculus
427	226	5.7	437	1	TMS4_HUMAN	Q9nre4 homo sapien	500	221	5.6	974	2	P91658	P91658 drosophila
428	226	5.7	430	2	Q6P7D7	Q6p7d7 rattus norv	501	221	5.6	1234	2	Q7PIQ7	Q7piq7 anopheles g
429	226	5.7	625	1	FALL1_HUMAN	P03951 homo sapien	502	221	5.6	1322	2	Q7PNR7	Q7pnr7 anopheles g
430	225.5	5.7	312	2	Q7M755	Q7m755 mus musculus	503	220.5	5.6	242	2	Q8QV84	Q8qv84 mus musculus
431	225.5	5.7	347	1	HPT_PIG	Q8sp87 sus scrofa	504	220.5	5.6	250	2	Q8QGR5	Q8qgr5 mus musculus
432	225.5	5.7	418	2	Q8SZK2	Q8szk2 drosophila	505	220.5	5.6	272	2	Q7Q9W5	Q7q9w5 anopheles g
433	225.5	5.7	418	2	Q9VA87	Q9va87 drosophila	506	220.5	5.6	277	2	Q8QWM7	Q8qwm7 mus musculus
434	225.5	5.7	429	2	Q8AVB0	Q8avb0 brachydanio	507	220.5	5.6	360	2	O17489	O17489 anopheles g
435	225.5	5.7	445	2	Q7Q956	Q7q956 anopheles g	508	220.5	5.6	360	2	Q7PEV7	Q7pev7 anopheles g
436	225.5	5.7	457	1	TMS5_HUMAN	Q9h3s3 homo sapien	509	220.5	5.6	468	2	Q9U0G3	Q9u0g3 pacifastacu
437	225	5.7	243	2	Q7PY20	Q7py20 anopheles g	510	220.5	5.6	506	2	Q7PR64	Q7pr64 anopheles g
438	225	5.7	328	2	Q8Q240	Q8q240 rattus norv	511	220.5	5.6	808	2	Q7YU36	Q7yu36 drosophila
439	225	5.7	387	2	Q9XY57	Q9xy57 ctenocephal	512	220.5	5.6	1067	1	TLD_DROME	P25723 drosophila
440	225	5.7	333	2	Q6RX66	Q6rx66 armigeres s	513	220	5.6	260	2	Q9W7P9	Q9w7p9 paralichthy
441	225	5.7	432	2	Q7QKL4	Q7qkl4 anopheles g	514	220	5.6	261	2	Q9G2G7	Q9g2g7 culex pipie
442	225	5.7	455	2	Q8CDR0	Q8cdr0 mus musculus	515	220	5.6	275	1	TRB1_HUMAN	Q1561 homo sapien
443	225	5.7	490	2	Q920K3	Q920k3 rattus norv	516	220	5.6	331	2	Q6B051	Q6b051 homo sapien
444	225	5.7	490	2	Q7TN04	P00748 homo sapien	517	220	5.6	331	2	Q8R1A6	Q8rx17 mus musculus
445	225	5.7	615	1	FAL12_HUMAN	Q88301 mus musculus	518	220	5.6	568	2	Q7Q064	Q7q064 anopheles g
446	224.5	5.7	246	2	Q88301	Q88301 mus musculus	519	220	5.6	568	2	Q7Q064	Q7q064 anopheles g
447	224.5	5.7	251	2	Q54854	Q54854 rattus norv	520	219.5	5.6	244	1	TRV2_XENLA	P70059 xenopus lae
448	224.5	5.7	253	2	Q91Y82	Q91y82 mus musculus	521	219.5	5.6	248	2	Q7QAX4	Q7qax4 anopheles g
449	224.5	5.7	271	1	EL2_RAT	Q91y82 mus musculus	522	219.5	5.6	248	2	Q7S2T1	Q7s2t1 xenopus lae
450	224.5	5.7	274	1	TRY1_ANOGA	P35035 anopheles g	523	219.5	5.6	255	2	Q9G1Y0	Q9g1y0 gallieria me
451	224.5	5.7	347	1	HPT_MOUSE	Q61646 mus musculus	524	219.5	5.6	255	2	Q6GNU2	Q6gnu2 xenopus lae
452	224.5	5.7	1022	1	TLD_BRARE	Q57460 brachydanio	525	219.5	5.6	271	1	EL2_MOUSE	P05208 mus musculus
453	224.5	5.7	1427	2	Q8VIB7	Q8vib7 mesocricetu	526	219.5	5.6	347	1	HPT_MUSCR	Q60574 mus caroli
454	224	5.7	222	2	Q8AV11	Q8av11 oncorhynchus	527	219.5	5.6	761	1	CFAB_MOUSE	P04186 mus musculus
455	224	5.7	242	2	Q7TIR8	Q7tir8 pangasius h	528	219.5	5.6	1378	2	Q68HV2	Q68hv2 mus musculus
456	224	5.7	245	1	CTRB_BOVIN	P00767 bos taurus	529	219.5	5.6	1444	2	Q6A051	Q6a051 mus musculus
457	224	5.7	248	2	O16126	O16126 boltenia vi	530	219	5.6	276	2	Q7QAM5	Q7qam5 anopheles g
458	224	5.7	261	1	KLK2_HORSE	Q6h321 equus cabal	531	219	5.6	318	1	Q80UR4	Q80ur4 mus musculus
459	224	5.7	490	1	TMS2_MOUSE	Q9j1q8 mus musculus	532	219	5.6	343	2	PS8_HUMAN	O16651 homo sapien
460	224	5.7	1174	2	Q9VYR4	Q9vyr4 drosophila	533	219	5.6	365	2	Q97366	Q97366 holotrichia
461	224	5.7	2622	2	Q7PSV8	Q7psv8 anopheles g	534	218.5	5.5	374	2	Q81862	Q81862 dermacentor
462	223.5	5.7	234	2	Q90244	Q90244 acipenser t	535	218.5	5.5	375	2	Q817W8	Q817w8 demacator
463	223.5	5.7	266	2	Q90244	Q9w7q0 paralichthy	536	218.5	5.5	435	1	TMS4_MOUSE	O8vc45 mus musculus
464	223.5	5.7	348	1	HPTR_HUMAN	P00739 homo sapien	537	218.5	5.5	787	2	Q6SIG0	O6sig0 naja kaouth
465	223.5	5.7	1242	1	JAG1_BRARE	Q90y57 brachydanio	538	218.5	5.5	1007	2	Q8J128	O8ji28 xenopus lae
466	223.5	5.7	1629	2	Q9V513	Q9v513 drosophila	539	218.5	5.5	1379	2	Q6T256	O6t256 homo sapien
467	223.5	5.7	1674	2	Q8SY35	Q8sy35 drosophila	540	218	5.5	232	2	Q7PG16	Q7pg16 anopheles g
468	223	5.7	242	2	Q9W7Q7	Q9w7q7 paralichthy	541	218	5.5	242	2	Q7SX90	Q7srx90 brachydanio
469	223	5.7	454	1	TMS3_HUMAN	P57727 homo sapien	542	218	5.5	271	2	Q54213	O54213 streptomyce

543	217.5	5.5	243	2	Q7MA13	Q7m413 megabombus	616	212.5	5.4	339	2	Q99L44	Q99L44 mus musculus
544	217.5	5.5	269	2	Q6ISU5	Q6ie14 homo sapien	617	212.5	5.4	420	2	Q6IE14	Q6ie14 rattus norv
545	217.5	5.5	324	2	Q7PXE3	Q7pxe3 anopheles g	618	212.5	5.4	425	2	Q7P285	Q7p285 anopheles g
546	217.5	5.5	3646	2	Q7Q737	Q7q737 anopheles g	619	212.5	5.4	778	2	Q9V519	Q9v519 drosophila
547	217.5	5.5	239	1	KLK2 CAVPO	P12323 cavia porce	620	212	5.4	260	1	NRPN MOUSE	Q61955 mus musculus
548	217.5	5.5	268	1	CLCR HUMAN	Q98955 homo sapien	621	212	5.4	274	2	Q6GNF0	Q6gnf0 xenopus lae
549	217.5	5.5	273	1	MCT7 MOUSE	Q28844 mus musculus	622	212	5.4	340	2	Q8BUV6	Q8bjv6 mus musculus
550	217.5	5.5	275	2	Q6ERZ6	Q6erz6 homo sapien	623	212	5.4	1322	2	Q9NJS5	Q9nj55 anopheles g
551	217.5	5.5	280	2	Q6GLK1	Q6glk1 xenopus lae	624	211.5	5.4	418	1	HATT HUMAN	Q60235 homo sapien
552	217.5	5.5	597	2	Q35727	Q35727 mus musculus	625	211.5	5.4	501	2	Q7QC70	Q7qc70 anopheles g
553	217.5	5.5	603	1	FA12 CAVPO	Q04622 cavia porce	626	211.5	5.4	629	2	Q6AZS7	Q6azs7 xenopus lae
554	217.5	5.5	2703	1	NOLC DROME	P07207 drosophila	627	211.5	5.4	719	2	Q6DJ90	Q6dj90 xenopus tro
555	216.5	5.5	235	2	Q6BAE4	Q6ba44 bos taurus	628	211	5.3	237	2	Q29464	Q29464 bos taurus
556	216.5	5.5	277	2	Q96899	Q96899 scolopendra	629	211	5.3	276	1	MCT6 MOUSE	F21845 mus musculus
557	216.5	5.5	346	2	Q7LE20	Q7le20 homo sapien	630	211	5.3	681	2	Q7Q554	Q7q554 anopheles g
558	216.5	5.5	346	2	Q28801	Q28801 pan troglod	631	211	5.3	1218	1	JAG1 HUMAN	P78504 homo sapien
559	216.5	5.5	2528	2	Q8AXP0	Q8axp0 cynops pyrr	632	211	5.3	2447	2	O13149	O13149 fugu rubrip
560	216.5	5.5	2616	1	NDL DROME	P98159 drosophila	633	210.5	5.3	247	1	TRYP SIMVI	P35048 simulium vi
561	216	5.5	255	2	Q7TNI0	Q7tni0 mus musculus	634	210.5	5.3	275	2	Q7PNF7	Q7pnf7 anopheles g
562	216	5.5	289	2	Q9CQ52	Q9cq52 m mus muscu	635	210.5	5.3	280	2	Q8N171	Q8n171 homo sapien
563	216	5.5	269	2	Q9D7T9	Q9d7t9 mus musculus	636	210.5	5.3	342	1	PS88 MOUSE	Q9esd1 mus musculus
564	216	5.5	355	2	Q7PEW0	Q7pew0 anopheles g	637	210.5	5.3	357	2	Q7QKX6	Q7qkx6 anopheles g
565	216	5.5	355	2	Q7POR9	Q7por9 anopheles g	638	210.5	5.3	360	2	Q9W1X6	Q9w1x6 drosophila
566	216	5.5	404	2	Q7QKL2	Q7qkl2 anopheles g	639	210.5	5.3	572	2	Q7RTY8	Q7rty8 homo sapien
567	216	5.5	418	2	Q7PGU3	Q7pgu3 anopheles g	640	210.5	5.3	754	2	Q28290	Q28290 canis fami
568	216	5.5	1218	1	JAG1 MOUSE	Q9qxx0 mus musculus	641	210.5	5.3	1219	1	JAG1 RAT	Q63722 rattus norv
569	215.5	5.5	243	2	Q9TXD8	Q9txd8 agelenopsis	642	210	5.3	2437	1	NTC1 BRARE	P46530 brachydanio
570	215.5	5.5	247	1	TRY3 CANFA	P06872 canis fami	643	209.5	5.3	280	2	Q6GNX6	Q6gnx6 canis fami
571	215.5	5.5	248	1	TRY3 CHICK	Q90629 gallus gall	644	209.5	5.3	313	2	Q8IN51	Q8in51 drosophila
572	215.5	5.5	254	2	Q6CGR4	Q6cgr4 mus musculus	645	209.5	5.3	321	2	Q96RZ8	Q96r28 homo sapien
573	215.5	5.5	269	2	Q6GN82	Q6gn82 xenopus lae	646	209.5	5.3	347	1	HPT MUSSA	Q62558 mus saxicol
574	215.5	5.5	317	1	BSS4 HUMAN	Q9gnz4 homo sapien	647	209.5	5.3	1441	2	Q7Z3G3	Q7z3g3 homo sapien
575	215.5	5.5	321	2	Q8DY38	Q8dy38 mus musculus	648	209	5.3	245	2	Q7PFF6	Q7pff6 anopheles g
576	215.5	5.5	326	2	Q9D9M0	Q9d9m0 mus musculus	649	209	5.3	263	2	Q63ZK0	Q63zk0 xenopus lae
577	215.5	5.5	334	2	Q6UXE0	Q6uxe0 homo sapien	650	209	5.3	307	2	Q6ZND6	Q6znd6 homo sapien
578	215.5	5.5	562	2	Q675X7	Q675x7 oikopleura	651	209	5.3	384	2	Q9W630	Q9w630 cyprinus ca
579	215.5	5.5	669	2	Q7PWE1	Q7pwe1 anopheles g	652	209	5.3	410	2	Q7QKD2	Q7qkd2 anopheles g
580	215.5	5.5	761	2	Q6MG74	Q6mg74 rattus norv	653	209	5.3	433	1	UROK MOUSE	P06869 mus musculus
581	215	5.4	241	1	TRYX GADMO	Q91041 gadus morhu	654	208.5	5.3	236	2	Q9TYH3	Q9tyh3 schistosoma
582	215	5.4	256	2	Q25081	Q25081 hypoderma 1	655	208.5	5.3	258	2	Q28803	Q28803 pan troglod
583	215	5.4	285	2	Q7Q5K4	Q7q5k4 anopheles g	656	208.5	5.3	279	2	Q7TNX3	Q7tnx3 mus musculus
584	215	5.4	301	2	Q7PXG5	Q7pxg5 anopheles g	657	208.5	5.3	311	2	Q80XZ3	Q80xz3 rattus norv
585	215	5.4	389	2	Q9PVX7	Q9pvx7 xenopus lae	658	208.5	5.3	417	2	Q8VHK8	Q8vhk8 mus musculus
586	215	5.4	609	2	Q6PER0	Q6per0 mus musculus	659	208.5	5.3	417	2	Q8VDV1	Q8vdv1 mus musculus
587	215	5.4	609	2	Q8QYC5	Q8qyc5 mus musculus	660	208.5	5.3	444	2	Q9V4W6	Q9v4w6 drosophila
588	215	5.4	749	2	Q9YGE8	Q9yge8 oncorhynch	661	208.5	5.3	464	2	Q6L7Z5	Q6l7z5 haemaphysal
589	215	5.4	760	2	Q8JG08	Q8jg08 tetraodon n	662	208.5	5.3	471	2	Q8CFE0	Q8cfe0 mus musculus
590	215	5.4	810	1	PLMN HUMAN	P00747 homo sapien	663	208	5.3	256	2	Q25082	Q25082 hypoderma 1
591	215	5.4	1116	2	Q7TP05	Q7tp05 rattus norv	664	208	5.3	271	2	Q8HYJ2	Q8hyj2 bos taurus
592	214.5	5.4	195	2	Q819P3	Q819p3 aurelia aur	665	208	5.3	275	2	Q8IXD7	Q8ixd7 homo sapien
593	214.5	5.4	247	1	TRY2 BOVIN	Q29463 bos taurus	666	208	5.3	282	2	Q7PX30	Q7px30 anopheles g
594	214.5	5.4	249	2	Q6DIW2	Q6diw2 xenopus tro	667	208	5.3	292	2	Q7Q6S2	Q7q6s2 anopheles g
595	214.5	5.4	357	2	Q7Q092	Q7q092 anopheles g	668	208	5.3	326	2	Q7RTY6	Q7rty6 homo sapien
596	214.5	5.4	266	2	Q70170	Q70170 mus musculus	669	208	5.3	558	2	Q86TM4	Q86tm4 homo sapien
597	214.5	5.4	505	2	Q966V4	Q966v4 halocynthia	670	207.5	5.3	195	2	Q8J006	Q8j006 homo sapien
598	214.5	5.4	593	1	FA12 BOVIN	P98140 bos taurus	671	207.5	5.3	239	2	Q91218	Q91218 oncorhynch
599	214.5	5.4	1130	2	Q9QIM7	Q9qim7 anopheles g	672	207.5	5.3	256	1	TRYB WANSE	P35046 manduca sex
600	214.5	5.4	1322	2	Q9NAT0	Q9nat0 anopheles g	673	207.5	5.3	266	2	Q92077	Q92077 gadus morhu
601	214.5	5.4	1428	1	ATRN MOUSE	Q9vu60 mus musculus	674	207.5	5.3	269	1	EL2A HUMAN	P08217 homo sapien
602	214	5.4	275	2	Q6FHB8	Q6fhb8 homo sapien	675	207.5	5.3	269	2	Q6ISN8	Q6isn8 homo sapien
603	214	5.4	342	1	PS88 RAT	Q9es87 rattus norv	676	207.5	5.3	278	2	Q7QHS0	Q7qhs0 anopheles g
604	213.5	5.4	241	2	Q98TG9	Q98tg9 engraulis j	677	207.5	5.3	298	2	Q9NH06	Q9nh06 heliothis z
605	213.5	5.4	248	2	Q9VQ98	Q9vg98 drosophila	678	207.5	5.3	900	2	Q6AX42	Q6ax42 xenopus lae
606	213.5	5.4	423	2	Q8BM10	Q8bm10 mus musculus	679	207.5	5.3	1282	2	Q8TER0	Q8ter0 homo sapien
607	213.5	5.4	562	2	Q7PN85	Q7pn85 anopheles g	680	207	5.2	238	1	TRY5 AEDAE	P29787 aedes aegyp
608	213.5	5.4	2352	2	Q61240	Q61240 halocynthia	681	207	5.2	240	2	Q7SYQ8	Q7syq8 xenopus lae
609	213	5.4	247	2	Q7PFF5	Q7pff5 anopheles g	682	207	5.2	260	1	NRPN RAT	Q88780 rattus norv
610	213	5.4	355	2	Q9NFU1	Q9nfui anopheles g	683	207	5.2	329	2	Q7QB72	Q7qb72 anopheles g
611	213	5.4	394	2	P91817	P91817 tachipleus	684	206.5	5.2	195	2	Q6SPC0	Q6spc0 homo sapien
612	213	5.4	615	2	Q81Z25	Q81zz5 homo sapien	685	206.5	5.2	256	1	TRYA WANSE	P35045 manduca sex
613	212.5	5.4	241	2	Q7PQB3	Q7pqb3 anopheles g	686	206.5	5.2	269	2	Q96QV5	Q96qv5 homo sapien
614	212.5	5.4	250	1	KLKE HUMAN	Q9ubx7 homo sapien	687	206.5	5.2	269	2	Q61CV2	Q61cv2 homo sapien
615	212.5	5.4	260	2	Q7RTY3	Q7rty3 homo sapien	688	206.5	5.2	269	2	Q9V929	Q9v929 drosophila

689	206.5	5.2	270	2	Q27824	Q27824	uca pugilator	762	202.5	5.1	339	2	Q6BDA8	Q6bda8	penaeus	jap
690	206.5	5.2	280	2	Q66NX5	Q66nx5	canis famill	763	202.5	5.1	372	2	Q9W2C8	Q9w2c8	drosofila	
691	206.5	5.2	284	2	Q8NF86	Q8nf86	homo sapien	764	202	5.1	190	2	Q9QXD5	Q9qxd5	mus musculus	
692	206.5	5.2	321	1	TRYG HUMAN	Q9nr12	homo sapien	765	202	5.1	241	1	TRV1_GADMO	P16049	gadus morhu	
693	206.5	5.2	467	2	Q86W2	Q86wx2	homo sapien	766	202	5.1	246	1	KLK_FIG	P00752	mus scrofa	
694	206.5	5.2	573	2	Q9V516	Q9v516	drosofila	767	202	5.1	380	2	Q68D21	Q68d21	homo sapien	
695	206.5	5.2	726	2	Q7QBP4	Q7qbp4	anopheles g	768	202	5.1	488	2	Q8IUv8	Q8iuv8	homo sapien	
696	206.5	5.2	1065	2	Q81OH2	Q81oh2	mus musculus	769	202	5.1	743	2	Q9YGE7	Q9yge7	oncorhynch	
697	206.5	5.2	1403	2	Q70E20	Q70e20	mus musculus	770	202	5.1	2321	1	NTC3_HUMAN	Q9um47	homo sapien	
698	206	5.2	269	2	Q9NE92	Q9nb92	agrotis ips	771	201.5	5.1	195	2	Q8JU07	Q8j007	homo sapien	
699	206	5.2	269	2	Q6A2F9	Q6axf9	anopheles lae	772	201.5	5.1	195	2	Q8JU08	Q8j008	homo sapien	
700	206	5.2	318	2	Q7Q9M4	Q7q9m4	anopheles g	773	201.5	5.1	246	1	TRY2_MOUSE	P07146	mus musculus	
701	206	5.2	424	2	Q6R559	Q6r559	ostrelinia nu	774	201.5	5.1	255	1	Q6ISi0	Q6iis0	homo sapien	
702	206	5.2	492	2	Q7Z155	Q7z155	chriomantes	775	201.5	5.1	256	1	KLKF_HUMAN	Q9h4r5	homo sapien	
703	206	5.2	458	1	APOA_HUMAN	P08159	homo sapien	776	201.5	5.1	320	2	Q7T0X2	Q7t0x2	anopheles lae	
704	205.5	5.2	269	1	TRYM_CANFA	P19236	canis famill	777	201.5	5.1	344	2	Q640F8	Q640f8	anopheles g	
705	205.5	5.2	269	2	Q6ISM5	Q6igm5	homo sapien	778	201.5	5.1	394	2	Q7FQ76	Q7fq76	homo sapien	
706	205.5	5.2	269	2	Q6ISP9	Q6isp9	homo sapien	779	201.5	5.1	438	2	Q6ZWK6	Q6zwk6	homo sapien	
707	205.5	5.2	347	1	HPT_RAT	P06866	rattus norv	780	201	5.1	247	2	Q42608	Q42608	petromyzon	
708	205.5	5.2	374	2	Q80YD5	Q80yd5	mus musculus	781	201	5.1	248	2	Q66105	Q66105	anopheles lae	
709	205.5	5.2	416	2	Q8BZ13	Q8bz13	mus musculus	782	201	5.1	260	2	Q81W69	Q81w69	homo sapien	
710	205.5	5.2	416	2	Q8BZ30	Q8bz30	mus musculus	783	201	5.1	275	2	Q66UD0	Q66ud0	culicoides	
711	205.5	5.2	492	1	TMS2_HUMAN	O15393	homo sapien	784	201	5.1	333	2	Q7Q5Z6	Q7q5z6	anopheles g	
712	205	5.2	256	1	HYPB_HYPLI	P35588	hypoderma l	785	201	5.1	351	2	Q816K0	Q816k0	holotrichia	
713	205	5.2	284	2	Q02569	O02569	culex quinq	786	201	5.1	392	2	Q9VMZ3	Q9vmz3	drosofila	
714	205	5.2	492	2	Q96T73	Q96t73	homo sapien	787	200.5	5.1	175	2	Q9UMV3	Q9umv3	homo sapien	
715	205	5.2	870	2	Q81QG6	Q81qg6	drosofila	788	200.5	5.1	231	1	TR1P_FIG	P00761	sus scrofa	
716	204.5	5.2	216	2	Q9QX83	Q9qx83	rattus norv	789	200.5	5.1	241	1	Q7PFF7	Q7pff7	anopheles g	
717	204.5	5.2	246	1	TRY2_RAT	P00763	rattus norv	790	200.5	5.1	246	2	Q792Z1	Q792z1	mus musculus	
718	204.5	5.2	247	2	Q9C9N9	Q9cpn9	m mus muscu	791	200.5	5.1	249	2	Q9W7Q1	Q9w7q1	paralichthy	
719	204.5	5.2	247	2	Q9DY77	Q9dy77	mus musculus	792	200.5	5.1	281	2	Q6NSB4	Q6nbs4	homo sapien	
720	204.5	5.2	256	1	TRYC_MANSE	P35047	manduca sex	793	200.5	5.1	358	2	O57434	O57434	fugu rubrip	
721	204.5	5.2	281	2	Q46137	Q46137	lumbicus r	794	200.5	5.1	415	2	Q9UKZ9	Q9ukz9	homo sapien	
722	204.5	5.2	367	2	Q70169	Q70169	mus musculus	795	200.5	5.1	752	1	CO2_HUMAN	F06681	homo sapien	
723	204.5	5.2	449	2	Q95RA3	Q95ra3	drosofila	796	200.5	5.1	810	1	PLMN_MACMU	P12545	macaca mula	
724	204.5	5.2	470	2	Q661F4	O661f4	anopheles tro	797	200.5	5.1	951	2	Q20176	Q20176	caenorhabdi	
725	204.5	5.2	510	2	Q9H4V1	Q9h4v1	homo sapien	798	200	5.1	241	2	Q7Q310	Q7q310	anopheles g	
726	204.5	5.2	752	1	CO2_PONPY	Q8sq75	pongo pygma	799	200	5.1	247	2	Q42158	Q42158	petromyzon	
727	204.5	5.2	1497	2	Q8NBT9	Q8nbt9	homo sapien	800	200	5.1	385	1	TS50_HUMAN	Q9ui18	homo sapien	
728	204.5	5.2	2470	1	NTC2_MOUSE	O35516	mus musculus	801	200	5.1	391	2	Q7PXJ5	Q7pxj5	anopheles g	
729	204	5.2	260	1	KLK8_HUMAN	O60259	homo sapien	802	200	5.1	454	2	Q46506	Q46506	papio hamad	
730	204	5.2	367	2	Q9QXD2	Q9qxd2	mus musculus	803	200	5.1	504	2	Q9VFM0	Q9vfm0	drosofila	
731	204	5.2	417	2	Q8VHL4	Q8vhl4	rattus norv	804	200	5.1	564	2	Q7RTZ1	Q7rtz1	homo sapien	
732	204	5.2	424	2	Q6R558	Q6r558	ostrelinia nu	805	199.5	5.1	223	2	Q9VBY4	Q9vby4	drosofila	
733	203.5	5.2	195	2	Q81XB4	Q81xb4	homo sapien	806	199.5	5.1	247	1	TRY3_RAT	P08426	rattus norv	
734	203.5	5.2	247	1	TRY2_HUMAN	P07478	homo sapien	807	199.5	5.1	257	1	KLKI_MACFA	Q07276	macaca fasc	
735	203.5	5.2	261	2	Q7Z5F3	Q7z5f3	homo sapien	808	199.5	5.1	258	2	Q8508	Q8508	macaca mula	
736	203.5	5.2	263	1	CFAD_RAT	P32038	rattus norv	809	199.5	5.1	275	1	TRY3_ANOGA	P35037	anopheles g	
737	203.5	5.2	285	1	FA9_CAVPO	P16295	cavia porce	810	199.5	5.1	348	2	Q86WS5	Q86ws5	homo sapien	
738	203.5	5.2	309	2	Q27083	P16295	tachypleus	811	199.5	5.1	378	2	Q90WP0	Q90wp0	trachemys s	
739	203.5	5.2	335	2	Q8VIF2	Q8vif2	mus musculus	812	199.5	5.1	390	2	Q7PVQ3	Q7pvq3	anopheles g	
740	203.5	5.2	404	2	Q7QF40	Q7qf40	anopheles g	813	199.5	5.1	1193	2	Q90819	Q90819	gallus gall	
741	203.5	5.2	664	2	Q9IAT6	Q9iat6	brachydania	814	199.5	5.1	1275	2	Q99FW0	Q99fw0	rattus norv	
742	203.5	5.2	734	2	Q69DL2	Q69dl2	sus scrofa	815	199.5	5.1	2556	1	NTC1_HUMAN	Q25253	lucilia cup	
743	203.5	5.2	750	2	Q9W633	Q9w633	cyprinus ca	816	199.5	5.1	2653	2	Q25253	Q25253	penaeus van	
744	203.5	5.2	1323	2	Q7Z387	Q7z387	homo sapien	817	199	5.0	263	2	Q62562	Q62562	anopheles lae	
745	203.5	5.2	1432	2	Q99J86	Q99j86	rattus norv	818	199	5.0	264	2	Q8QGF6	Q8qgf6	anopheles lae	
746	203.5	5.2	3494	2	Q7LCS3	Q7lcs3	homo sapien	819	199	5.0	264	2	Q6GPY5	Q6gpy5	anopheles lae	
747	203.5	5.2	3623	2	Q60494	O60494	homo sapien	820	199	5.0	401	2	Q6LH17	Q6lhi7	photobacter	
748	203	5.1	177	2	Q9QX86	Q9qx86	rattus norv	821	199	5.0	441	2	Q9XXV0	Q9xxv0	bombyx mori	
749	203	5.1	185	2	Q9QX88	Q9qx88	rattus norv	822	199	5.0	1303	2	Q9ULC7	Q66S84	oikopleura	
750	203	5.1	185	2	Q9QXA4	Q9qxa4	mus musculus	823	198.5	5.0	181	2	Q9ULC7	Q66S84	oikopleura	
751	203	5.1	186	2	Q9QXD4	Q9qxd4	rattus norv	824	198.5	5.0	237	2	Q17035	Q17035	anopheles g	
752	203	5.1	289	2	Q7PUU1	Q7puu1	anopheles g	825	198.5	5.0	243	1	TRY1_BOVIN	P00760	bos caurus	
753	203	5.1	370	2	Q9VA44	Q9va44	drosofila	826	198.5	5.0	260	2	Q7SZC3	Q7szc3	gallus gall	
754	203	5.1	403	2	Q9KSQ6	Q9ksq6	vibriio chol	827	198.5	5.0	279	2	Q9Z774	Q9z774	rattus norv	
755	203	5.1	537	2	Q9BYE1	Q9bye1	homo sapien	828	198.5	5.0	311	1	TRYG_MOUSE	Q9qul7	mus musculus	
756	203	5.1	575	2	Q7Q9W3	Q7q9w3	anopheles g	829	198.5	5.0	364	2	Q9NA59	Q9nas9	anopheles g	
757	203	5.1	581	2	Q9BYE2	Q9bye2	homo sapien	830	198.5	5.0	365	2	Q7Q1D1	Q7q1d1	anopheles g	
758	203	5.1	833	2	Q9YIC5	Q9yic5	cyprinus ca	831	198.5	5.0	388	2	O44330	Q44330	manduca sex	
759	202.5	5.1	239	2	O8N1C9	Q8n1c9	homo sapien	832	198.5	5.0	461	2	Q8T4N2	Q8t4n2	thripicephal	
760	202.5	5.1	255	2	Q7JIG6	Q7jig6	sagunus oe	833	198.5	5.0	752	2	Q863A0	Q863a0	gorilla gor	
761	202.5	5.1	274	2	O16133	O16133	anopheles s	834	198.5	5.0	1214	2	Q90YD2	Q90yd2	anopheles lae	

835	198	5.0	235	1	TRYD_HUMAN	Q9bzj3	homo sapien	908	194	4.9	806	1	PLMN_MACEU	018783	macropus eu
836	198	5.0	259	1	DEF3_DERFA	P49275	dermatophag	909	193.5	4.9	183	2	Q6PLJ7	Q6plj7	fennaropena
837	198	5.0	261	2	Q6QX60	Q6qx60	lepeophthei	910	193.5	4.9	245	2	Q792Y9	Q792y9	mus musculus
838	198	5.0	293	2	Q7Q8F9	Q7q8f9	anopheles g	911	193.5	4.9	246	2	Q9QK9	Q9qk9	mus musculus
839	198	5.0	427	2	Q6Y2X4	Q6y2x4	manduca sex	912	193.5	4.9	247	2	Q6T376	Q6t376	eisenia foe
840	198	5.0	760	1	CO2_MOUSE	P21180	mus musculus	913	193.5	4.9	247	2	Q9W7Q5	Q9w7q5	paralichthy
841	198	5.0	1023	2	Q6UXD4	Q6uxd4	homo sapien	914	193.5	4.9	256	2	Q27540	Q27540	choristoneu
842	198	5.0	1024	1	SZ6L_HUMAN	Q9b9h1	homo sapien	915	193.5	4.9	263	2	Q9V5X7	Q9v5x7	drosofila
843	197.5	5.0	226	1	COGS_UCAPU	P00771	uca pugilat	916	193.5	4.9	271	2	Q7Q820	Q7q820	anopheles g
844	197.5	5.0	242	2	Q6NTB8	Q6ntb8	homo sapien	917	193.5	4.9	282	2	Q7PVQ2	Q7pvq2	anopheles g
845	197.5	5.0	246	2	Q6I866	Q6ie66	rattus norv	918	193.5	4.9	317	2	Q9DGR3	Q9dgr3	xenopus lae
846	197.5	5.0	248	1	KLKC_HUMAN	Q9ukr0	homo sapien	919	193.5	4.9	327	2	Q7Q530	Q7q530	anopheles g
847	197.5	5.0	255	2	Q96RQ0	Q96rq0	homo sapien	920	193.5	4.9	402	2	Q7QB73	Q7qb73	anopheles g
848	197.5	5.0	258	2	Q28805	Q28805	pan troglod	921	193.5	4.9	789	2	Q8N1E9	Q8n1e9	homo sapien
849	197.5	5.0	263	2	Q6H319	Q6h319	sus scrofa	922	193.5	4.9	1089	2	Q8T3A0	Q8t3a0	ciona intes
850	197.5	5.0	267	2	Q7Q4H6	Q7q4h6	anopheles g	923	193.5	4.9	1317	2	Q6IQ50	Q6iq50	homo sapien
851	197	5.0	222	2	Q91W20	Q91w20	rattus norv	924	193.5	4.9	2471	1	NTC2_RAT	Q9q230	rattus norv
852	197	5.0	245	2	Q7Q2X3	Q7q2x3	anopheles g	925	193	4.9	253	1	CAC3_BOVIN	P05805	bos taurus
853	197	5.0	260	2	Q7PWE3	Q7pwe3	anopheles g	926	193	4.9	258	2	Q867B0	Q867b0	canis famil
854	197	5.0	261	2	Q9VXC7	Q9vxc7	drosofila	927	193	4.9	268	2	Q9XY56	Q9xy56	ctenoccephal
855	197	5.0	338	1	PLMN_HORSE	P80010	equus cabal	928	193	4.9	269	2	Q95KW7	Q95kw7	bos taurus
856	197	5.0	421	2	Q95RS6	Q95rs6	drosofila	929	193	4.9	405	2	Q7QAC0	Q7qac0	anopheles g
857	197	5.0	585	2	Q9U0B2	Q9u0e2	tribolium c	930	193	4.9	423	2	Q57433	Q57433	fugu rubrip
858	197	5.0	745	2	Q91701	Q91701	xenopus lae	931	193	4.9	481	2	Q9H284	Q9h284	homo sapien
859	197	5.0	760	2	Q70350	Q70350	mus musculus	932	193	4.9	543	2	Q6PHN6	Q6phn6	mus musculus
860	196.5	5.0	219	2	Q91036	Q91036	gadus morhu	933	193	4.9	962	2	Q8C420	Q8c420	mus musculus
861	196.5	5.0	237	2	Q6GJY5	Q6gyj5	struthio ca	934	193	4.9	963	2	Q6PID5	Q6pid5	mus musculus
862	196.5	5.0	259	2	Q8IRE0	Q8ire0	drosofila	935	192.5	4.9	178	2	Q93594	Q93594	dicertrarch
863	196.5	5.0	269	1	EL2B_HUMAN	P08218	homo sapien	936	192.5	4.9	232	2	Q94508	Q94508	dermatophag
864	196.5	5.0	298	2	Q8T4N4	Q8t4n4	rhhipcephal	937	192.5	4.9	246	2	Q9Z1R9	Q9z1r9	mus musculus
865	196.5	5.0	373	2	Q6LBY9	Q6lby9	homo sapien	938	192.5	4.9	247	2	Q8NHM4	Q8nhm4	homo sapien
866	195.5	5.0	570	1	FBP3_STRPU	P49013	strongyloce	939	192.5	4.9	249	2	Q9QYN4	Q9qyn4	mus musculus
867	196.5	5.0	829	2	Q6NUL9	Q6nul9	homo sapien	940	192.5	4.9	250	2	Q63ZF2	Q63zf2	rattus norv
868	196.5	5.0	2524	1	NOTC_XENLA	P21783	xenopus lae	941	192.5	4.9	256	1	TRYP_CHOFU	P35042	choristoneu
869	196	5.0	248	2	Q6GPX7	Q6gpx7	xenopus lae	942	192.5	4.9	276	2	Q9QVN3	Q9qvn3	m hippostas
870	196	5.0	270	1	EL3B_HUMAN	P08861	homo sapien	943	192.5	4.9	381	2	Q8MQY4	Q8mqy4	drosofila
871	196	5.0	275	2	Q66UC8	Q66uc8	culicoides	944	192.5	4.9	438	2	Q9H804	Q9h804	homo sapien
872	196	5.0	347	2	Q7QSV3	Q7qsv3	anopheles g	945	192.5	4.9	703	2	Q7Q6S1	Q7q6s1	anopheles g
873	196	5.0	400	2	Q9QSG2	Q9qsg2	tenebrio mo	946	192.5	4.9	754	2	P79816	P79816	oryzias lat
874	196	5.0	3623	2	Q70244	Q70244	rattus norv	947	192	4.9	244	2	Q42159	Q42159	petromyzon
875	195.5	5.0	257	1	GRAM_HUMAN	P51124	homo sapien	948	192	4.9	246	2	Q9BLI7	Q9bli7	lumbricus r
876	195.5	5.0	267	2	Q9GP27	Q9gp27	drosofila	949	192	4.9	254	2	Q9XYI0	Q9xyi0	rhypopertha
877	195.5	5.0	271	1	FA9_FIG	P16293	sus scrofa	950	192	4.9	256	2	Q6MJY6	Q6mjiy6	bdellovibri
878	195.5	5.0	274	2	Q17086	Q17086	anopheles s	951	192	4.9	376	2	Q7PTP7	Q7ptp7	anopheles g
879	195.5	5.0	276	2	O18443	O18443	helicoverpa	952	192	4.9	380	2	Q9Y1K5	Q9y1k5	anopheles g
880	195.5	5.0	752	1	CO2_PANTR	Q8sq74	pan troglod	953	192	4.9	383	2	Q77102	Q77102	manduca sex
881	195.5	5.0	948	2	Q6IEZ4	Q6ibz4	homo sapien	954	192	4.9	410	2	Q7QJ44	Q7qj44	anopheles g
882	195.5	5.0	2471	1	NTC2_HUMAN	Q04721	homo sapien	955	191.5	4.9	247	1	TRT1_HUMAN	P07477	homo sapien
883	195	4.9	261	1	KLK6_MOUSE	P15947	mus musculus	956	191.5	4.9	247	2	Q17039	Q17039	anopheles g
884	195	4.9	262	2	Q7Z0G3	Q7z0g3	phlebotomus	957	191.5	4.9	265	2	Q6QX61	Q6qx61	lepeophthei
885	195	4.9	276	2	Q9BRH3	Q9brh3	homo sapien	958	191.5	4.9	281	2	Q76898	Q76898	drosofila
886	195	4.9	320	2	Q7PBV6	Q7pav6	anopheles g	959	191.5	4.9	284	2	Q8IRX5	Q8irx5	drosofila
887	195	4.9	432	1	UROK_RAT	P29598	rattus norv	960	191.5	4.9	360	2	Q8SX54	Q8sx54	drosofila
888	194.5	4.9	246	1	TRY1_RAT	P00762	rattus norv	961	191.5	4.9	385	2	Q8SXE1	Q8sxe1	drosofila
889	194.5	4.9	246	2	Q9R0T7	Q9rot7	m pancreati	962	191.5	4.9	480	2	Q66IT1	Q66it1	xenopus lae
890	194.5	4.9	261	2	Q7Z5F4	Q7z5f4	homo sapien	963	191.5	4.9	579	2	Q96DQ9	Q96dq9	homo sapien
891	194.5	4.9	283	2	Q95V22	Q95v22	lumbricus b	964	191.5	4.9	713	2	Q80TP0	Q80tp0	mus musculus
892	194.5	4.9	343	1	PLMN_SHEEP	P81286	ovis aries	965	191.5	4.9	830	1	LEM3_HUMAN	P16109	homo sapien
893	194.5	4.9	1374	2	Q9VSU0	Q9vsu0	drosofila	966	191.5	4.9	2468	2	Q800E4	Q800e4	brachydanio
894	194.5	4.9	1449	2	Q9UII2	Q9uii2	drosofila	967	191.5	4.9	3396	2	Q9VM55	Q9vm55	drosofila
895	194.5	4.9	1450	2	Q8IQB8	Q8iqb8	drosofila	968	191	4.8	228	2	Q6PEJ8	Q6pej8	homo sapien
896	194.5	4.9	1462	2	Q9UII3	Q9uii3	drosofila	969	191	4.8	254	1	KLK4_HUMAN	Q9y5k2	homo sapien
897	194.5	4.9	2382	2	Q9BI19	Q9bi19	drosofila	970	191	4.8	255	2	Q25227	Q25227	lucilia cup
898	194.5	4.9	2409	2	Q960G6	Q960g6	drosofila	971	191	4.8	256	2	Q818E5	Q818e5	ochlerotatu
899	194.5	4.9	2428	2	Q816X6	Q816x6	boophilus m	972	191	4.8	277	2	Q81Q10	Q81q10	drosofila
900	194.5	4.9	2786	2	Q9VSU2	Q9vsu2	drosofila	973	191	4.8	317	2	Q8K4D1	Q8k4d1	mus musculus
901	194	4.9	245	2	Q42160	Q42160	petromyzon	974	191	4.8	317	2	Q8K4I7	Q8k4i7	mus musculus
902	194	4.9	247	2	Q70T74	Q70t74	equus cabal	975	191	4.8	415	2	Q9GRW0	Q9grw0	holotrichia
903	194	4.9	253	2	Q9VAG3	Q9vag3	drosofila	976	191	4.8	646	2	Q29097	Q29097	sus scrofa
904	194	4.9	259	1	CFAD_PIG	P51779	sus scrofa	977	191	4.8	758	2	Q6MG73	Q6mg73	rattus norv
905	194	4.9	267	1	TRY7_ANOGA	P35041	anopheles g	978	190.5	4.8	246	2	Q79220	Q79220	mus musculus
906	194	4.9	556	2	Q803D5	Q803d5	brachydanio	979	190.5	4.8	257	2	Q818E3	Q818e3	aedes polyn
907	194	4.9	593	2	Q6PJN5	Q6pjn5	homo sapien	980	190.5	4.8	270	2	Q7QON6	Q7qon6	anopheles g

981	190.5	4.8	329	2	Q7PEV8	Q7pev8 anopheles g	1054	187	4.7	246	1	TRVA_RAT	P32821 rattus norv
982	190.5	4.8	579	2	Q9BY79	Q9by79 homo sapien	1055	187	4.7	256	2	Q18439	O18439 helicoverpa
983	190.5	4.8	762	1	Q9YIC6	Q9yic6 cyprinus ca	1056	187	4.7	261	2	Q29474	Q29474 canis famil
984	190.5	4.8	768	1	LEM3_MOUSE	Q01102 mus musculus	1057	187	4.7	271	1	CTRL_PENVA	Q00871 penaeus van
985	190.5	4.8	1064	1	FBPI_STRPU	P10079 strongyloce	1058	187	4.7	291	2	Q25510	Q25510 manduca sex
986	190.5	4.8	2037	1	Q7QFS2	Q7qfs2 anopheles g	1059	187	4.7	890	2	Q7QJ41	Q7qj41 anopheles g
987	190	4.8	243	2	Q86VJ5	Q86vj5 homo sapien	1060	186.5	4.7	235	2	Q9GTK7	Q9gkt7 aedes albop
988	190	4.8	245	2	Q6DKQ3	Q6dkq3 eisenia foe	1061	186.5	4.7	250	2	O93265	O93265 pseudopleur
989	190	4.8	253	2	Q8WZB4	Q8wzb4 homo sapien	1062	186.5	4.7	257	2	Q818E2	Q818e2 aedes trise
990	190	4.8	277	2	Q8SQ44	Q8sq44 mus scrofa	1063	186.5	4.7	397	2	Q9WTV2	Q9wvt2 drosophila
991	190	4.8	282	2	Q25395	Q25395 lumbricus r	1064	186.5	4.7	323	2	Q7QCP4	Q7qcp4 anopheles g
992	190	4.8	299	2	Q7Q9S0	Q7q9s0 anopheles g	1065	186.5	4.7	352	2	O9GSM1	O9gsn1 chrysomya b
993	190	4.8	334	2	Q4E507	Q4e507 papio hamad	1066	186	4.7	181	2	Q7QGSN1	Q7qgsn1 chrysomya b
994	190	4.8	378	2	Q8SY50	Q8sy50 drosophila	1067	186	4.7	249	2	O92046	O92046 dissostichu
995	190	4.8	414	2	Q8R4W6	Q8r4w6 mus musculus	1068	186	4.7	280	2	Q7Q494	Q7q494 anopheles g
996	189.5	4.8	241	2	Q9Z135	Q9z135 rattus norv	1069	186	4.7	324	2	Q6BD05	Q6bd05 anopheles g
997	189.5	4.8	246	2	Q7M754	Q7m754 mus musculus	1070	186	4.7	449	2	Q9VDU8	Q9vdu8 drosophila
998	189.5	4.8	255	2	Q9Y7A9	Q9y7a9 metarhizium	1071	186	4.7	1176	2	Q6ZWI6	Q6zwi6 homo sapien
999	189.5	4.8	257	2	Q27440	Q27440 aedes aegypt	1072	186	4.7	1594	2	Q95218	Q95218 oryctolagus
1000	189.5	4.8	258	2	Q28804	Q28804 pan troglod	1073	185.5	4.7	211	2	O8J009	O8j009 homo sapien
1001	189.5	4.8	263	2	Q02570	Q02570 culex quinq	1074	185.5	4.7	256	2	Q9XY51	Q9xy51 ctenoccephal
1002	189.5	4.8	263	2	Q9TY16	Q9ty16 penaeus van	1075	185.5	4.7	261	1	DER3_DERPT	DER355 dermatophag
1003	189.5	4.8	266	2	Q27761	Q27761 penaeus van	1076	185.5	4.7	292	2	O18438	O18438 helicoverpa
1004	189.5	4.8	271	2	Q9VRS6	Q9vrs6 drosophila	1077	185.5	4.7	292	2	Q7PWM9	Q7pwm9 anopheles g
1005	189.5	4.8	281	2	Q8SYB5	Q8syb5 drosophila	1078	185.5	4.7	310	1	DIGF_MOUSE	D9qvz9 mus musculus
1006	189.5	4.8	369	2	Q7Q928	Q7q928 anopheles g	1079	185.5	4.7	439	2	O8BHM9	O8bhm9 m mus muscu
1007	189.5	4.8	381	2	Q9VB66	Q9vb66 drosophila	1080	185.5	4.7	542	2	Q7MK56	Q7mk56 vibrio vuln
1008	189.5	4.8	385	2	Q9OWS2	Q9ows2 elaphe sp.	1081	185.5	4.7	711	1	HGFL_HUMAN	H26227 homo sapien
1009	189.5	4.8	470	2	Q8T3A1	Q8t3a1 ciona intes	1082	185.5	4.7	928	1	NRP1_XENLA	P28824 xenopus lae
1010	189.5	4.8	572	2	Q8BIK6	Q8bik6 mus musculus	1083	185.5	4.7	1115	2	Q7QB67	Q7qb67 anopheles g
1011	189.5	4.8	649	2	Q28657	Q28657 oryctolagus	1084	185.5	4.7	1254	2	Q90Y56	Q90y56 brachydanio
1012	189.5	4.8	2386	1	EFL4_HUMAN	Q7z7m0 homo sapien	1085	185.5	4.7	1254	2	Q90YH2	Q90yh2 brachydanio
1013	189	4.8	181	2	Q9GSM5	Q9gsm5 chrysomya b	1086	185	4.7	230	2	Q7PG50	Q7pg50 anopheles g
1014	189	4.8	245	1	Q9BLI8	Q9bli8 lumbricus r	1087	185	4.7	256	1	KLK4_MOUSE	P00757 mus musculus
1015	189	4.8	246	1	TRYB_RAT	P32822 rattus norv	1088	185	4.7	258	1	KLK1_PAPHA	Q28773 papio hamad
1016	189	4.8	246	2	Q7TT42	Q7tt42 mus musculus	1089	185	4.7	287	2	Q9NH10	Q9nh10 agrotis ips
1017	189	4.8	247	1	TRY4_RAT	P12788 rattus norv	1090	185	4.7	320	2	Q7OKL3	Q7okl3 anopheles g
1018	189	4.8	253	1	KLK7_HUMAN	P49862 homo sapien	1091	185	4.7	508	2	O8DA23	O8da23 vibrio vuln
1019	189	4.8	414	2	Q9CX06	P42201 bos taurus	1092	185	4.7	709	2	Q6ZTN9	Q6ztn9 xenopus lae
1020	189	4.8	646	1	LEM3_BOVIN	Q8cip8 rattus norv	1093	184.5	4.7	247	2	Q66PG9	Q66pg9 helicoverpa
1021	189	4.8	758	2	Q8CIP8	O6plj5 neocaridina	1094	184.5	4.7	295	2	O18445	O18445 helicoverpa
1022	188.5	4.8	182	2	Q6PLJ5	O6lcu4 lumbricus r	1095	184.5	4.7	295	2	O18450	O18450 helicoverpa
1023	188.5	4.8	239	2	Q6LCU4	Q792y8 mus musculus	1096	184.5	4.7	321	2	O6GNK3	O6gnk3 xenopus lae
1024	188.5	4.8	246	2	Q792Y8	Q6azc0 brachydanio	1097	184.5	4.7	427	2	O8BQH6	O8bqh6 mus musculus
1025	188.5	4.8	266	2	Q6AZC0	P16296 rattus norv	1098	184.5	4.7	923	2	Q6PAR3	Q6par3 mus musculus
1026	188.5	4.8	282	1	FA9_RAT	Q9bqr3 homo sapien	1099	184.5	4.7	1203	2	Q7QH41	Q7qh41 anopheles g
1027	188.5	4.8	290	1	PR27_HUMAN	O6ie62 rattus norv	1100	184.5	4.7	1213	1	JAG3_BRARE	Q90y54 brachydanio
1028	188.5	4.8	330	2	Q6I5E2	Q90w44 crocodylus	1101	184.5	4.7	1582	2	Q7PN18	Q7pnl8 anopheles g
1029	188.5	4.8	382	2	Q90WT4	Q962w9 podocoryne	1102	184	4.7	246	2	Q8I7P0	O8i7p0 lumbricus b
1030	188.5	4.8	713	2	Q962W9	P97677 rattus norv	1103	184	4.7	246	1	TEST_HUMAN	O6dkq2 eisenia foe
1031	188.5	4.8	714	1	DLI1_RAT	F60882 mus musculus	1104	184	4.7	314	1	Q7QK70	Q7qk70 rattus norv
1032	188.5	4.8	2330	1	EFL4_MOUSE	O6fhw3 homo sapien	1105	184	4.7	350	2	Q7QK70	Q7qk70 drosophila
1033	188	4.8	228	2	Q8FHW3	O8n460 homo sapien	1106	184	4.7	381	2	Q7TP23	Q7tsp23 rattus norv
1034	188	4.8	235	2	Q8N4E0	P00746 homo sapien	1107	184	4.7	395	2	Q7KSK1	Q7ksk1 drosophila
1035	188	4.8	233	1	CFAD_HUMAN	Q8n5n9 homo sapien	1108	184	4.7	405	2	Q8S260	Q8sz60 drosophila
1036	188	4.8	253	1	Q8NSN9	P32824 praomys nat	1109	184	4.7	745	2	O90WF9	O90wf9 triakis scy
1037	188	4.8	263	1	KLK9_PRANA	O6p326 xenopus tro	1110	184	4.7	988	2	Q8IHW4	O8iwy4 homo sapien
1038	188	4.8	265	2	Q6P326	Q6p326 xenopus tro	1111	183.5	4.7	229	2	Q7PKD3	Q7pkd3 anopheles g
1039	188	4.8	266	2	Q8WR10	O8wri0 paralithode	1112	183.5	4.7	245	2	Q6R670	Q6r670 oreochromis
1040	188	4.8	271	2	O18487	O18487 penaeus van	1113	183.5	4.7	329	2	O6R671	O6r671 oreochromis
1041	188	4.8	276	2	Q9VXP8	Q9vxp8 drosophila	1114	183.5	4.7	247	2	Q9CPN7	Q9cpn7 mus musculus
1042	188	4.8	278	2	Q6EFN6	Q6efn6 brachydanio	1115	183.5	4.7	257	2	Q86PL8	O86pl8 aedes aegyp
1043	188	4.8	282	2	Q7K2R3	P80009 canis famil	1116	183.5	4.7	305	2	Q7Q6S4	Q7q6s4 anopheles g
1044	188	4.8	333	1	PLMN_CANFA	Q64id3 anthonomus	1117	183.5	4.7	306	2	Q7PZP8	Q7pzp8 anopheles g
1045	188	4.8	404	2	Q64ID3	Q64id3 anthonomus	1118	183.5	4.7	329	2	O42272	O42272 xenopus lae
1046	188	4.8	505	2	Q7QCVD	Q7qcvd anopheles g	1119	183.5	4.7	387	2	Q7PZP9	Q7pzp9 anopheles g
1047	187.5	4.8	250	2	Q17036	Q17036 anopheles g	1120	183.5	4.7	431	2	Q7PV05	Q7pv05 anopheles g
1048	187.5	4.8	251	2	Q8N2U3	Q8n2u3 homo sapien	1121	183.5	4.7	1372	2	P91526	P91526 caenorhabdi
1049	187.5	4.8	257	2	Q9NB49	Q9nb49 aedes aegyp	1122	183	4.6	161	1	PRTC_MACMU	Q28506 macaca mula
1050	187.5	4.8	283	2	Q25394	Q25394 lumbricus r	1123	183	4.6	257	2	O19023	O19023 macaca mula
1051	187.5	4.8	283	2	Q8ITU7	Q8itu7 lumbricus r	1124	183	4.6	261	1	KLK1_RAT	P00758 rattus norv
1052	187.5	4.8	304	1	TRY3_HUMAN	P35030 homo sapien	1125	183	4.6	265	2	Q68G17	Q68g17 rattus norv
1053	187.5	4.8	1216	2	Q90Y55	Q90y55 brachydanio	1126	183	4.6	266	2	Q7Z0B3	Q7z0b3 stomoxys ca

1127	183	4.6	267	2	Q9MZ26	Q9mz26 macaca fasc	1200	180.5	4.6	264	2	O62561	O62561 penaeus van
1128	183	4.6	272	2	Q9V5X6	Q9v5x6 drosophila	1201	180.5	4.6	266	2	O81916	O81916 blomia trop
1129	183	4.6	309	2	Q6DH4	Q6dh4 brachydanio	1202	180.5	4.6	275	1	FA9_RABIT	FA9_RABIT
1130	183	4.6	322	2	Q9V215	Q9v215 drosophila	1203	180.5	4.6	293	2	Q7Z5A4	Q7z5a4 homo sapien
1131	183	4.6	387	2	Q7RTV4	Q7rtv4 homo sapien	1204	180.5	4.6	330	2	Q8MP08	Q8mp08 bombyx mori
1132	183	4.6	392	1	EAST_DROME	E13562 drosophila	1205	180.5	4.6	436	1	ACRO_MOUSE	ACRO_MOUSE
1133	183	4.6	417	2	Q6J590	Q6j590 homo sapien	1206	180.5	4.6	520	2	Q8SY93	Q8sy93 mus musculus
1134	183	4.6	752	2	Q42374	Q42374 brachydanio	1207	180.5	4.6	717	2	P70006	P70006 xenopus lae
1135	182.5	4.6	157	2	Q6ZJW3	Q6zjw3 homo sapien	1208	180	4.6	157	1	PRTC_HORSE	PRTC_HORSE
1136	182.5	4.6	248	1	TRY1_CHICK	Q9627 gallus galli	1209	180	4.6	203	2	Q9NE77	Q9nb77 heliothis z
1137	182.5	4.6	257	2	Q8IS83	Q8is83 aedes albop	1210	180	4.6	234	2	Q9CV76	Q9cv76 mus musculus
1138	182.5	4.6	259	2	Q7QK17	Q7qk17 anopheles g	1211	180	4.6	254	2	Q01136	Q01136 metathizium
1139	182.5	4.6	274	2	Q9VRS7	Q9vr57 drosophila	1212	180	4.6	256	2	Q9Y842	Q9y842 metathizium
1140	182.5	4.6	285	2	Q9NCC6	Q9nc6c heliothis z	1213	180	4.6	261	1	KLKE_MOUSE	KLKE_MOUSE
1141	182.5	4.6	297	2	Q86M89	Q86m89 spodoptera	1214	180	4.6	274	2	Q6DHC9	Q6dhc9 brachydanio
1142	182.5	4.6	337	2	Q8MG77	Q8mg77 drosophila	1215	180	4.6	275	1	TRY4_ANOGA	TRY4_ANOGA
1143	182.5	4.6	330	2	Q6NVR7	Q6nvr7 xenopus tro	1216	180	4.6	292	2	Q7PVQ5	Q7pvq5 anopheles g
1144	182.5	4.6	371	2	Q8MRV3	Q8mr3 drosophila	1217	180	4.6	324	2	Q6BD16	Q6bd16 drosophila
1145	182.5	4.6	375	2	Q7PWE2	Q7pwe2 anopheles g	1218	180	4.6	472	2	Q6TGB2	Q6tgb2 drosophila
1146	182.5	4.6	468	1	PCO1_RAT	Q8628 rattus norv	1219	180	4.6	511	2	Q9VZH5	Q9vzh5 drosophila
1147	182.5	4.6	470	2	Q7QIS5	Q7qis5 anopheles g	1220	180	4.6	546	2	Q8SXG6	Q8sxg6 anopheles g
1148	182.5	4.6	482	2	Q28982	Q28982 sus scrofa	1221	180	4.6	1823	2	Q7PRP5	Q7prp5 anopheles g
1149	182.5	4.6	484	1	LEM2_PIG	P98110 sus scrofa	1222	179.5	4.6	243	1	TRY1_XENLA	TRY1_XENLA
1150	182.5	4.6	520	2	O8ING0	O8ing0 drosophila	1223	179.5	4.6	250	1	KLK9_HUMAN	KLK9_HUMAN
1151	182.5	4.6	722	1	DLLE_MOUSE	Q61483 mus musculus	1224	179.5	4.6	258	1	TRYU_DROER	TRYU_DROER
1152	182.5	4.6	722	2	Q6PFV7	Q6pfv7 mus musculus	1225	179.5	4.6	259	1	CFAD_MOUSE	CFAD_MOUSE
1153	182.5	4.6	1551	2	Q9NGV4	Q9ngv4 drosophila	1226	179.5	4.6	274	1	FA9_SHEEP	FA9_SHEEP
1154	182.5	4.6	2531	2	O16004	O16004 lytechinus	1227	179.5	4.6	277	2	Q7QID2	Q7qid2 anopheles g
1155	182	4.6	240	2	Q9GQ03	Q9gq03 biophalari	1228	179.5	4.6	354	2	Q9U611	Q9u611 drosophila
1156	182	4.6	241	2	Q917L2	Q917l2 drosophila	1229	179.5	4.6	416	2	Q6DJ32	Q6dj32 xenopus tro
1157	182	4.6	284	2	O18434	O18434 helioverpa	1230	179.5	4.6	581	2	Q96015	Q96015 drosophila
1158	182	4.6	261	1	KLK5_MOUSE	P15945 mus musculus	1231	179.5	4.6	728	2	Q90656	Q90656 gallus gall
1159	182	4.6	262	1	TRYT_DROER	P54628 drosophila	1232	179.5	4.6	1047	2	Q24019	Q24019 drosophila
1160	182	4.6	278	2	Q7PNF6	Q7pnf6 anopheles g	1233	179.5	4.6	1047	2	Q9VZH2	Q9vzh2 drosophila
1161	182	4.6	280	2	Q9V5X8	Q9v5x8 drosophila	1234	179	4.5	253	1	TRYB_DROER	TRYB_DROER
1162	182	4.6	301	2	Q9V3Z2	Q9v3z2 drosophila	1235	179	4.5	266	1	EL1_PIG	EL1_PIG
1163	182	4.6	421	2	Q6ZMR5	Q6zmr5 homo sapien	1236	179	4.5	270	2	Q8WR11	Q8wr11 paralithode
1164	182	4.6	726	2	Q8AW87	Q8aw87 cynops pyrr	1237	179	4.5	280	1	TRYZ_DROME	TRYZ_DROME
1165	182	4.6	1238	1	JAG2_HUMAN	Q9y219 homo sapien	1238	179	4.5	282	2	O18655	O18655 plodia inte
1166	181.5	4.6	227	2	Q7PJQ1	Q7pjq1 anopheles g	1239	179	4.5	282	2	Q76B45	Q76b45 blarina bre
1167	181.5	4.6	229	2	Q7RHP2	Q7rhp2 anopheles g	1240	179	4.5	283	2	Q7PVP9	Q7pvp9 anopheles g
1168	181.5	4.6	247	1	GRAB_MOUSE	P04187 mus musculus	1241	179	4.5	290	2	Q6UDQ6	Q6udq6 penaeus mon
1169	181.5	4.6	258	1	GRAM_RAT	Q03238 rattus norv	1242	179	4.5	384	2	Q9XI63	Q9xy63 ctenocephal
1170	181.5	4.6	269	2	Q7Q6S6	Q7q6s6 anopheles g	1243	179	4.5	440	2	Q8MRF6	Q8mrf6 drosophila
1171	181.5	4.6	284	2	Q96089	Q96089 haemaphysal	1244	179	4.5	474	2	Q68EF1	Q68ef1 mus musculus
1172	181.5	4.6	284	2	Q7Q493	Q7q493 anopheles g	1245	179	4.5	549	1	LEM2_RAT	LEM2_RAT
1173	181.5	4.6	295	2	Q9NH07	Q9nh07 heliothis z	1246	179	4.5	606	2	P70412	P70412 mus musculus
1174	181.5	4.6	437	1	ACRO_RAT	P29293 rattus norv	1247	179	4.5	609	2	Q7M761	Q7m761 mus musculus
1175	181.5	4.6	450	2	Q7SI99	Q7sy99 xenopus lae	1248	179	4.5	612	1	LEM2_MOUSE	LEM2_MOUSE
1176	181.5	4.6	487	2	Q7ZWR8	Q7zwr8 xenopus lae	1249	179	4.5	675	2	Q9W6J8	Q9w6j8 dissostichu
1177	181.5	4.6	754	2	Q98UI6	Q98ui6 cyprinus ca	1250	179	4.5	905	2	Q800L4	Q800l4 gallus gall
1178	181	4.6	249	2	Q788V0	Q788v0 dissostichu	1251	179	4.5	919	2	Q8UVR0	Q8uvr0 gallus gall
1179	181	4.6	254	2	O18436	O18436 helioverpa	1252	179	4.5	936	2	Q8UVQ9	Q8uvq9 gallus gall
1180	181	4.6	254	2	Q76954	Q76954 laccanobia o	1253	179	4.5	2998	2	Q9VLT6	Q9vlt6 drosophila
1181	181	4.6	255	2	O34289	O34289 salvelinus	1254	178.5	4.5	201	2	Q7QAX3	Q7qax3 anopheles g
1182	181	4.6	258	2	Q632F4	Q632f4 rattus norv	1255	178.5	4.5	243	2	Q7SZ06	Q7sz06 xenopus lae
1183	181	4.6	261	1	KLK3_MOUSE	P00756 mus musculus	1256	178.5	4.5	255	1	TRY4_LUCCU	TRY4_LUCCU
1184	181	4.6	261	2	Q7PXE5	Q7pxe5 anopheles g	1257	178.5	4.5	256	2	Q6R561	Q6r561 ostrinia nu
1185	181	4.6	270	2	Q8L9P2	Q8l9p2 aplysina fi	1258	178.5	4.5	262	2	Q7PT73	Q7pt73 anopheles g
1186	181	4.6	318	2	Q7QC37	Q7qc37 anopheles g	1259	178.5	4.5	292	2	O18444	O18444 helioverpa
1187	181	4.6	370	2	Q6GQQ3	Q6gqq3 rattus norv	1260	178.5	4.5	300	2	Q9NH08	Q9nh08 agrotis ips
1188	181	4.6	405	2	Q8MQS8	Q8mq8 apis mellif	1261	178.5	4.5	346	2	Q7P243	Q7p243 anopheles g
1189	181	4.6	412	2	Q7SYT3	Q7sy73 xenopus lae	1262	178.5	4.5	400	2	Q9VCJ8	Q9vcj8 drosophila
1190	181	4.6	494	2	Q9VJD7	Q9vjd7 drosophila	1263	178.5	4.5	468	1	PCO1_MOUSE	PCO1_MOUSE
1191	181	4.6	674	2	Q7QFM7	Q7qfm7 anopheles g	1264	178.5	4.5	922	1	NRE1_RAT	NRE1_RAT
1192	181	4.6	840	2	Q9UJ45	Q9uj45 homo sapien	1265	178.5	4.5	923	1	NRE1_MOUSE	NRE1_MOUSE
1193	181	4.6	910	2	Q6UXD5	Q6uxd5 homo sapien	1266	178	4.5	212	2	O90920	O90920 rattus norv
1194	181	4.6	1271	1	YC81_CAEEL	Q19981 caenorhabdi	1267	178	4.5	253	1	TRYD_DROER	TRYD_DROER
1195	181	4.6	1329	2	Q9EMB0	Q9emb0 caenorhabdi	1268	178	4.5	256	2	O18599	O18599 drosophila
1196	180.5	4.6	182	2	Q6PLJ6	Q6plj6 penaeus jap	1269	178	4.5	259	2	Q632F5	Q632f5 rattus norv
1197	180.5	4.6	248	1	TRY2_CHICK	Q90628 gallus gall	1270	178	4.5	289	2	Q8MR67	Q8mr67 drosophila
1198	180.5	4.6	261	1	EUM3_EURMA	Q97370 euroglyphus	1271	178	4.5	290	2	Q9VRT2	Q9vrt2 drosophila
1199	180.5	4.6	263	2	Q7Q298	Q7q298 anopheles g	1272	178	4.5	292	2	Q7QK16	Q7qk16 anopheles g

1273	178	4.5	313	2	Q706S3	Q7q6s3 anopheles g	1346	175	4.4	555	2	Q9H2E2	Q9h2e2 homo sapien
1274	178	4.5	434	1	Q9V7S7	Q9v7e7 drosophila	1347	175	4.4	901	2	Q9H2D5	Q9h2d5 homo sapien
1275	178	4.5	528	1	GD_WDRME	Q62589 drosophila	1348	175	4.4	901	2	Q9H2E4	Q9h2e4 homo sapien
1276	178	4.5	596	2	Q8TD25	Q8td25 homo sapien	1349	175	4.4	906	2	Q9H2D4	Q9h2d4 homo sapien
1277	178	4.5	1212	2	Q42347	Q42347 rattus norv	1350	175	4.4	906	2	Q9H2E3	Q9h2e3 homo sapien
1278	177.5	4.5	248	1	NKP1_RAT	P18291 gallus gall	1351	175	4.4	931	1	NRP2_HUMAN	Q60462 homo sapien
1279	177.5	4.5	261	2	Q00344	Q00344 cochiobola	1352	175	4.4	931	2	Q723T9	Q723t9 homo sapien
1280	177.5	4.5	267	2	Q9VLF5	Q9vlf5 drosophila	1353	174.5	4.4	232	2	Q9TXE6	Q9txe6 bombyx mori
1281	177.5	4.5	328	2	Q61RA4	Q61ra4 xenopus lae	1354	174.5	4.4	246	1	TRV1_CANFA	P06871 canis fami
1282	177.5	4.5	556	2	Q6DEK7	Q6dek7 brachydanio	1355	174.5	4.4	371	2	Q7P2E6	Q7p2p6 anopheles g
1283	177.5	4.5	691	2	Q7PKC4	Q7pkc4 anopheles g	1356	174.5	4.4	1676	2	Q81NW2	Q81nw2 drosophila
1284	177.5	4.5	1364	1	NTC4_MOUSE	P31695 mus musculus	1357	174	4.4	250	2	Q8T4P4	Q8t4p4 lepeophthei
1285	177.5	4.5	2524	2	Q9GP45	Q9gpa5 brachiososto	1358	174	4.4	257	2	Q7Q2X4	Q7qt24 anopheles g
1286	177.5	4.5	2811	2	Q70434	Q7g434 anopheles g	1359	174	4.4	258	1	ELI_HUMAN	Q9un11 homo sapien
1287	177	4.5	233	2	Q6GRZ7	Q96rz7 homo sapien	1360	174	4.4	259	1	KLAM_MOUSE	P15948 mus musculus
1288	177	4.5	257	2	Q61E61	Q61e61 rattus norv	1361	174	4.4	261	1	KLX1_MOUSE	P00755 mus musculus
1289	177	4.5	258	2	Q9W5U8	Q9w5u8 drosophila	1362	174	4.4	261	2	Q9NIQ1	Q9niq1 saguinus oe
1290	177	4.5	271	1	CTR2_PENVA	P36178 penaeus van	1363	174	4.4	262	2	Q8T4P7	Q8t4p7 lepeophthei
1291	177	4.5	328	2	Q8BJR6	Q8bjr6 mus musculus	1364	174	4.4	263	1	KLKO_MOUSE	Q61754 mus musculus
1292	177	4.5	385	2	Q25101	Q25101 herdmania m	1365	174	4.4	266	1	ELI_BOVIN	Q28153 bos taurus
1293	177	4.5	425	2	Q9W1Q9	Q9wiq9 drosophila	1366	174	4.4	280	2	Q7ONE3	Q7qne3 anopheles g
1294	177	4.5	452	2	Q7P2E6	Q7p2e6 anopheles g	1367	174	4.4	280	2	Q8BLH5	Q8blh5 mus musculus
1295	177	4.5	473	1	FP2_MYTGA	Q25464 mytilus gal	1368	174	4.4	280	2	Q86T59	Q86t59 homo sapien
1296	177	4.5	536	2	Q7PX72	Q7px72 anopheles g	1369	174	4.4	1295	1	GLP1_CABEL	P13508 caenorhabdi
1297	177	4.5	737	2	Q90422	Q90422 brachydanio	1370	174	4.4	1295	2	Q6MG89	P13508 caenorhabdi
1298	177	4.5	747	2	Q91900	Q91900 xenopus lae	1371	173.5	4.4	205	2	Q96JE0	Q96je0 homo sapien
1299	177	4.5	927	2	Q69DB6	Q69db6 brachydanio	1372	173.5	4.4	205	2	Q96JE2	Q96je2 homo sapien
1300	176.5	4.5	182	2	Q6PLJ8	Q6plj8 procamburus	1373	173.5	4.4	236	2	Q7SIG3	Q7sig3 salmo salar
1301	176.5	4.5	267	2	Q9VRU0	Q9vru0 drosophila	1374	173.5	4.4	260	1	COGS_HYPLI	Q9bpq4 hypoderma l
1302	176.5	4.5	269	2	Q7PW17	Q7pw17 anopheles g	1375	173.5	4.4	260	2	Q9BPFQ4	Q9nb91 agrotis ips
1303	176.5	4.5	413	2	Q7SV25	Q7sv25 brachydanio	1376	173.5	4.4	262	2	Q6NNB3	Q6nnb3 drosophila
1304	176.5	4.5	716	2	Q91691	Q91691 xenopus lae	1377	173.5	4.4	279	2	Q7PWD4	Q7pwd4 anopheles g
1305	176.5	4.5	925	1	NRP2_RAT	Q35276 rattus norv	1378	173.5	4.4	319	2	Q6Q6S3	Q6q6s3 callinectes g
1306	176.5	4.5	926	2	Q8QZY7	Q8qzy7 mus musculus	1379	173.5	4.4	348	2	Q9KRJ1	Q9krj1 vibrio chol
1307	176.5	4.5	931	1	NRP2_MOUSE	Q35375 mus musculus	1380	173.5	4.4	607	2	Q35360	Q35360 rattus norv
1308	176.5	4.5	2003	1	NTC4_HUMAN	Q99466 homo sapien	1381	173.5	4.4	607	2	Q9QZT0	Q9qzt0 rattus norv
1309	176	4.5	243	2	Q8AVB3	Q8avb3 brachydanio	1382	173.5	4.4	684	2	Q81498	Q81498 cuplennius
1310	176	4.5	260	2	Q8T4P5	Q8t4p5 lepeophthei	1383	173.5	4.4	717	2	P87357	P87357 brachydanio
1311	176	4.5	261	1	KLK7_RAT	P36373 rattus norv	1384	173.5	4.4	720	2	Q8UWJ4	Q8uwj4 brachydanio
1312	176	4.5	261	1	KLK9_MOUSE	P15949 mus musculus	1385	173.5	4.4	809	2	Q9BW82	Q9bw82 homo sapien
1313	176	4.5	264	1	VDP_BOMMO	Q07943 bombyx mori	1386	173.5	4.4	853	2	Q9UU47	Q9uj47 homo sapien
1314	176	4.5	265	2	Q6GNG0	Q6gng0 xenopus lae	1387	173.5	4.4	913	2	Q6NUE0	Q6nue0 xenopus lae
1315	176	4.5	270	1	EL3A_HUMAN	P09093 homo sapien	1388	173.5	4.4	914	1	NRP1_CHICK	Q6ue0 gallus gall
1316	176	4.5	270	2	Q96OL8	Q96ol8 homo sapien	1389	173.5	4.4	927	2	Q6T868	Q6t868 brachydanio
1317	176	4.5	282	2	Q7QCX2	Q7qcx2 anopheles g	1390	173.5	4.4	159	2	Q28286	Q28286 canis fami
1318	176	4.5	297	2	Q9W174	Q9w174 drosophila	1391	173	4.4	229	1	TRYP_SQUAC	P00764 squalus aca
1319	176	4.5	389	2	Q9V517	Q9v517 drosophila	1392	173	4.4	246	2	Q6F3Z0	Q6p320 mus musculus
1320	176	4.5	575	2	Q22328	Q22328 caenorhabdi	1393	173	4.4	248	1	MCTR_RAT	P97594 rattus norv
1321	176	4.5	594	2	Q8K480	Q8k480 mus musculus	1394	173	4.4	248	2	Q8HYV6	Q8hyv6 oryctolagus
1322	176	4.5	891	2	Q9VV38	Q9vv38 drosophila	1395	173	4.4	253	2	Q9NGY5	Q9ngy5 heliothis v
1323	176	4.5	2318	1	NTC3_MOUSE	Q61982 mus musculus	1396	173	4.4	253	2	Q9NGY5	P91894 arenicola m
1324	176	4.5	2319	1	NTC3_RAT	Q9r172 rattus norv	1397	173	4.4	276	2	P91894	Q7q1d4 anopheles g
1325	175.5	4.4	220	2	Q7QM61	Q7qm61 anopheles g	1398	173	4.4	276	2	Q8QGR6	Q8qgr6 mus musculus
1326	175.5	4.4	220	2	Q81BE4	Q81be4 ochlerotatu	1399	173	4.4	287	2	Q675S0	Q675s0 oikopleura
1327	175.5	4.4	257	2	Q6R560	Q6r560 ostrinia nu	1400	173	4.4	406	2	Q25059	Q25059 helioctidari
1328	175.5	4.4	257	2	Q9VRS3	Q9vrs3 drosophila	1401	173	4.4	421	2	Q6ICK2	Q6ick2 homo sapien
1329	175.5	4.4	274	1	TRY5_ANOGA	P35039 anopheles g	1402	173	4.4	421	2	Q9VRT1	Q9vrt1 drosophila
1330	175.5	4.4	459	2	Q9V4W7	Q9v4w7 drosophila	1403	173	4.4	438	2	Q9VRT1	Q8i6j9 tenebrio mo
1331	175.5	4.4	522	2	Q8MQM9	Q8mqm9 drosophila	1404	173	4.4	444	2	Q816J9	Q8b9p4 bos taurus
1332	175.5	4.4	617	2	Q8JTS1	Q8jts1 triakis scy	1405	173	4.4	504	2	Q28BPP4	Q28b94 mus musculus
1333	175.5	4.4	677	2	Q9VVC7	Q9vvc7 drosophila	1406	173	4.4	578	2	Q8BPP4	P98106 rattus norv
1334	175.5	4.4	921	2	Q9QX38	Q9qx38 rattus norv	1407	173	4.4	768	1	LEM3_RAT	Q9gm3 paracentrot
1335	175.5	4.4	1316	2	Q96QU7	Q96qu7 homo sapien	1408	173	4.4	2656	2	Q9GNJ3	P08892 mus musculus
1336	175	4.4	249	2	Q6QX62	Q6qx62 lepeophthei	1409	172.5	4.4	248	1	GRAC_MOUSE	Q91ve3 m thymopsin
1337	175	4.4	260	2	Q8T4P6	Q8t4p6 lepeophthei	1410	172.5	4.4	249	2	Q91VE3	Q7q927 anopheles g
1338	175	4.4	261	2	Q62598	Q62598 plodia inte	1411	172.5	4.4	274	2	Q7Q927	P35036 anopheles g
1339	175	4.4	263	2	Q7Z1D5	Q7z1d5 lepeophthei	1412	172.5	4.4	277	1	TRY2_ANOGA	P91893 arenicola m
1340	175	4.4	264	2	Q81PY7	Q81py7 drosophila	1413	172.5	4.4	278	2	P91893	Q7q929 anopheles g
1341	175	4.4	284	2	Q71S89	Q7ys89 lepeophthei	1414	172.5	4.4	306	2	Q7Q929	Q9vj28 drosophila
1342	175	4.4	266	2	Q46644	Q46644 macaca fasc	1415	172.5	4.4	355	2	Q9VJZ8	Q9vj28 oryctolagus
1343	175	4.4	301	2	Q6U8A8	Q6u8a8 ornithodoro	1416	172.5	4.4	431	1	ACRO_RABIT	P48038 oryctolagus
1344	175	4.4	344	2	Q9W679	Q9w679 dissostichu	1417	172.5	4.4	433	2	Q8T3A2	Q8t3a2 ciona intes
1345	175	4.4	421	1	ACRO_HUMAN	P10323 homo sapien	1418	172.5	4.4	439	2	Q9Y122	Q9y122 drosophila



1419	172.5	4.4	4.4	1	PCOL HUMAN	Q15113	homo sapien
1420	172.5	4.4	4.4	863	Q6AXF9	Q6axf9	mus musculus
1421	172.5	4.4	4.4	923	Q91X64	Q91x64	mus musculus
1422	172.5	4.4	4.4	1202	1 JAG2 RAT	P97607	rattus norv
1423	172	4.4	4.4	157	1 PRTC CAPHI	Q28315	capra hircu
1424	172	4.4	4.4	235	2 Q66P68	Q66p68	fugu rubrip
1425	172	4.4	4.4	242	1 FIBC LUNRU	P83238	lumbriacus r
1426	172	4.4	4.4	242	2 Q96687	Q96687	lumbriacus r
1427	172	4.4	4.4	249	2 Q7KRDO	Q7krdo	notothenia
1428	172	4.4	4.4	249	2 Q9W6K0	Q9w6k0	notothenia
1429	172	4.4	4.4	254	1 TRYP SARBU	P51588	sarcophaga
1430	172	4.4	4.4	254	2 Q765Z0	Q765z0	stomoxys ca
1431	172	4.4	4.4	260	1 ESTA CANFA	P09582	canis famil
1432	172	4.4	4.4	260	2 Q9V7G4	Q9v7g4	canis famil
1433	172	4.4	4.4	261	1 KLK8 MOUSE	P07628	mus musculus
1434	172	4.4	4.4	261	2 Q6H320	Q6h320	bos taurus
1435	172	4.4	4.4	262	1 TRYT DROME	P42278	drosofila
1436	172	4.4	4.4	262	2 Q8S2G7	Q8szg7	drosofila
1437	172	4.4	4.4	262	2 Q9V8Y0	Q9v8y0	drosofila
1438	172	4.4	4.4	390	2 Q81927	Q81927	hyphantria
1439	172	4.4	4.4	415	1 ACRO PIG	P08001	sus scrofa
1440	172	4.4	4.4	415	2 Q29015	Q29015	sus sp. pre
1441	172	4.4	4.4	441	2 Q81917	Q81917	manduca sex
1442	172	4.4	4.4	441	2 Q81925	Q81925	hyphantria
1443	172	4.4	4.4	655	2 Q7KKR0	Q7kkro	drosofila
1444	172	4.4	4.4	721	2 Q95YG0	Q95yg0	ciona savig
1445	172	4.4	4.4	721	2 Q91902	Q91902	xenopus lae
1446	172	4.4	4.4	1208	2 Q80YAB	Q80yab	mus musculus
1447	172	4.4	4.4	1247	1 JAG2 MOUSE	Q9qye5	mus musculus
1448	171.5	4.3	4.3	241	2 Q9G0G2	Q9g0g2	biophalari
1449	171.5	4.3	4.3	248	2 Q8IR82	Q8ir82	drosofila
1450	171.5	4.3	4.3	261	2 Q6H322	Q6h322	equus cabal
1451	171.5	4.3	4.3	262	1 KLK1 HUMAN	P06870	homo sapien
1452	171.5	4.3	4.3	262	2 Q7PX38	Q7px38	anopheles g
1453	171.5	4.3	4.3	277	2 Q8VPM8	Q8vpm8	drosofila
1454	171.5	4.3	4.3	278	2 Q8MQ02	Q8mq02	drosofila
1455	171.5	4.3	4.3	282	2 Q9NGY4	Q9ngy4	heliothis v
1456	171.5	4.3	4.3	321	2 Q61860	Q61e60	rattus norv
1457	171.5	4.3	4.3	373	2 Q7PVJ0	Q7pvj0	anopheles g
1458	171.5	4.3	4.3	1785	2 Q9Y211	Q9y211	homo sapien
1459	171.5	4.3	4.3	1785	2 Q9Y4V9	Q9y4v9	homo sapien
1460	171.5	4.3	4.3	2403	2 Q9UGM2	Q9ugm2	homo sapien
1461	171.5	4.3	4.3	2413	2 Q96DU4	Q96du4	homo sapien
1462	171.5	4.3	4.3	2413	2 Q9UKJ4	Q9ukj4	homo sapien
1463	171.5	4.3	4.3	2426	2 Q9UGM3	Q9ugm3	homo sapien
1464	171	4.3	4.3	175	2 Q6PLJ9	Q6plj9	squilla ora
1465	171	4.3	4.3	245	2 Q17439	Q17439	boltenia vi
1466	171	4.3	4.3	248	2 Q8T4P2	Q8t4p2	leptophthei
1467	171	4.3	4.3	258	2 Q61SM6	Q61sm6	homo sapien
1468	171	4.3	4.3	260	1 GRAA MOUSE	P11032	mus musculus
1469	171	4.3	4.3	262	2 Q7Z1D6	Q7z1d6	leptophthei
1470	171	4.3	4.3	266	1 EL1 RAT	P00773	rattus norv
1471	171	4.3	4.3	273	1 TRY5 ANOGA	P35040	anopheles g
1472	171	4.3	4.3	277	1 KLK0 HUMAN	Q9ukr3	homo sapien
1473	171	4.3	4.3	319	2 Q9VAQ4	Q9vaq4	drosofila
1474	171	4.3	4.3	358	2 Q45029	Q45029	drosofila
1475	171	4.3	4.3	426	2 Q8CFX9	Q8cfx9	mus musculus
1476	171	4.3	4.3	454	2 Q8TB42	Q8tb42	homo sapien
1477	171	4.3	4.3	609	2 Q9GLF0	Q9glf0	canis famil
1478	171	4.3	4.3	611	1 LEM2 CANFA	P33730	canis famil
1479	171	4.3	4.3	737	2 Q81YTO	Q81yto	homo sapien
1480	171	4.3	4.3	737	2 Q8NFT8	Q8nft8	homo sapien
1481	171	4.3	4.3	832	2 Q9JLB4	Q9jlb4	mus musculus
1482	171	4.3	4.3	2139	1 CRB DROME	P10040	drosofila
1483	171	4.3	4.3	2146	2 Q9VC97	Q9vc97	drosofila
1484	171	4.3	4.3	2412	2 Q9UJ57	Q9uj57	homo sapien
1485	170.5	4.3	4.3	259	2 Q45048	Q45048	anopheles g
1486	170.5	4.3	4.3	273	2 Q57659	Q57659	gallus gall
1487	170.5	4.3	4.3	282	2 Q7PVP7	Q7pvp7	anopheles g
1488	170.5	4.3	4.3	328	2 Q6BEA2	Q6bea2	rattus norv
1489	170.5	4.3	4.3	350	2 Q9VSE3	Q9vse3	drosofila
1490	170.5	4.3	4.3	377	2 Q9VB68	Q9vb68	drosofila
1491	170.5	4.3	4.3	390	2 Q9Y157	Q9y157	drosofila

1492	170.5	4.3	408	2	Q8MR95	Q8mr95	drosofila
1493	170.5	4.3	473	2	Q7PV63	Q7pv63	anopheles g
1494	170.5	4.3	669	2	Q922H0	Q922h0	mus musculus
1495	170.5	4.3	705	2	Q6MZN4	Q6mzn4	homo sapien
1496	170.5	4.3	772	2	Q6DI48	Q6di48	brachydanio
1497	170.5	4.3	802	2	Q57462	Q57462	brachydanio
1498	170	4.3	239	2	Q8T4P3	Q8t4p3	leptophthei
1499	170	4.3	239	2	Q63275	Q63275	rattus norv
1500	170	4.3	245	1	MCT1_SHEEP	P80931	ovis aries

## ALIGNMENTS

## RESULT 1

Q6UXH9	PRELIMINARY;	PRT;	720 AA.
ID	Q6UXH9		
AC	Q6UXH9		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	ELGCG99.		
GN	ORFName=UNO699;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
NCBI_TaxID=9606;			
[1]			
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-22887236; PubMed-12975309; DOI-10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.U., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandien R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
CC	Genome Res. 13:2265-2270(2003).		
CC	-/- SIMILARITY: Belongs to peptidase family S1.		
CC	-/- SIMILARITY: Contains 1 EGF-like domain.		
DR	EMBL; AY358346; AAQ88712.1; -		
DR	HSSP; P00734; 1BB0.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR000859; CUB.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR006209; EGF-like.		
DR	InterPro; IPR006210; IEGF.		
DR	InterPro; IPR001254; Peptidase S1.		
DR	InterPro; IPR001314; Peptidase S1A.		
DR	InterPro; IPR009003; Pept_Ser_Cys.		
DR	Pfam; PF00431; CUB; 1.		
DR	Pfam; PF00008; EGF; 1.		
DR	Pfam; PF00084; Sushi; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	SMART; SM00032; CCF; 2.		
DR	SMART; SM00042; CUB; 1.		
DR	SMART; SM00181; EGF; 2.		
DR	SMART; SM00179; EGF_Ca; 1.		
DR	SMART; SM00020; Tryp_Spc; 1.		
DR	PROSITE; PS01180; CUB; 1.		
DR	PROSITE; PS00022; EGF_1; 1.		
DR	PROSITE; PS01186; EGF_2; 1.		



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DR PROSITE; PS50026; EGF 3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80196 MW; DC898BC7241289D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.6e-287;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
DB 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
QY 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
DB 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
QY 121 YGDCMRCGOVLRAPKGQILLESYPLNAHCETIHAKEPFIQLRVFMLSLEFDYMCQYD 180
DB 121 YGDCMRCGOVLRAPKGQILLESYPLNAHCETIHAKEPFIQLRVFMLSLEFDYMCQYD 180
QY 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSIGSSILHLVLFHSDGSKNFGFHAIEEITACS 240
DB 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSIGSSILHLVLFHSDGSKNFGFHAIEEITACS 240
QY 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKKTCCQNGEWSGKQPICIKACREPISDLVRRRL 360
DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKKTCCQNGEWSGKQPICIKACREPISDLVRRRL 360
QY 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTCKKPPALPGDLPNGYQHLHTQLQYECISPFYR 420
DB 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTCKKPPALPGDLPNGYQHLHTQLQYECISPFYR 420
QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWQAAIYRRTSGVHDGSL 480
DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWQAAIYRRTSGVHDGSL 480
QY 481 HKGAWFLVCSGALVNERVTVVAACHVTDLGKVTMIKTADLKVLGKPYRDDRDDEKTIQS 540
DB 481 HKGAWFLVCSGALVNERVTVVAACHVTDLGKVTMIKTADLKVLGKPYRDDRDDEKTIQS 540
QY 541 LQISAILHPNYDPIILLDADIALILKLDKARISTRVQPICLAASRDILSTSFQESHITVAG 600
DB 541 LQISAILHPNYDPIILLDADIALILKLDKARISTRVQPICLAASRDILSTSFQESHITVAG 600
QY 601 WNVLDVRSFGKNDLTRSGVSVVDSLLCEEQEDHGIPVSVTDNMFCASWEPTAPSDI 660
DB 601 WNVLDVRSFGKNDLTRSGVSVVDSLLCEEQEDHGIPVSVTDNMFCASWEPTAPSDI 660
QY 661 CTAETGGIAAVSPGRASPRRHLMLGVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK 720
DB 661 CTAETGGIAAVSPGRASPRRHLMLGVSWSYDKTCSHRLSTAFTKVLFPKDWIERNMK 720

RESULT 2
Q6N062 PRELIMINARY; PRT; 720 AA.
AC Q6N062;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686N24154.
GN Name=DKFZp686N24154;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Colon endothel.
RG The German CDNA Consortium;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BX640676; CAE45808.1; -.
DR HSSP; P00734; 1BBO.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;
SQ Serine protease.
SQ SEQUENCE 720 AA; 80196 MW; E98A9F9948EE777D CRC64;

Query Match 99.8%; Score 3936; DB 2; Length 720;
Best Local Similarity 99.7%; Pred. No. 7.5e-287;
Matches 718; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
DB 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
QY 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
DB 61 VVGTYTPCCNNEECDSCLIHPGCTIFENCKSCRNCSWGGLTDDFVVGKGYCAECRAGW 120
QY 121 YGDCMRCGOVLRAPKGQILLESYPLNAHCETIHAKEPFIQLRVFMLSLEFDYMCQYD 180
DB 121 YGDCMRCGOVLRAPKGQILLESYPLNAHCETIHAKEPFIQLRVFMLSLEFDYMCQYD 180
QY 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSIGSSILHLVLFHSDGSKNFGFHAIEEITACS 240
DB 181 YVEVRDGDNRDQGIIRKVCNERNPAPIQSIGSSILHLVLFHSDGSKNFGFHAIEEITACS 240
QY 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSKYKACLAGYTGRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKKTCCQNGEWSGKQPICIKACREPISDLVRRRL 360
DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKKTCCQNGEWSGKQPICIKACREPISDLVRRRL 360
QY 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTCKKPPALPGDLPNGYQHLHTQLQYECISPFYR 420
DB 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTCKKPPALPGDLPNGYQHLHTQLQYECISPFYR 420
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Db 541 LGRFYRDDDRDEXTQISLQISAILHPNVDPILLDADIALKLLDKARISTRVQPICLAA 600  
QY 584 SRDLSTSFQESHITVAGNVNVLADVRSPGFKNDTLRSGVSVVDSILCEQHEHGHGIPVSU 643  
Db 601 SRDLSTSFQESHITVAGNVNVLADVRSPGFKNDTLRSGVSVVDSILCEQHEHGHGIPVSU 660  
QY 644 TDMNFCASWEPTAPSDICTAETGIIAASVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLST 703  
Db 661 TDMNFCASWEPTAPSDICTAETGIIAASVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLST 720  
QY 704 APTKVLFPKDWIERNMK 720  
Db 721 APTKVLFPKDWIERNMK 737  
RESULT 4  
Q8BU25 PRELIMINARY; PRT; 720 AA.  
AC Q8BU25;  
DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430002G05 product:hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine proteases, trypsin family domain containing protein, full insert sequence.  
DE Name=E430002G05Rik;  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
[3]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RA The FANTOM Consortium;  
RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
RL "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
RN Nature 420:563-573(2002).  
[4]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
RN Genome Res. 10:1617-1630(2000).  
[5]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."  
RN Genome Res. 10:1757-1771(2000).  
[6]  
RN SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akanishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
CC 1- SIMILARITY: Belongs to peptidase family S1.  
CC 1- SIMILARITY: Contains 1 EGF-like domain.  
DR EMBL; AK088017; BAC40098.1; -.  
DR HSSP; P00736; IGPZ.  
DR MGD; MGI:2445082; E430002G05Rik.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS00923; SUSHI; 2.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;  
KW Serine protease.  
SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;  
Query Match 91.6%; Score 3612; DB 2; Length 720;  
Best Local Similarity 90.1%; Pred. No. 1.6e-262;  
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;  
QY 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPKRE 60  
DB 1 MELDRWAQLGLVFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECLCPKKE 60  
QY 61 VVGVTTPCCFNEEDSCSLIHFGCTIFENCKSCRNCSWGGLTDDFYVKGFGYCAECRAG 120  
DB 61 VVGVTTPCCFNEEDSCSLIHFGCTIFENCKSCRNCSWGGLTDDFYVKGFGYCAECRAG 120  
QY 121 YGGDMRCGGVLRAPKGQILLESYPNAHCETWTHAKPGFVIQLRFWLSLEFDYMCQYD 180  
DB 121 YGGDMRCGGVLRAPKGQILLESYPNAHCETWTHAKPGFVIQLRFWLSLEFDYMCQYD 180  
QY 181 YVEVRGDNRDGOIIRKVCNNEPAPQSTIGSSILHVLFDSDGSKNPDGFFHAYVEEITACS 240  
DB 181 YVEVRGDNRDSDPIIRKFCNNEPAPQSTIGSSILHVLFDSDGSKNPDGFFHAYVEEITACS 240  
QY 241 SSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDFPGPVNGYQKITGGPLI 300

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Db 241 SSPCFHDTCLLDTTGSFKACACAGYTGRCENLLEBRNCSLDGGPVNGYKLTGEGPLL 300
Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Db 301 NEHHVIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Qy 361 PMQVSRRTPLHQLYSNFAFSKQKLSQAPTAKKPPALPGDLPNGYHQLHTLOQYECISPPFYR 420
Db 361 SMQVSRRTPLHQLYSTAFSKQKLDASTKKPAPLPGDLPNGYHQLHTLOQYECISPPFYR 420
Qy 421 RLSSRRRTCLRTGWSRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480
Db 421 RLSSRRRTCLRTGWSRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480
Qy 481 HKGAWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLKVVLGKFRYRDDDEKTIQS 540
Db 481 HKGAWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLKVVLGKFRYRDDDEKTIQS 540
Qy 541 LQISAILHPNYDPIILDADIALKLDKARISTRVQPICLAAASRLDLSFQBSHITVAG 600
Db 541 LRVSAIILHPNYDPIILDADIALKLDKARISTRVQPICLAAASRLDLSFQBSHITVAG 600
Qy 601 WNLADVRSPGFKNDTLRSQVSVVDSLCEOEHDGPIVSVTDNMFCASWPTAPSDI 660
Db 601 WNLADVRSPGFKNDTLHYGVRVVDPMLECEQHDGPIVSVTDNMFCASKDPSTPSDI 660
Qy 661 CTAETGGIAAVSPGPRPRLHMLGLVSWSDYDKTSKRLSTAFKTVLPFKDWIERNMK 720
Db 661 CTAETGGIAALSPGPRPRLHMLGLVSWSDYDKTSKRLSTAFKTVLPFKDWIERNMK 720

RESULT 5
Q8K2B8 PRELIMINARY; PRT; 720 AA.
AC Q8K2B8;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, last annotation update)
DE Regeneration associated muscle protease.
GN Name=E430002G05Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.P., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; BC031841; AAH31841.1; -.
DR EMBL; BC057685; AAH57685.1; -.
DR HSSP; P00736; 1GPZ.
DR MGD; MGI:2445082; E430002G05Rik.
DR CO; Q0:0005615; C:extracellular space; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS09923; SUSHI; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;

Query Match 91.6%; Score 3612; DB 2; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.6e-262;
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

Qy 1 MELGCVTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60
Db 1 MELDRWAQLGLVFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECLCPGKKE 60

Qy 61 VVGTYTPCCRNENECDSCLIHPGCTIPENCCKSCRNCSGGTLLDDPVVKGFFCAECRAGW 120
Db 61 VVGTYTPCCRNENECDSCLIHPGCTIPENCCKSCRNCSGGTLLDDPVVKGFFCAECRAGW 120

Qy 121 YGDCMRCQVLRAPKQGLLESYPLNAHCEWTIHAKPGFVQLRFLVMSLEFDYMCQYD 180
Db 121 YGDCMRCQVLRAPKQGLLESYPLNAHCEWTIHAKPGFVQLRFLVMSLEFDYMCQYD 180

Qy 181 YVEVRDGNRDQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPDGFHAIYEETACS 240
Db 181 YVEVRDGNDSPIIKRFGNERPAPIRSTGSSLHVLPHSDGSKNPDGFHAFVEETACS 240

Qy 241 SSPCFHDTCLLDTTGSFKACACAGYTGRCENLLEBRNCSLDGGPVNGYKLTGEGPLL 300
Db 241 SSPCFHDTCLLDTTGSFKACACAGYTGRCENLLEBRNCSLDGGPVNGYKLTGEGPLL 300

Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360
Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCIKACREPKISDLVRRVRL 360

Qy 361 PMQVSRRTPLHQLYSNFAFSKQKLSQAPTAKKPPALPGDLPNGYHQLHTLOQYECISPPFYR 420
Db 361 SMQVSRRTPLHQLYSTAFSKQKLDASTKKPAPLPGDLPNGYHQLHTLOQYECISPPFYR 420

Qy 421 RLSSRRRTCLRTGWSRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480
Db 421 RLSSRRRTCLRTGWSRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480

Qy 481 HKGAWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLKVVLGKFRYRDDDEKTIQS 540
Db 481 HKGAWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLKVVLGKFRYRDDDEKTIQS 540
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ID Q71RES PRELIMINARY; PRT; 417 AA.  
AC Q71RES; 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE FP938  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,  
RA Wan D.F., Gu J.R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; AF370388; AAQ15224.1; -  
DR HSSP; P00734; 1BB0.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Peptidase\_S1A.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS50923; SUSHI; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;  
  
Query Match 52.2%; Score 2059; DB 2; Length 417;  
Best Local Similarity 95.6%; Pred. No. 3 5e-146;  
Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;  
  
QY 314 FCNNSVYLGNEKRTCCQNGESGKQPIKACREPKISDLVRRRLPMQVQSRTEPLHQ 373  
DB 11 FVTTPMFLVAMRKELASRMERWSGKQPIKACREPKISDLVRRRLPMQVQSRTEPLHQ 70  
  
QY 374 LYSAAFSKQKQAPTKKPPALPGDLPNGYQHLLTQYECISPPFRRLLGSSRRTCIRTG 433  
DB 71 LYSAAFSKQKQAPTKKPPALPGDLPNGYQHLLTQYECISPPFRRLLGSSRRTCIRTG 130  
  
QY 434 KNSGRAPSCIPICGKENTITAPKTQGLRWPMQAAIYRRTSVGHDSLHKGAWFLVCSGAL 493  
DB 131 KNSGRAPSCIPICGKENTITAPKTQGLRWPMQAAIYRRTSVGHDSLHKGAWFLVCSGAL 190  
  
QY 494 VNERTVVAACHVTDLGKVTIMKTADLKVVLGKPYRDDDRDEKTIQSLQISAILLHPNYD 553  
DB 191 VNERTVVAACHVTDLGKVTIMKTADLKVVLGKPYRDDDRDEKTIQSLQISAILLHPNYD 250  
  
QY 554 PILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVAGWNVLDVRSFGPK 613  
DB 251 PILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVAGWNVLDVRSFGPK 310  
  
QY 614 NDLTRSGVSVVDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSF 673  
DB 311 NDLTRSGVSVVDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSF 370  
  
QY 674 PGRASPEPRHMLGLVSWSDYKTCSHRLSTAFTKVLPFKDWIERNM 720  
DB 371 PGRASPEPRHMLGLVSWSDYKTCSHRLSTAFTKVLPFKDWIERNM 417  
  
RESULT 8  
QY432  
ID QY432 PRELIMINARY; PRT; 181 AA.  
AC QY432;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein DKF2p586H2123 (Fragment).  
GN Name=DKF2p586H2123;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ansoorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AL050214; CAB43317.1; -  
DR PIR; T08805; T08805.  
DR HSSP; P00736; 1MD7.  
DR MEROPS; S01.998; -  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR009003; Peptidase\_S1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW Hydrolase; Hypothetical protein; Protease; Serine protease.  
FT NON\_TER 1  
SQ SEQUENCE 181 AA; 19962 MW; ABC793BE8682D439 CRC64;  
  
Query Match 24.1%; Score 949; DB 2; Length 181;  
Best Local Similarity 99.4%; Pred. No. 2.9e-63;  
Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 540 SLQISAILLHPNYDPIILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVA 599  
DB 1 SLRISAILLHPNYDPIILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVA 60  
  
QY 600 GNVLDVRSFGPKNDLRSVGVSVDLSLCEQHEHDGIPVSVTDNMFCASWEPTAPSD 659  
DB 61 GNVLDVRSFGPKNDLRSVGVSVDLSLCEQHEHDGIPVSVTDNMFCASWEPTAPSD 120  
  
QY 660 ICTAETGGIAAVSFPGRASPEPRHMLGLVSWSDYKTCSHRLSTAFTKVLPFKDWIERNM 719  
DB 121 ICTAETGGIAAVSFPGRASPEPRHMLGLVSWSDYKTCSHRLSTAFTKVLPFKDWIERNM 180  
  
QY 720 K 720  
DB 181 K 181  
  
RESULT 9  
QY432  
ID QY432 PRELIMINARY; PRT; 1019 AA.  
AC QY432;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Factor C precursor.  
OS Tachypleus tridentatus (Japanese horseshoe crab).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
OC Limulidae; Tachypleus.  
OX NCBI\_TaxID=6853;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21955715; PubMed=11958140;  
RA Wang D., Liu J., Chen L., Wang L., Yang G., Wu X., Zhang W.;  
RT "Cloning and expression of Tachypleus tridentatus factor C";  
RL Acta Biochim. Biophys. Sin. 34:77-82(2002).  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
DR EMBL; AF467804; AAL75577.1; -  
DR HSSP; P00746; 1FDP.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.



```

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR009003; Pept_Ser_Cys.
DR Pfam: PF003815; LCCL; 1.
DR Pfam: PF00059; Lectin_C; 1.
DR Pfam: PF00084; Sushi; 3.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 5.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00041; C_TYPE_LECTIN_2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00820; LCCL; 1.
DR PROSITE: PS00923; SUSHI; 5.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1
FT CHAIN 26 1019
SQ SEQUENCE 1019 AA; 112248 MW; B8E51730AE595993 CRC64;

Query Match 17.2%; Score 678; DB 2; Length 1019;
Best Local Similarity 25.68; Pred No. 5.5e-42;
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAEWNIM-----CRECEYDQIE---CVCFGKREVGVGTIPCCRNENECDCLIHGCT 86
DB 184 PNGQWSFPKPCIRECAKVSPEHGKVTAPSGNMIEGATL-----RFSCHS-----PHYL 233
QY 87 IFENCKSCR-NGSWGGL-----CGQVLR--APKG 137
DB 234 IGOETLTTCOGNGQWSGQIPQCKLVFCPDLDPVNHAEHVQKIGVEQKYGFPQGTETVYT 293
QY 104 --DDFYVKGFYCAECR--AGWYGG--DCMR-----CGQVLR--APKG 137
DB 294 CSGNYFLMGNTLTKNLDGWSGSQPSCKVADREVDVDCSKAVDFLDDVGEVRIHCPAG 353
QY 138 QILLES-----YPLNACHEWTIHA-----KPGFVI-----Q 163
DB 354 CSLTAGTVGCTATYVHELSSVCRAIHAAGKLPNSGGAHVHVNNGPYSDFLGSLDNGIKSEE 413
QY 164 LRFVMSLEFDYM-----COYDVVEVRD-----GNRDQIIRKVCN--ERPAP 206
DB 414 LKSLARSFRFDYVSSSTAGRSGCPDGMFVEENCVVYTSQRAWERAQGVCTNNAARLAV 473
QY 207 IQS--IGSSLHLVLFHSDG--SKNFDGEH-----ALYEBITACSSSPCF 245
DB 474 LKDVIPSSITEALRGKGLTTTIGLRLDAEKFVWELMDRNVNLDNLTFWASGEPG 533
QY 246 HDGTCV-LDKAGS-----YKCACLAGYTGORCENLLEARN---CSDPGGPNVGKIQKIGP 297
DB 534 NETNCVYLDIRDQIQPVWKTCKSCFPSSFACMMDLSDRNAKAKDDPGSLENGHATLHGQS 593
QY 298 GLINGRAHAKGTVVVFFCNNSYVLSGNEKTCQONGEWSGKQPCIK--ACRPEKISDLV 355
DB 594 --IDGFYA--GSSIRYCEVHLVLSGTETVCTTNGTWSAPKPKRCIKVITCONPPVPSYG 649
QY 356 RRRVLPQVQOSRETFPLHQLYSAAPSKQLQ---SAPTKKPAALPGD-----LP 400

```

## RESULT 10

## LFC\_TACTR

## ID LFC TACTR

## STANDARD; PRT; 1019 AA.

## AC

## P28175;

## DT

## 01-OCT-1994 (Rel. 30, Created)

## DT

## 01-OCT-1994 (Rel. 30, Last sequence update)

## DT

## 25-OCT-2004 (Rel. 45, Last annotation update)

## DE

## Fimulus clotting factor C precursor (EC 3.4.21.84) (FC).

## OS

## Tachyplesus tridentatus (Japanese horseshoe crab).

## OC

## Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;

## OC

## Limulidae; Tachyplesus.

## OX

## NCBI\_TaxID=6853;

## RN

## SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.

## RP

## MEDLINE=91177916; PubMed=2007602;

## RX

## Muta T., Miyata T., Misumi Y., Tokunaga F., Nakamura T., Toh Y.,

## RA

## Ikehara Y., Iwanaga S.

## RA

## "Limulus factor C. An endotoxin-sensitive serine protease zymogen with

## RT

## a mosaic structure of complement-like, epidermal growth factor-like,

## RT

## and lectin-like domains.";

## RL

## J. Biol. Chem. 266:6554-6561(1991).

## CC

## - FUNCTION: This enzyme is closely associated with an endotoxin-

## CC

## sensitive hemolymph coagulation system which may play important

## CC

## roles in both hemostasis and host defense mechanisms. Its active

## CC

## form catalyzes the activation of factor B.

## CC

## - CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and

## CC

## 124-Ile-Ile-125 bonds in Limulus clotting factor B to form

## CC

## activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic

## CC

## substrates.

## CC

## - ENZYME REGULATION: Activated by Gram-negative bacterial

## CC

## lipopolysaccharides and chymotrypsin.

## CC

## - SUBUNIT: Heterodimer of a light chain and a heavy chain linked by

## CC

## a disulfide bond.

## CC

## - SUBCELLULAR LOCATION: Secreted in hemolymph.

## CC

## - ALTERNATIVE PRODUCTS:

## CC

## Event=Alternative splicing; Named isoforms=2;

## CC

## Name=Long;

## CC

## IsoId=P28175-1; Sequence=Displayed;

## CC

## Name=Short;

## CC

## IsoId=P28175-2; Sequence=VSP\_005413, VSP\_005414;

## CC

## - SIMILARITY: Belongs to the peptidase S1 family.

## CC

## - SIMILARITY: Contains 1 C-type lectin family domain.

## CC

## - SIMILARITY: Contains 1 EGF-like domain.

## CC

## - SIMILARITY: Contains 1 LCCL domain.

## CC

## - SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.

## CC

## - SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.

## CC





QY 689 VMSYDKTCSH-RLSTAFKTLVLPKDWIER 717  
 DB 988 VSWGSPSGCKANQYGGFTKVNFLSWIRQ 1017

RESULT 11  
 LFC\_CARRO STANDARD; PRT; 1019 AA.  
 AC Q26422;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).  
 OS Carinoscorpius rotundicauda (Southeast Asian horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 OC Limulidae; Carinoscorpius.  
 OX NCBI\_TaxID=6848;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=95268506; PubMed=7538401;  
 RA Ding J.L., Navas M.A. III, Ho B.;  
 RT "Molecular cloning and sequencing analysis of factor C cDNA from the  
 RL Singapore horseshoe crab, Carinoscorpius rotundicauda.";  
 RL Mol. Mar. Biol. Biotechnol. 4:90-103(1995).  
 CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-  
 sensitive hemolymph coagulation system which may play important  
 roles in both hemostasis and host defense mechanisms. Its active  
 form catalyzes the activation of factor B.  
 CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-104 and  
 124-Ile-125 bonds in Limulus clotting factor B to form  
 CC activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic  
 CC substrates.  
 CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial  
 CC lipopolysaccharides and chymotrypsin (By similarity).  
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by  
 CC a disulfide bond (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted in hemolymph.  
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -!- SIMILARITY: Contains 1 EGF-like domain.  
 CC -!- SIMILARITY: Contains 1 LCCL domain.  
 CC -!- SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; S77063; AAB34361.1; -.  
 CC HSP; P00746; 1PDP.  
 CC DR MEROPS; S01.219; -.  
 CC InterPro; IPR000742; EGF 2  
 CC InterPro; IPR006209; EGF\_like.  
 CC InterPro; IPR006210; IEGF.  
 CC InterPro; IPR004043; LCCL.  
 CC InterPro; IPR001304; Lectin C.  
 CC InterPro; IPR001254; Peptidase S1.  
 CC InterPro; IPR001314; Peptidase\_S1.  
 CC InterPro; IPR009003; Pept\_Ser\_Cys.  
 CC InterPro; IPR004036; Sushi\_SCR\_CCP.  
 CC Pfam; PF03815; LCCL; 1.  
 CC Pfam; PF00059; Lectin C; 1.  
 CC Pfam; PF00084; Sushi; 5.  
 CC Pfam; PF00089; Trypsin; 1.  
 CC PRINTS; PR00722; CHYMOTRYPSIN.  
 CC SMART; SM00032; CCP; 5.  
 CC SMART; SM00034; CLECT; 1.  
 CC SMART; SM00181; EGF; 1.  
 CC SMART; SM00603; LCCL; 1.

DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00441; C\_TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS00820; LCCL; 1.  
 DR PROSITE; PS00923; SUSHI; 5.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Cell adhesion; EGF-like domain; Glycoprotein; Hemolymph clotting;  
 KW Hydrolase; Lectin; Repeat; Serine protease; Signal; Sushi.  
 FT SIGNAL 1 25 By similarity.  
 FT CHAIN 26 1019 Limulus clotting factor C.  
 FT CHAIN 26 690 Limulus clotting factor C heavy chain.  
 FT CHAIN 691 1019 Limulus clotting factor C light chain.  
 FT CHAIN 691 762 Limulus clotting factor C chain A.  
 FT CHAIN 763 1019 Limulus clotting factor C chain B.  
 FT DOMAIN 102 137 EGF-like.  
 FT DOMAIN 140 197 Sushi 1.  
 FT DOMAIN 198 256 Sushi 2.  
 FT DOMAIN 258 323 Sushi 3.  
 FT DOMAIN 325 421 LCCL.  
 FT DOMAIN 436 568 C-type lectin.  
 FT DOMAIN 574 636 Sushi 4.  
 FT DOMAIN 689 750 Sushi 5.  
 FT DOMAIN 763 1019 Serine protease.  
 FT ACT\_SITE 809 809 Charge relay system (By similarity).  
 FT ACT\_SITE 865 865 Charge relay system (By similarity).  
 FT ACT\_SITE 966 966 Charge relay system (By similarity).  
 FT BINDING 960 960 Substrate (By similarity).  
 FT DOMAIN 643 689 Pro-rich.  
 FT DISULFID 106 118 By similarity.  
 FT DISULFID 112 125 By similarity.  
 FT DISULFID 127 136 By similarity.  
 FT DISULFID 436 447 By similarity.  
 FT DISULFID 464 564 By similarity.  
 FT DISULFID 538 556 By similarity.  
 FT DISULFID 794 810 By similarity.  
 FT DISULFID 932 951 By similarity.  
 FT DISULFID 962 996 By similarity.  
 FT CARBOHYD 523 523 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 534 534 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 624 624 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 740 740 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 767 767 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 912 912 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 1019 AA; 112429 MW; 918A1ED8B817B6C3 CRC64;

Query Match 16.9%; Score 665; DB 1; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 5.2e-41;  
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWIMCECEYDQIECVCPGKRE-----VVGYYTIPCCRNENECDSCLIH 82  
 DB 184 PNGQSNFPFKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS---- 229  
 QY 83 PGCTIFENCKSCR-NGSWGOTL-----  
 DB 230 PYYLIGQETLTCCQNGQWNGQIPQCKNLVFCPLDVPVNHAEHKVKGVEQYGFPGQTE 289  
 QY 104 -----DDFYVKGIFYCAECR--AGWYGG--DCMR-----CQQVLR-- 133  
 DB 290 VVTCTGNYFLMGFDTLKCNPDGSGWSGSQSCVKVADREVDCKSKAVDFLDDVGEPRIH 349  
 QY 134 APKQIILLES-----YPLNAHCETIHA-----KPGFVI----- 162  
 DB 350 CPAGCSLTAGTVNGTAIYHELSSVCRAAIHAGKLPNSSGAVHVNNNGPYSDFLGSLNGI 409  
 QY 163 ----QLRFVMLSLEFDYM-----CQDYVEVRD-----GDRNGQIHKVCGN--E 202  
 DB 410 KSEELKSLARSFDFYVRSSTAGSKGCPDGWFEVDENCVVYTSKQRAWERAQGVCTNMAA 469



Db 827 IWNGNSTEQWQAGISRWLA-----DHNWFLQCGSLNKKWVTAACVITYSA 879  
QY 511 KVTMIKTADLKVVGLKGYRDRDDREKTIQSLQISAILLHPNYDPILLDADIALIKLLDKA 570  
Db 880 TABIIDPNQPMVGLKGYRDRDDREKTIQSLQISAILLHPNYDPILLDADIALIKLLDKA 570  
QY 571 RIGTRVQICLAASRDLSFQESH-----TVAGNVLADVRSPGKNDTLRSQVSV 624  
Db 940 TLTRVQICLPT-DITT---REHLKEGLAVVTGWG-----LNENVTSETTQAVLVP 990  
QY 625 VDSLLCEEQHEHGPVSTNNMFCASWEPTAPSDICTAETGGIAAVSPGGRASPFRPH 684  
Db 991 VAASTCEGYKEADPLVTENNFCAGYK-KGRYDACSQSGG-PLVFADDSKTRRRW 1047  
QY 685 LMGLVSHSYDKTCSH-RLSTAFKVLFPKDWIER 717  
Db 1048 LEGIVSWGSPSGCGKANQYGFTKVNVLFWLSIRQ 1081

## RESULT 13

Q868H7 PRELIMINARY; PRT; 680 AA.  
ID Q868H7  
AC Q868H7  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mannose-binding lectin associated serine protease-1.  
GN Name=MASP-1;  
OS Branchiostoma belcheri (Amphioxus).  
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
OC Branchiostoma.  
OX NCBI\_TaxID=7741;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Notochord;  
RX MEDLINE=22593355; PubMed=12707349;  
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,  
Matsushita M., Fujita T;  
RT "Origin of mannose-binding lectin-associated serine protease (MASP)-1  
and MASP-3 involved in the lectin complement pathway traced back to  
the invertebrate, amphioxus";  
RT J. Immunol. 170:4701-4707(2003).  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
DR ENBL; AB089267; BAC75886.1; -;  
DR HSP; P00736; IAPQ.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006956; P:complement activation; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR00152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR011361; Pept\_S1 Comp Act.  
DR InterPro; IPR009003; Pept\_Set\_Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 2.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001155; Clr\_Cls\_MASP; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.

DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS0923; SUSHI; 2.  
DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Lectin; Protease; Serine protease.  
SQ SEQUENCE 680 AA; 75871 MW; 496985A94A728318 CRC64;  
  
Query Match 15.4%; Score 608.5; DB 2; Length 680;  
Best Local Similarity 26.3%; Pred. No. 5; Se-37;  
Matches 195; Conservative 92; Mismatches 239; Indels 215; Gaps 35;  
  
QY 46 CEYDQIECV-----CFGKEV-----VGYT 65  
Db 84 CEYDYVKVMEGDKLVGLFCGTEDTTEKVPGRVIESTGSQLSEPKSPSNVDRHGFV 143  
QY 66 IPCRNEENECDCLHPGCTIFENCKSCRNGSWGGLDDFYVYKGFYCAECRAG-WYGGD 124  
Db 144 VHYRVVDRDEC-AVDNGGCHP-----CHN-----YISGYCS-CRAGYWMKD 185  
QY 125 ---C-MRCG-QVLRAPKQIILLES---YPLNAHCEWTTHAKPGFVQLRFVMSLEFD- 174  
Db 186 RETCKFGCGQVLTQLSGTISSEYPRLYPKVLDCDCKIQVEPGYVVTLQF---DDDFDV 242  
QY 175 ---YMCQYDYVEVDGNRDQIIRKVCNERPAPIQSIGSSSLVHLHSDGSKNFDGF 229  
Db 243 EQHPEVSCFYDHLKVQAGDEKYP---YCGKTVPTTITSTDHKMHVFFHSDSGENKGF 298  
QY 230 HAIYEBITACSSSPCPHDGTCVLDDKAGSYKACLAGVTGQRCENLLEERNCSDPGGPVNG 289  
Db 299 RATYFT-----TAPCEAL-----SAP----- 315  
QY 290 YQKITGGPGLNGRHAKIGTVVTSFFCNNSYVSGNEKRTCCQNGEWSGKQPICAKREP 349  
Db 316 ---AYGTMESNFTYSQVSFACGEGYLDGPDHRCVQADGWSGVQPTC----- 362  
QY 350 KISDIARRRVLPQVOSRTPPLHOLYSAAFSKQLOSAPTKKFPALPGDLPMGYQHLHTQ 409  
Db 363 ---ELVNCGLP-NISNGEIVDGNFS-----YADIRI----- 391  
QY 410 LOYECISPFYRLGSSRRTRCLRTKWSGRAPSCIPICGKIENITAPKTOGLR-----WP 463  
Db 392 --YRC-DQFEMAGEGTRFCEADGKKTGNEPSCKPGKPEFVTRGKLVGRRPAMRGAWP 448  
QY 464 WQAAIYRTSGVHDSGLHKGAMFLVCSGALVNBRTVVVAACHVTDLGKVTMIKTADLKVV 523  
Db 449 WMAHLRTPRG-----FCGGTLLGQWVLTAAHCLVSPVTSPIILKDSFSVI 496  
QY 524 LGKF-YRDDRDRKTIQSLQISAILLHPNYDPILLDADIALIKLLDKARISTRVQICLA 582  
Db 497 LGHKARDKDTTETQV---QVAQIVVHPAFPTFTFLADALLKLESFARLNYITPICLL 553  
QY 583 ASRDLTSF---QESHITVAGNVLADVRSPGKNDTLRSQVSVVDSLLCEQHEDHGI 639  
Db 554 SEEEATATLVPGREAAVT--GWG-----HSDQGFANLELREVFLPLVDTSTCNKTYD---- 603  
QY 640 PVSVDNMFCAWSEPTAPSDICTAETGGIAAVSPGGRASPFRPHLMGLVSHSYDKTCSH 699  
Db 604 -FTVTSMDICAGFQ-EGGKDACRDSGG--PLAFFERTA--EKWQGVGVVTVGWG--CGR 655  
QY 700 RLS-TAFTKVLFPKDWIERNM 719  
Db 656 KNYGYVTNVIQYLPWIDEVM 676

## RESULT 14

Q868H5 PRELIMINARY; PRT; 680 AA.  
ID Q868H5  
AC Q868H5  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

Qy	240	SSSPCFHDGTCVLKAGSYKACACLAGYTGQRCENLEERNCSDDPGPVNGYQKITGGPGL	299
Ds	305	-----TARPEAL-----SAP-----AYGT	319
Qy	300	INGRHAKIGTVSPFCNNSYVLSGNEKKTCCOONGEWSGKOPIC-IKACREPKISDLVRRR	358
Ds	320	MEGNNFTYSQKVSFACGGYVLDGPDHRVCOADGSWSGVPQTCELVNCGPP-----	370
Qy	359	VLPQVOSRETPLHLQLYSAAFSKOKLSAPTKKCPALPFQDLPMGYQHLHTQLQ-YECISP	417
Ds	371	-----PNIENGEIEVDGNFSYADIAIYRC-DQ	396
Qy	418	PYRLGSSRRTCRLRTGKWSGRAPSCIPICGKIENITAPKTOGLR-----WPQAAIYRR	471
Ds	397	PYEMAGEGTRFCEADGKWTGNPSCKPTCGKPEFVTRGKLGVGRPAMRGWPNMAMLRHT	456
Qy	472	TSGVHDGSLHKGANFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKF-YED	530
Ds	457	PRGP-----FCGGTLLGDQWVLTAAHCLVSPVTSPIILKDSFVILGKHKARD	504
Qy	531	DDRDEKTIQSLQISAILHPNVDPTLLDADIAILKLDKARISTRVQVPICLAASRDLS	590
Ds	505	KOTTEQIVQVAQIAA---HPAFNTTSLADIALKLASPARLNPYITPCLLSESEATAT	561
Qy	591	F---QESHITVAGNVNLADVRSFGKNDTLRSGVSVVDSLLCEQEHEDHGIPVSVTDNM	647
Ds	562	LVPREGAVT---GWG-----HSDQGFIANELREVFLPLVDTNCTNKTYD-----FTVTS	610
Qy	648	FCASWEPTAPSDICTAETGGTAANVSFPGRASPEPRWHLMLGLVSWSYDTCSHRLS-TAFT	706
Ds	611	ICAGFO---EGGKADCRGDSGG---PLAFFERTA---EKWQGVVSWGNG---CGRKNKYGVYT	663
Qy	707	KVLPFKDWIERNM	719
Ds	664	NVIQYLPWIDVEM	676

RESULT 15

Q868HG

Q868HG6

PRELIMINARY;

PRT;

688 AA.

ID

Q868HG6

AC

Q868HG6;

DT

01-JUN-2003

DT

01-JUN-2003

DT

01-MAR-2004

DE

Mannose-binding lectin associated serine protease-3.

GN

Name=MASP-3;

OS

Branchiostoma belcheri (Amphioxus).

OC

Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC

Branchiostoma.

OX

NCBI\_TaxID=7741;

RN

[1]

RP

SEQUENCE FROM N.A.

RS

TISSUE=Notochord;

RX

MEDLINE=22593355; PubMed=12707349;

RA

Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,

RA

Matsushita M., Fujita T.;

RT

"Origin of mannose-binding lectin-associated serine protease (MASP)-1

RT

and MASP-3 involved in the lectin complement pathway traced back to

RT

the invertebrate, amphioxus.";

RL

J. Immunol. 170:4701-4707(2003).

CC

EMBL; AB089268; BAC75887.1; --

DR

HSSP; P00760; 1EZKX.

DR

GO; GO:0005576; C:extracellular;

DR

GO; GO:0005509; F:calcium ion binding;

DR

GO; GO:0004263; F:chymotrypsin activity;

DR

GO; GO:0008233; F:peptidase activity;

DR

GO; GO:0005529; F:sugar binding;

DR

GO; GO:0004295; F:trypsin activity;

DR

GO; GO:0006956; P:complement activation;

DR

GO; GO:0006508; P:proteolysis and peptidolysis;

DR

InterPro; IPR000152; Abx hydroxyl S.

DR InterPro; IPR000859; CUB.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR001361; Pept\_S1\_Comp\_Act.  
DR InterPro; IPR009003; Pept\_Set\_Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 2.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001155; Chr\_Cls\_MASP; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00923; SUSHI; 2.  
DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Lectin; Protease; Serine protease.  
SQ. SEQUENCE 688 AA; 76890 MW; 14B3AD8215BD4D15 CRC64;

Query Match 15.1%; Score 597; DB 2; Length 688;  
Best Local Similarity 26.6%; Pred. No. 4.1e-36;  
Matches 197; Conservative 88; Mismatches 244; Indels 212; Gaps 36;

QY 46 CEYDQIECV-----CPGREV-----VGYT 65  
DB 84 CEYDYKVMESGKLVGLFCGTEDTDEQVFGDRVIESTGSLSEPKSDFSNADRHKGFA 143

QY 66 IPCRNEENECDSCLHPGCTIFENCKSCRNKSGWGTLDLDFYKGYCAECRAG-WYGGD 124  
DB 144 VHYRVVDRDEC--AVDNGGCHF-----CHN-----YISGYYS-CRAGYIMKD 185

QY 125 ---C-MRCG-QVLRAPKQILLES---YPLNAHCWTIHAKGFIQLRPFVMSLEFD- 174  
DB 186 RETCKFGCGQVLTLSGTSPEYPRLYPKVLDCKWKIQVEFGYVVTLPF---DDDFDV 242

QY 175 -----YMCQYDYVEVRDGNRDGQIIKRVCGNERPAPIQISGSLHVLPHSDGSKNPDGF 229  
DB 243 EQHPEVSCPYDHLKVKAGDEKYP---YCGKTVPTTITTDHNMHVFFHSDSGENKGF 298

QY 230 HAIYEITACSSPFCFHDGTCVLDKAGYKACACLAGYTGQRCENLLEERNCSDPGGPVNG 289  
DB 299 RATYFT-----TARPCAL-----SAP----- 315

QY 290 YQKITGGPGLNGRHAKIGTVSPFCNNSVYLSGNEKRTCOQNGESGKOPICIKACREP 349  
DB 316 -----AYGTWEGSNFTYSQKVPACGEGYLDGPHRVQADGWSGVQPTC----- 362

QY 350 KISDLVRRRLPMQVQSRETPLHQLYSAFSAKQLQSAPTKKPPALPFGDLPMGYQHLHTQ 409  
DB 363 ---ELVNCGPLP-NISNGEIEVDGNFS-----YADIAI----- 391

QY 410 LQYECISPFYRRLLGSSRRCTCLRTCKWGRAPSCIPICGKI-----ENIT--APKTQGLRW 462  
DB 392 --YRC-DQFYEMAGEGRFCEAGGKWTGNEFPSCPKPICGESFPSPDRIRVGGGPKKG-AW 447

QY 463 PWQAAIVRRITSGVHDGSLHKGAWFL---VCSGALVNERTVVAHCVTDLGKVTMIKTAD 519  
DB 448 PWQAMV-----IHQAPRIRKPFCCGALVDKKWILTAAHCV---GENDILPTGY 493

QY 520 LKVVILGKFYRDDREKTIQSLQISAIILHPNVDPIILLDADIALKLLDKARISTRVQPI 579  
DB 494 FNVSLGLHKRKEPDNDVFPF--EVERVIRHPDWDKDNFDSIALLELKEEVDLTDYIRPV 551

QY 580 CLAAS--RDLSTSFQBSHI-TVAGMNVLADVRSPGFKNDTLRSGVSVVVDLLICEQEHED 636  
DB 552 CLQRSGRQSAQDVQEGRAGVVTGWGRTSNLP--GSEANTLQEBVEVPVVDQEECVSAYEG 609

QY 637 HGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVFPGRASPEPRKWHLMGLVSWSYDKT 696  
DB 610 ---DYPVTGNMLCAGLR-IGGKSDCDGSGPILLQDPDTT-----RFFVAGLVSWGEPSE 661

QY 697 CSH-RLSTAFATKVLFPKDWIE 716  
DB 662 CGRARKYGYVYARVENFVQMIK 682

Search completed: May 8, 2005, 16:08:27  
Job time : 109 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 13:11:48 ; Search time 25 Seconds  
(without alignments)  
2149.893 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGWTQGLTFLQLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits.satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2946.5	74.7	570	4	US-10-067-422-9
2	665	16.9	1019	1	US-08-296-014A-4
3	665	16.9	1019	2	US-08-596-405-4
4	665	16.9	1019	2	US-08-877-620-4
5	665	16.9	1019	4	US-09-287-368-4
6	665	16.9	1019	4	US-09-626-795-4
7	665	16.9	1083	1	US-08-296-014A-2
8	665	16.9	1083	2	US-08-596-405-2
9	665	16.9	1083	4	US-08-877-620-2
10	665	16.9	1083	4	US-09-287-368-2
11	665	16.9	1083	4	US-09-626-795-2
12	482	12.2	699	4	US-09-949-016-6138
13	475	12.0	717	4	US-09-949-016-11182
14	399.5	10.1	691	4	US-09-949-016-7775
15	337	8.3	855	4	US-09-027-337-2
16	337	8.3	855	4	US-09-644-600-2
17	337	8.3	855	4	US-09-654-600A-2
18	321	8.1	460	6	5270178-16
19	321	8.1	460	6	5270178-16
20	317.5	8.0	798	1	US-08-200-900A-2
21	317.5	8.0	798	4	US-08-794-042-2
22	317.5	8.0	798	5	PCT-US94-00616-2
23	311.5	7.9	461	6	5460953-3
24	311.5	7.9	461	6	5460953-3
25	310.5	7.9	409	3	US-09-065-872-2
26	310.5	7.9	409	4	US-09-667-570A-2
27	310.5	7.9	410	3	US-09-065-872-1

28	310.5	7.9	410	4	US-09-667-570A-1	Sequence 1, Appli
29	310.5	7.9	419	1	US-08-295-411-1	Sequence 1, Appli
30	310.5	7.9	419	2	US-08-955-471-1	Sequence 1, Appli
31	310.5	7.9	419	4	US-09-667-570A-3	Sequence 3, Appli
32	310.5	7.9	419	4	US-10-182-263-1	Sequence 1, Appli
33	310.5	7.9	419	5	PCT-US92-10242-1	Sequence 1, Appli
34	310.5	7.9	460	2	US-08-756-506-2	Sequence 2, Appli
35	310.5	7.9	460	2	US-08-756-506-4	Sequence 2, Appli
36	310.5	7.9	461	4	US-10-182-263-2	Sequence 32, Appli
37	310.5	7.9	461	4	US-09-054-272-32	Sequence 32, Appli
38	310.5	7.9	461	4	US-09-949-016-5921	Sequence 5921, Ap
39	310.5	7.9	461	6	5255537-2	Patent No. 5255537
40	310.5	7.9	461	6	5255537-2	Patent No. 5255537
41	310.5	7.9	485	4	US-09-949-016-10882	Sequence 10882, A
42	310	7.9	419	4	US-10-182-263-6	Sequence 6, Appli
43	309	7.8	419	4	US-10-182-263-3	Sequence 3, Appli
44	309	7.8	419	4	US-10-182-263-5	Sequence 5, Appli
45	309	7.8	461	6	5270178-2	Patent No. 5270178
46	309	7.8	461	6	5270178-2	Patent No. 5270178
47	308	7.8	419	4	US-10-182-263-4	Sequence 4, Appli
48	307	7.8	460	6	5270178-15	Patent No. 5270178
49	307	7.8	460	6	5270178-15	Patent No. 5270178
50	305	7.7	460	6	5270178-13	Patent No. 5270178
51	305	7.7	460	6	5270178-14	Patent No. 5270178
52	305	7.7	460	6	5270178-13	Patent No. 5270178
53	305	7.7	460	6	5270178-14	Patent No. 5270178
54	302.5	7.7	461	6	5270178-17	Patent No. 5270178
55	302.5	7.7	461	6	5270178-18	Patent No. 5270178
56	302.5	7.7	461	6	5270178-17	Patent No. 5270178
57	302.5	7.7	461	6	5270178-18	Patent No. 5270178
58	288.5	7.3	902	4	US-09-644-600-10	Sequence 10, Appli
59	288.5	7.3	902	4	US-09-654-600A-10	Sequence 10, Appli
60	287.5	7.3	356	4	US-09-054-272-18	Sequence 18, Appli
61	283.5	7.2	587	4	US-09-949-016-11501	Sequence 11501, A
62	282	7.1	527	6	5520913-1	Patent No. 5520913
63	282	7.1	527	6	5520913-1	Patent No. 5520913
64	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appli
65	281	7.1	487	2	US-08-469-658-53	Sequence 53, Appli
66	281	7.1	488	4	US-09-367-777-44	Sequence 44, Appli
67	281	7.1	488	4	US-09-367-791A-27	Sequence 27, Appli
68	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appli
69	281	7.1	492	2	US-08-469-658-2	Sequence 2, Appli
70	280.5	7.1	267	4	US-09-949-016-9575	Sequence 9575, Ap
71	280	7.1	527	1	US-07-609-510B-16	Sequence 16, Appli
72	280	7.1	527	2	US-08-811-949-39	Sequence 39, Appli
73	280	7.1	527	2	US-09-600-985-1	Sequence 1, Appli
74	280	7.1	527	4	US-09-612-314A-51	Sequence 51, Appli
75	280	7.1	527	5	PCT-US91-01025A-2	Sequence 2, Appli
76	280	7.1	527	6	5185259-8	Patent No. 5185259
77	280	7.1	527	6	5185259-8	Patent No. 5185259
78	280	7.1	562	2	US-08-811-949-43	Sequence 43, Appli
79	280	7.1	562	2	US-08-560-098A-50	Sequence 50, Appli
80	280	7.1	562	2	US-08-883-795A-38	Sequence 38, Appli
81	280	7.1	562	4	US-09-703-695A-4	Sequence 4, Appli
82	280	7.1	562	4	US-10-443-701-4	Sequence 4, Appli
83	280	7.1	562	6	5185259-3	Sequence 4, Appli
84	280	7.1	562	6	5200340-2	Patent No. 5200340
85	280	7.1	562	6	5344773-2	Patent No. 5344773
86	280	7.1	562	6	5185259-3	Patent No. 5185259
87	280	7.1	562	6	5200340-2	Patent No. 5200340
88	280	7.1	562	6	5344773-2	Patent No. 5344773
89	279	7.1	527	4	US-09-600-985-2	Sequence 2, Appli
90	278.5	7.1	466	1	US-07-882-202A-4	Sequence 4, Appli
91	278.5	7.1	466	1	US-08-021-615A-4	Sequence 4, Appli
92	278.5	7.1	466	1	US-08-321-777-4	Sequence 4, Appli
93	278.5	7.1	466	3	US-09-009-217-14	Sequence 14, Appli
94	278.5	7.1	466	3	US-09-009-656-14	Sequence 14, Appli
95	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appli
96	278.5	7.1	483	4	US-09-949-016-9523	Sequence 9523, Ap
97	278	7.0	448	5	PCT-US92-10068-1	Sequence 1, Appli
98	278	7.0	496	4	US-09-949-016-9524	Sequence 9524, Ap
99	276.5	7.0	655	1	US-08-148-910-12	Sequence 12, Appli
100	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appli

101	276	7.0	448	1	US-08-295-411-3	Sequence 3, Appli	174	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appli
102	276	7.0	448	2	US-08-955-471-3	Sequence 3, Appli	175	248	6.3	230	2	US-08-944-483-62	Sequence 62, Appl
103	276	7.0	448	5	PCT-US92-10242-3	Sequence 3, Appli	176	248	6.3	231	3	US-09-027-337-6	Sequence 6, Appli
104	276	7.0	527	4	US-09-600-985-3	Sequence 3, Appli	177	248	6.3	231	4	US-09-644-600-6	Sequence 6, Appli
105	275.5	7.0	406	1	US-08-295-411-5	Sequence 5, Appli	178	248	6.3	231	4	US-09-654-600A-6	Sequence 2, Appli
106	275.5	7.0	406	2	US-08-955-471-5	Sequence 5, Appli	179	247	6.3	764	2	US-08-177-109A-2	Sequence 2, Appli
107	275.5	7.0	406	4	US-09-782-587B-1	Sequence 1, Appli	180	247	6.3	764	2	US-08-687-706-2	Sequence 2, Appli
108	275.5	7.0	406	4	US-09-782-587B-1	Sequence 3, Appli	181	247	6.3	798	4	US-09-949-016-11021	Sequence 11021, A
109	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appli	182	247	6.3	986	4	US-09-949-016-6690	Sequence 6690, Ap
110	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appli	183	246.5	6.2	259	3	US-08-944-483-52	Sequence 52, Appl
111	275.5	7.0	444	2	US-08-327-690-2	Sequence 2, Appli	184	246.5	6.2	295	3	US-08-338-368-2	Sequence 2, Appli
112	275.5	7.0	444	2	US-08-660-289-2	Sequence 2, Appli	185	246.5	6.2	376	3	US-08-558-269-10	Sequence 10, Appl
113	275.5	7.0	444	2	US-08-537-807-2	Sequence 2, Appli	186	246.5	6.2	376	3	US-09-410-882-10	Sequence 10, Appl
114	275.5	7.0	444	2	US-08-871-003-2	Sequence 2, Appli	187	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appli
115	275.5	7.0	444	3	US-08-464-233-2	Sequence 2, Appli	188	246.5	6.2	579	2	US-08-955-471-4	Sequence 4, Appli
116	275.5	7.0	444	3	US-09-189-607-2	Sequence 2, Appli	189	246.5	6.2	579	3	US-09-117-708-14	Sequence 14, Appl
117	275.5	7.0	444	3	US-09-378-907-2	Sequence 2, Appli	190	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appli
118	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appli	191	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appli
119	275.5	7.0	461	4	US-09-949-016-8839	Sequence 8839, Ap	192	246.5	6.2	615	1	US-08-463-953-3	Sequence 3, Appli
120	275	7.0	562	6	5244676-5	Patent No. 5244676	193	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appli
121	275	7.0	562	6	5244676-5	Patent No. 5244676	194	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appli
122	275	7.0	1113	4	US-09-959-392-4	Sequence 4, Appli	195	246.5	6.2	622	3	US-08-952-967-8	Sequence 8, Appli
123	273	6.9	560	4	US-09-949-016-6458	Sequence 6458, Ap	196	246.5	6.2	622	4	US-09-054-272-42	Sequence 42, Appl
124	273	6.9	560	4	US-09-912-559-3	Sequence 3, Appli	197	246	6.2	812	4	US-08-991-761A-7	Sequence 7, Appli
125	273	6.9	560	4	US-09-912-559-4	Sequence 4, Appli	198	245	6.2	828	1	US-08-278-091-10	Sequence 10, Appl
126	272	6.9	488	1	US-08-487-037-1	Sequence 1, Appli	199	245	6.2	228	1	US-08-483-859-10	Sequence 10, Appl
127	271.5	6.9	244	4	US-08-361-393-1	Sequence 1, Appli	200	245	6.2	228	1	US-08-472-173-10	Sequence 10, Appl
128	271.5	6.9	325	4	US-09-949-016-7713	Sequence 7713, Ap	201	245	6.2	228	2	US-08-487-167-10	Sequence 10, Appl
129	270.5	6.9	415	1	US-08-295-411-2	Sequence 2, Appli	202	245	6.2	228	2	US-08-482-816-10	Sequence 10, Appl
130	270.5	6.9	415	2	US-08-955-471-2	Sequence 2, Appli	203	245	6.2	228	2	US-08-296-149-10	Sequence 10, Appl
131	270.5	6.9	415	5	PCT-US92-10242-2	Sequence 2, Appli	204	245	6.2	228	2	US-08-801-499-10	Sequence 10, Appl
132	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl	205	245	6.2	228	2	US-08-615-271-10	Sequence 10, Appl
133	264.5	6.7	415	2	US-08-073-531B-1	Sequence 1, Appli	206	245	6.2	228	3	US-09-074-660-10	Sequence 10, Appl
134	264.5	6.7	415	2	US-08-766-288-1	Sequence 1, Appli	207	245	6.2	228	3	US-09-106-468-10	Sequence 10, Appl
135	263	6.7	431	4	US-09-101-272G-1	Sequence 1, Appli	208	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl
136	263	6.7	431	6	5188829-1	Patent No. 5188829	209	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl
137	263	6.7	431	6	5188829-1	Patent No. 5188829	210	244.5	6.2	269	4	US-09-715-994-2	Sequence 2, Appli
138	262.5	6.7	461	3	US-08-742-877-2	Sequence 2, Appli	211	244.5	6.2	416	2	US-09-000-846-2	Sequence 2, Appli
139	262.5	6.7	461	3	US-09-053-871A-21	Sequence 21, Appl	212	242.5	6.1	416	2	US-08-872-757-2	Sequence 2, Appli
140	262.5	6.7	461	3	US-10-133-907-5	Sequence 5, Appli	213	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appli
141	262.5	6.7	461	6	5521070-2	Sequence 5, Appli	214	242	6.1	730	4	US-08-811-949-1	Sequence 1, Appli
142	262.5	6.7	461	6	5521070-2	Patent No. 5521070	215	241.5	6.1	347	2	US-08-572-225-1	Sequence 1, Appli
143	262.5	6.7	480	4	US-09-949-016-11123	Sequence 11123, A	216	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appli
144	262.5	6.7	1042	4	US-09-959-392-2	Sequence 2, Appli	217	241	6.1	354	2	US-08-811-949-61	Sequence 61, Appl
145	261.5	6.6	415	4	US-09-118-748-2	Sequence 2, Appli	218	241	6.1	986	3	US-08-872-757-4	Sequence 4, Appli
146	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appli	219	241	6.1	986	3	US-08-872-757-4	Sequence 4, Appli
147	260	6.6	477	2	US-08-560-098A-51	Sequence 51, Appl	220	240.5	6.1	356	1	US-08-427-640-8	Sequence 8, Appli
148	258.5	6.6	411	1	US-08-087-163-1	Sequence 18, Appl	221	240.5	6.1	3571	4	US-09-911-842A-2	Sequence 2, Appli
149	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl	222	240	6.1	432	4	US-09-959-392-34	Sequence 34, Appl
150	258.5	6.6	411	1	US-08-153-799-18	Sequence 18, Appl	223	240	6.1	432	2	US-08-560-098A-47	Sequence 47, Appl
151	258.5	6.6	411	3	US-09-181-816-1	Sequence 1, Appli	224	239.5	6.1	1015	4	US-09-285-385C-2	Sequence 2, Appli
152	258.5	6.6	411	4	US-09-880-503-3	Sequence 3, Appli	225	239.5	6.1	3594	4	US-09-911-842A-4	Sequence 4, Appli
153	257.5	6.5	430	6	5219569-2	Patent No. 5219569	226	239	6.1	356	4	US-09-601-318-3	Sequence 3, Appli
154	257.5	6.5	430	6	5219569-2	Patent No. 5219569	227	239	6.1	356	4	US-08-681-151-1	Sequence 1, Appli
155	256.5	6.5	411	4	US-09-403-736-2	Sequence 2, Appli	228	239	6.1	389	2	US-08-811-949-67	Sequence 67, Appl
156	256.5	6.5	430	1	US-07-942-157A-3	Sequence 3, Appli	229	238.5	6.0	437	2	US-08-811-949-49	Sequence 49, Appl
157	255.5	6.5	244	4	US-09-618-259-11	Sequence 11, Appl	230	238.5	6.0	437	2	US-08-811-949-51	Sequence 51, Appl
158	254.5	6.5	437	1	US-08-487-037-3	Sequence 3, Appli	231	238.5	6.0	437	2	US-08-811-949-55	Sequence 55, Appl
159	254	6.4	261	6	5270178-21	Patent No. 5270178	232	238.5	6.0	437	2	US-08-811-949-57	Sequence 57, Appl
160	254	6.4	261	6	5270178-21	Patent No. 5270178	233	238	6.0	237	3	US-08-163-919A-3	Sequence 3, Appli
161	251	6.4	261	6	5270178-5	Patent No. 5270178	234	238	6.0	237	4	US-08-462-515-3	Sequence 3, Appli
162	251	6.4	261	6	5270178-5	Patent No. 5270178	235	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appli
163	250.5	6.3	229	2	US-08-557-146-13	Sequence 13, Appl	236	236.5	6.0	274	2	US-08-978-404B-5	Sequence 5, Appli
164	250.5	6.3	229	2	US-09-154-344-13	Sequence 13, Appl	237	236.5	6.0	355	1	US-08-137-116-1	Sequence 1, Appli
165	250.5	6.3	411	2	US-08-560-098A-48	Sequence 48, Appl	238	236.5	6.0	355	1	US-08-217-618-1	Sequence 2, Appli
166	249.5	6.3	403	4	US-09-880-503-6	Sequence 6, Appli	239	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appli
167	249.5	6.3	986	4	US-09-285-385C-19	Sequence 19, Appl	240	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appli
168	249	6.3	251	3	US-08-944-483-47	Sequence 47, Appl	241	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appli
169	248.5	6.3	250	3	US-08-944-483-51	Sequence 51, Appl	242	236.5	6.0	355	2	US-08-217-616-1	Sequence 1, Appli
170	248.5	6.3	261	6	5270178-19	Patent No. 5270178	243	236.5	6.0	355	2	US-08-811-949-45	Sequence 45, Appl
171	248.5	6.3	261	6	5270178-20	Patent No. 5270178	244	236.5	6.0	355	2	US-08-811-949-47	Sequence 47, Appl
172	248.5	6.3	261	6	5270178-19	Patent No. 5270178	245	236.5	6.0	355	3	US-08-794-528-1	Sequence 1, Appli
173	248.5	6.3	261	6	5270178-20	Patent No. 5270178	246	236.5	6.0	355	6	5223256-1	Patent No. 5223256



247	236.5	6.0	355	6	5223256-1	Patent No. 5223256	320	228	5.8	812	4	US-09-192-012-3	Sequence 3, Appli
248	236.5	6.0	356	1	US-08-427-640-4	Sequence 4, Appli	321	228	5.8	812	4	US-09-335-325-1	Sequence 1, Appli
249	236.5	6.0	378	3	US-09-553-498-10	Sequence 10, Appl	322	228	5.8	812	4	US-08-991-761A-12	Sequence 12, Appl
250	236.5	6.0	378	4	US-09-618-869-10	Sequence 10, Appl	323	228	5.8	812	5	PCr-US95-05107-1	Sequence 1, Appli
251	236.5	6.0	472	2	US-08-811-949-63	Sequence 63, Appl	324	227	5.8	241	4	US-09-657-986B-2	Sequence 2, Appli
252	236.5	6.0	871	3	US-09-245-041-19	Sequence 19, Appl	325	227	5.8	285	4	US-09-023-942A-26	Sequence 26, Appl
253	236.5	6.0	871	4	US-09-358-055B-19	Sequence 19, Appl	326	227	5.8	308	3	US-08-705-875A-10	Sequence 10, Appl
254	236.5	6.0	871	4	US-09-893-238-19	Sequence 19, Appl	327	227	5.8	308	4	US-09-242-999-10	Sequence 10, Appl
255	236.5	6.0	1013	2	US-08-866-650-3	Sequence 3, Appli	328	226.5	5.7	2787	3	US-09-518-046-2	Sequence 2, Appli
256	236.5	6.0	1013	3	US-09-021-287-3	Sequence 3, Appli	329	226.5	5.7	2787	3	US-09-245-041-15	Sequence 15, Appl
257	236.5	6.0	1013	3	US-09-240-473-3	Sequence 3, Appli	330	226.5	5.7	2787	4	US-09-358-055B-15	Sequence 15, Appl
258	236.5	6.0	1350	4	US-09-445-041-17	Sequence 17, Appl	331	226.5	5.7	2787	4	US-09-893-238-15	Sequence 15, Appl
259	236.5	6.0	1350	4	US-09-358-055B-17	Sequence 17, Appl	332	226	5.7	406	4	US-09-851-588-6	Sequence 6, Appli
260	236.5	6.0	1350	4	US-09-893-238-17	Sequence 17, Appl	333	226	5.7	423	3	US-09-656-002-2	Sequence 2, Appli
261	236	6.0	355	2	US-08-811-949-53	Sequence 53, Appl	334	226	5.7	435	3	US-09-008-271A-6	Sequence 6, Appli
262	236	6.0	355	2	US-08-811-949-59	Sequence 59, Appl	335	226	5.7	435	4	US-09-607-745-2	Sequence 2, Appli
263	235	6.0	270	2	US-08-978-404B-8	Sequence 8, Appli	336	226	5.7	437	4	US-09-851-588-8	Sequence 8, Appli
264	233.5	5.9	252	3	US-08-944-483-72	Sequence 72, Appl	337	226	5.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
265	233.5	5.9	253	4	US-09-027-337-8	Sequence 8, Appli	338	226	5.7	481	4	US-09-949-016-9239	Sequence 9239, Ap
266	233.5	5.9	253	4	US-09-644-600-8	Sequence 8, Appli	339	226	5.7	637	4	US-09-949-016-11538	Sequence 11538, A
267	233.5	5.9	253	4	US-09-654-600A-8	Sequence 8, Appli	340	226	5.7	637	4	US-09-949-016-11539	Sequence 11539, A
268	233.5	5.9	383	2	US-08-558-269-6	Sequence 6, Appli	341	225.5	5.7	348	4	US-09-949-016-6979	Sequence 6979, Ap
269	233.5	5.9	383	3	US-09-410-882-6	Sequence 6, Appli	342	224.5	5.7	232	4	US-09-959-392-32	Sequence 32, Appl
270	233.5	5.9	546	6	5200340-6	Patent No. 5200340	343	224.5	5.7	235	3	US-08-944-483-65	Sequence 65, Appl
271	233.5	5.9	546	6	5200340-6	Patent No. 5200340	344	224	5.7	275	2	US-09-016-366A-17	Sequence 17, Appl
272	232.5	5.9	259	4	US-10-165-442-2	Sequence 2, Appli	345	224	5.7	275	2	US-08-978-404B-12	Sequence 12, Appl
273	232.5	5.9	295	4	US-10-165-442-1	Sequence 1, Appli	346	224	5.7	276	4	US-09-880-503-5	Sequence 5, Appli
274	232.5	5.9	1013	2	US-08-866-650-5	Sequence 5, Appli	347	224	5.7	306	2	US-08-560-098A-45	Sequence 45, Appl
275	232.5	5.9	1013	2	US-09-021-287-5	Sequence 5, Appli	348	224	5.7	323	4	US-09-880-503-7	Sequence 7, Appli
276	232.5	5.9	1013	3	US-08-991-408-2	Sequence 2, Appli	349	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appl
277	232.5	5.9	1013	3	US-09-240-473-5	Sequence 5, Appli	350	223.5	5.7	245	3	US-08-944-483-69	Sequence 69, Appl
278	232.5	5.9	1013	3	US-09-432-472-2	Sequence 2, Appli	351	223.5	5.7	346	4	US-09-949-016-9000	Sequence 9000, Ap
279	232.5	5.9	1013	4	US-09-285-385C-20	Sequence 20, Appl	352	223	5.7	521	3	US-08-944-483-64	Sequence 64, Appl
280	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appli	353	223	5.7	521	4	US-09-949-016-11081	Sequence 11081, A
281	231.5	5.9	389	2	US-08-811-949-65	Sequence 65, Appl	354	223	5.7	521	4	US-09-949-016-11082	Sequence 11082, A
282	231.5	5.9	417	4	US-09-820-002-4	Sequence 4, Appli	355	223	5.7	521	4	US-09-949-016-11083	Sequence 11083, A
283	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl	356	222.5	5.6	452	4	US-09-949-016-7182	Sequence 1182, Ap
284	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl	357	222.5	5.6	790	4	US-08-991-761A-13	Sequence 13, Appl
285	231	5.9	393	2	US-08-560-098A-44	Sequence 44, Appl	358	222	5.6	274	2	US-09-016-366A-21	Sequence 21, Appl
286	231	5.9	393	3	US-08-967-024C-24	Sequence 24, Appl	359	222	5.6	274	2	US-08-978-404B-16	Sequence 16, Appl
287	231	5.9	393	3	US-08-967-024C-25	Sequence 25, Appl	360	222	5.6	407	3	US-09-734-675-4	Sequence 4, Appli
288	231	5.9	1012	4	US-09-285-385C-4	Sequence 4, Appli	361	221	5.6	253	3	US-08-944-483-73	Sequence 73, Appl
289	230.5	5.8	259	4	US-10-165-442-4	Sequence 4, Appli	362	221	5.6	273	2	US-08-978-404B-6	Sequence 6, Appli
290	230.5	5.8	295	4	US-10-165-442-3	Sequence 3, Appli	363	221	5.6	300	3	US-08-705-875A-6	Sequence 6, Appli
291	230.5	5.8	302	3	US-09-220-731-26	Sequence 26, Appl	364	221	5.6	300	4	US-09-242-999-6	Sequence 6, Appli
292	230.5	5.8	302	4	US-09-242-999-22	Sequence 22, Appl	365	221	5.6	1193	4	US-09-949-016-10498	Sequence 10498, A
293	230	5.8	232	3	US-09-959-392-31	Sequence 31, Appl	366	220.5	5.6	376	4	US-09-820-002-2	Sequence 2, Appli
294	230	5.8	248	3	US-08-944-483-63	Sequence 63, Appl	367	220	5.6	273	2	US-09-016-366A-19	Sequence 19, Appl
295	230	5.8	387	3	US-09-032-215-8	Sequence 8, Appli	368	220	5.6	273	2	US-08-978-404B-14	Sequence 14, Appl
296	230	5.8	387	3	US-09-032-215-13	Sequence 13, Appl	369	219.5	5.6	254	3	US-08-944-483-50	Sequence 50, Appl
297	229	5.8	242	3	US-09-004-731-36	Sequence 36, Appl	370	219.5	5.6	255	2	US-09-027-337-7	Sequence 7, Appli
298	229	5.8	242	3	US-08-749-699-36	Sequence 36, Appl	371	219.5	5.6	255	4	US-09-644-600-7	Sequence 7, Appli
299	229	5.8	242	4	US-09-004-729-36	Sequence 36, Appl	372	219.5	5.6	255	4	US-09-654-600A-7	Sequence 7, Appli
300	229	5.8	400	3	US-09-004-731-30	Sequence 30, Appl	373	218.5	5.5	244	4	US-09-601-318-4	Sequence 4, Appli
301	229	5.8	400	3	US-09-004-731-33	Sequence 33, Appl	374	218.5	5.5	244	4	US-09-601-318-5	Sequence 5, Appli
302	229	5.8	400	3	US-08-749-699-30	Sequence 30, Appl	375	218.5	5.5	244	4	US-09-601-318-6	Sequence 6, Appli
303	229	5.8	400	3	US-08-749-699-33	Sequence 33, Appl	376	218.5	5.5	244	4	US-09-601-318-7	Sequence 7, Appli
304	229	5.8	400	4	US-09-004-729-30	Sequence 30, Appl	377	218.5	5.5	245	3	US-09-079-970A-6	Sequence 6, Appli
305	229	5.8	400	4	US-09-004-729-33	Sequence 33, Appl	378	218.5	5.5	245	4	US-09-601-318-1	Sequence 1, Appli
306	228.5	5.8	235	3	US-08-807-151-3	Sequence 3, Appli	379	218.5	5.5	249	3	US-09-079-970A-5	Sequence 5, Appli
307	228.5	5.8	235	3	US-09-478-957-3	Sequence 3, Appli	380	217.5	5.5	1198	3	US-09-245-041-131	Sequence 131, App
308	228	5.8	591	3	US-08-991-408-4	Sequence 4, Appli	381	217.5	5.5	1198	3	US-09-794-236-3	Sequence 3, Appli
309	228	5.8	591	3	US-09-432-473-4	Sequence 4, Appli	382	217.5	5.5	1198	4	US-09-358-055B-132	Sequence 132, App
310	228	5.8	809	4	US-08-991-761A-9	Sequence 9, Appli	383	217.5	5.5	1429	3	US-09-245-041-130	Sequence 130, App
311	228	5.8	812	1	US-08-248-629A-1	Sequence 1, Appli	384	217.5	5.5	1429	3	US-09-358-055B-131	Sequence 131, App
312	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appli	385	217	5.5	239	3	US-08-944-483-61	Sequence 61, Appl
313	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appli	386	217	5.5	268	4	US-09-613-822B-2	Sequence 2, Appli
314	228	5.8	812	1	US-08-326-785-1	Sequence 1, Appli	387	217	5.5	273	2	US-08-978-404B-3	Sequence 3, Appli
315	228	5.8	812	2	US-08-612-788-1	Sequence 1, Appli	388	217	5.5	791	3	US-08-643-219-1	Sequence 1, Appli
316	228	5.8	812	2	US-08-605-988B-1	Sequence 1, Appli	389	217	5.5	791	3	US-08-851-350-1	Sequence 1, Appli
317	228	5.8	812	2	US-08-429-743-1	Sequence 1, Appli	390	217	5.5	2703	1	US-08-185-432-19	Sequence 19, Appl
318	228	5.8	812	2	US-08-866-735-1	Sequence 1, Appli	391	217	5.5	2703	4	US-08-899-232-4	Sequence 4, Appli
319	228	5.8	812	3	US-09-066-028-1	Sequence 1, Appli	392	217	5.5	2703	4	US-09-121-457-4	Sequence 4, Appli



393	216	5.5	267	2	US-09-016-366A-23	Sequence 23, Appl	466	211	5.3	1218	4	US-09-917-254-85	Sequence 85, Appl
394	216	5.5	267	2	US-08-978-404B-18	Sequence 18, Appl	467	211	5.3	1218	4	US-09-195-524-6	Sequence 6, Appl
395	216	5.5	267	4	US-09-917-254-101	Sequence 101, App	468	211	5.3	1218	4	US-09-579-536C-1	Sequence 1, Appl
396	216	5.5	268	1	US-08-568-031-2	Sequence 2, Appl	469	211	5.3	1218	4	US-09-949-016-10297	Sequence 10297, A
397	216	5.5	268	2	US-08-966-319-2	Sequence 2, Appl	470	211	5.3	1254	4	US-09-949-016-10297	Sequence 62, Appl
398	216	5.5	268	3	US-09-153-304-2	Sequence 2, Appl	471	210.5	5.3	418	4	US-09-370-838-62	Sequence 62, Appl
399	216	5.5	299	3	US-08-944-483-66	Sequence 66, Appl	472	210.5	5.3	418	4	US-08-854-133-62	Sequence 5, Appl
400	216	5.5	319	4	US-09-386-642-12	Sequence 12, Appl	473	210.5	5.3	1219	3	US-08-882-046-5	Sequence 5, Appl
401	216	5.5	328	4	US-09-386-642-11	Sequence 11, Appl	474	210.5	5.3	1219	4	US-09-566-047-5	Sequence 5, Appl
402	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appl	475	210	5.3	154	3	US-09-261-416-5	Sequence 24, Appl
403	216	5.5	790	2	US-08-469-658-54	Sequence 54, Appl	476	210	5.3	248	3	US-08-944-483-24	Sequence 2, Appl
404	216	5.5	810	6	5200340-8	Patent No. 5200340	477	210	5.3	446	4	US-10-177-661-4	Sequence 2, Appl
405	216	5.5	810	6	5200340-8	Patent No. 5200340	478	209.5	5.3	477	4	US-10-177-661-2	Sequence 12, Appl
406	215.5	5.5	317	4	US-09-386-629-7	Sequence 7, Appl	479	209.5	5.3	562	4	US-09-879-792-12	Sequence 82, Appl
407	215.5	5.5	317	4	US-09-907-794A-263	Sequence 263, App	480	208.5	5.3	492	4	US-09-685-168A-895	Sequence 14, Appl
408	215.5	5.5	317	4	US-09-905-125A-263	Sequence 263, App	481	208.5	5.3	492	4	US-09-879-792-14	Sequence 895, App
409	215.5	5.5	317	4	US-09-902-775A-263	Sequence 263, App	482	208.5	5.3	492	4	US-09-679-426-895	Sequence 895, App
410	215.5	5.5	317	4	US-09-906-700-263	Sequence 263, App	483	208.5	5.3	492	4	US-09-759-143-895	Sequence 2, Appl
411	215.5	5.5	317	4	US-09-903-603A-263	Sequence 263, App	484	208	5.3	268	1	US-08-270-584A-2	Sequence 2, Appl
412	215.5	5.5	317	4	US-09-904-920A-263	Sequence 263, App	485	208	5.3	268	2	US-08-765-192-2	Sequence 2, Appl
413	215.5	5.5	317	4	US-09-909-064-263	Sequence 263, App	486	208	5.3	268	3	US-09-199-793-2	Sequence 10, Appl
414	215.5	5.5	317	4	US-09-905-381A-263	Sequence 263, App	487	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appl
415	215.5	5.5	317	4	US-09-906-618-263	Sequence 263, App	488	208	5.3	271	2	US-08-628-198-10	Sequence 10, Appl
416	215	5.4	713	4	US-09-949-016-9983	Sequence 9983, Ap	489	208	5.3	271	3	US-09-201-038-10	Sequence 10, Appl
417	215	5.4	791	2	US-09-131-995-1	Sequence 1, Appl	490	208	5.3	271	5	PCT-US96-07343-10	Sequence 59, Appl
418	215	5.4	791	2	US-08-832-087B-1	Sequence 1, Appl	491	207.5	5.3	241	3	US-08-944-483-59	Sequence 5, Appl
419	215	5.4	791	3	US-09-132-154-1	Sequence 1, Appl	492	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appl
420	215	5.4	791	3	US-08-991-761A-6	Sequence 6, Appl	493	206.5	5.2	255	3	US-08-984-417-5	Sequence 5, Appl
421	215	5.4	791	4	US-08-924-287A-1	Sequence 1, Appl	494	206.5	5.2	284	3	US-09-387-375-7	Sequence 7, Appl
422	215	5.4	810	1	US-07-854-603-2	Sequence 2, Appl	495	206.5	5.2	284	4	US-10-041-400A-7	Sequence 7, Appl
423	215	5.4	810	1	US-08-147-000B-29	Sequence 29, Appl	496	206.5	5.2	284	4	US-10-042-091A-7	Sequence 9, Appl
424	215	5.4	810	3	US-09-086-514-1	Sequence 1, Appl	497	206.5	5.2	316	4	US-09-387-375-9	Sequence 9, Appl
425	215	5.4	810	4	US-09-192-012-5	Sequence 5, Appl	498	206.5	5.2	316	4	US-10-041-400A-9	Sequence 9, Appl
426	215	5.4	810	4	US-09-403-736-1	Sequence 1, Appl	499	206.5	5.2	316	4	US-10-042-091A-9	Sequence 9, Appl
427	215	5.4	810	4	US-09-701-265-1	Sequence 1, Appl	500	205.5	5.2	235	3	US-08-944-483-48	Sequence 48, Appl
428	214	5.4	254	2	US-08-560-098A-49	Sequence 49, Appl	501	205.5	5.2	269	2	US-08-978-404B-10	Sequence 10, Appl
429	214	5.4	292	4	US-09-607-745-9	Sequence 9, Appl	502	205.5	5.2	288	4	US-09-386-642-13	Sequence 13, Appl
430	213.5	5.4	255	3	US-08-944-483-67	Sequence 67, Appl	503	205.5	5.2	327	4	US-09-386-629-8	Sequence 8, Appl
431	213.5	5.4	256	2	US-09-027-337-3	Sequence 3, Appl	504	205.5	5.2	492	3	US-09-342-749-2	Sequence 2, Appl
432	213.5	5.4	256	4	US-09-644-600-3	Sequence 3, Appl	505	205.5	5.2	492	4	US-09-691-840-2	Sequence 2, Appl
433	213.5	5.4	256	4	US-09-654-600A-3	Sequence 3, Appl	506	205.5	5.2	492	4	US-09-759-143-932	Sequence 932, App
434	212.5	5.4	250	4	US-09-205-258-427	Sequence 427, App	507	205.5	5.2	510	4	US-09-949-016-11074	Sequence 11074, A
435	212.5	5.4	282	3	US-09-025-059-1	Sequence 1, Appl	508	205	5.2	393	4	US-09-759-143-934	Sequence 934, App
436	212.5	5.4	289	4	US-09-386-642-14	Sequence 14, Appl	509	204.5	5.2	260	3	US-09-949-016-9260	Sequence 9260, App
437	212	5.4	260	3	US-09-025-059-3	Sequence 3, Appl	510	204	5.2	260	3	US-09-070-526-2	Sequence 2, Appl
438	212	5.4	260	4	US-09-618-259-8	Sequence 8, Appl	511	204	5.2	260	4	US-09-618-253-7	Sequence 7, Appl
439	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appl	512	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appl
440	211.5	5.4	418	1	US-08-508-448C-19	Sequence 19, Appl	513	203.5	5.2	249	4	US-09-949-016-8770	Sequence 8770, Ap
441	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appl	514	203.5	5.2	3623	3	US-09-341-461-2	Sequence 2, Appl
442	211.5	5.4	418	4	US-09-370-838-82	Sequence 82, Appl	515	203	5.1	283	3	US-08-807-151-1	Sequence 1, Appl
443	211.5	5.4	418	4	US-09-370-838-82	Sequence 82, Appl	516	203	5.1	283	4	US-09-478-957-1	Sequence 1, Appl
444	211.5	5.4	418	4	US-09-854-133-82	Sequence 82, Appl	517	202	5.1	2321	4	US-09-230-652-2	Sequence 2, Appl
445	211.5	5.4	418	4	US-09-854-133-83	Sequence 83, Appl	518	200.5	5.1	226	1	US-08-650-129-4	Sequence 4, Appl
446	211	5.3	276	2	US-09-016-366A-15	Sequence 15, Appl	519	200.5	5.1	226	3	US-08-984-417-4	Sequence 4, Appl
447	211	5.3	276	2	US-08-978-404B-21	Sequence 21, Appl	520	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appl
448	211	5.3	300	3	US-08-705-875A-4	Sequence 4, Appl	521	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appl
449	211	5.3	300	3	US-09-220-731-21	Sequence 21, Appl	522	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appl
450	211	5.3	300	4	US-09-242-999-4	Sequence 4, Appl	523	200.5	5.1	232	2	US-08-487-167-8	Sequence 8, Appl
451	211	5.3	433	4	US-09-949-016-8220	Sequence 8220, Ap	524	200.5	5.1	232	2	US-08-482-816-8	Sequence 8, Appl
452	211	5.3	1010	3	US-08-882-046-7	Sequence 7, Appl	525	200.5	5.1	232	2	US-08-296-149-8	Sequence 8, Appl
453	211	5.3	1010	3	US-09-566-047-7	Sequence 7, Appl	526	200.5	5.1	232	2	US-08-801-499-8	Sequence 8, Appl
454	211	5.3	1036	3	US-09-068-740A-6	Sequence 6, Appl	527	200.5	5.1	232	2	US-08-615-271-8	Sequence 8, Appl
455	211	5.3	1067	3	US-09-579-536C-18	Sequence 18, Appl	528	200.5	5.1	232	3	US-09-074-660-8	Sequence 8, Appl
456	211	5.3	1187	3	US-09-068-740A-7	Sequence 7, Appl	529	200.5	5.1	232	3	US-09-074-659-8	Sequence 8, Appl
457	211	5.3	1208	4	US-09-199-865-1	Sequence 1, Appl	530	200.5	5.1	232	3	US-09-106-468-8	Sequence 8, Appl
458	211	5.3	1208	4	US-10-213-329-1	Sequence 1, Appl	531	200.5	5.1	232	3	US-09-106-466A-8	Sequence 8, Appl
459	211	5.3	1218	2	US-08-400-159-6	Sequence 6, Appl	532	200.5	5.1	232	2	US-08-956-267A-2	Sequence 2, Appl
460	211	5.3	1218	3	US-08-611-729A-6	Sequence 6, Appl	533	200.5	5.1	247	2	US-08-936-382A-2	Sequence 2, Appl
461	211	5.3	1218	3	US-08-882-046-2	Sequence 2, Appl	534	200.5	5.1	414	4	US-09-907-794A-104	Sequence 104, App
462	211	5.3	1218	3	US-09-214-278-7	Sequence 7, Appl	535	200.5	5.1	415	4	US-09-905-125A-104	Sequence 104, App
463	211	5.3	1218	3	US-09-068-740A-11	Sequence 11, Appl	536	200.5	5.1	415	4	US-09-902-775A-104	Sequence 104, App
464	211	5.3	1218	4	US-09-855-722-7	Sequence 7, Appl	537	200.5	5.1	415	4	US-09-906-700-104	Sequence 104, App
465	211	5.3	1218	4	US-09-566-047-2	Sequence 2, Appl	538	200.5	5.1	415	4		

539	200.5	5.1	415	4	US-09-903-603A-104	Sequence 104, App	612	193	4.9	228	3	US-08-944-483-44	Sequence 44, Appl
540	200.5	5.1	415	4	US-09-904-520A-104	Sequence 104, App	613	193	4.9	253	6	5223425-8	Patent No. 5223425
541	200.5	5.1	415	4	US-09-909-064-104	Sequence 104, App	614	193	4.9	253	6	5223425-8	Patent No. 5223425
542	200.5	5.1	415	4	US-09-905-381A-104	Sequence 104, App	615	193	4.9	268	3	US-09-032-215-42	Sequence 12, Appl
543	200.5	5.1	415	4	US-09-906-618-104	Sequence 104, App	616	192.5	4.9	225	2	US-08-557-146-12	Sequence 42, Appl
544	200.5	5.1	769	4	US-09-949-016-11019	Sequence 11019, A	617	192.5	4.9	225	2	US-09-154-344-12	Sequence 12, Appl
545	200.5	5.1	810	4	US-08-991-761A-11	Sequence 11, Appl	618	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl
546	200	5.1	385	4	US-09-163-951-16	Sequence 16, Appl	619	192.5	4.9	281	1	US-08-628-198-7	Sequence 7, Appl
547	200	5.1	385	4	US-09-345-881-16	Sequence 16, Appl	620	192.5	4.9	281	1	US-08-628-198-7	Sequence 7, Appl
548	199.5	5.1	1193	2	US-08-400-159-10	Sequence 10, Appl	621	192.5	4.9	281	5	PCT-US96-07343-7	Sequence 7, Appl
549	199.5	5.1	1193	3	US-08-611-729A-10	Sequence 10, Appl	622	192	4.9	149	3	US-09-518-046-20	Sequence 20, Appl
550	199.5	5.1	1193	4	US-09-195-524-10	Sequence 10, Appl	623	191.5	4.9	221	4	US-09-959-392-33	Sequence 33, Appl
551	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl	624	191.5	4.9	224	2	US-08-766-982-13	Sequence 13, Appl
552	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	625	191.5	4.9	224	3	US-08-944-483-36	Sequence 36, Appl
553	199.5	5.1	2556	3	US-08-532-384-20	Sequence 20, Appl	626	191.5	4.9	224	3	US-09-296-219-13	Sequence 13, Appl
554	199.5	5.1	2556	4	US-08-899-232-2	Sequence 2, Appl	627	191.5	4.9	225	2	US-09-027-337-5	Sequence 5, Appl
555	199.5	5.1	2556	4	US-09-121-457-2	Sequence 2, Appl	628	191.5	4.9	225	4	US-09-644-600-5	Sequence 5, Appl
556	199	5.0	249	4	US-09-949-016-8151	Sequence 8151, Ap	629	191.5	4.9	225	4	US-09-654-600A-5	Sequence 5, Appl
557	199	5.0	260	3	US-09-008-271A-7	Sequence 7, Appl	630	191.5	4.9	233	4	US-09-636-382A-24	Sequence 24, Appl
558	199	5.0	278	1	US-08-392-828C-4	Sequence 4, Appl	631	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl
559	199	5.0	278	3	US-09-330-945-4	Sequence 4, Appl	632	191	4.8	250	6	5223425-4	Patent No. 5223425
560	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl	633	191	4.8	250	6	5223425-4	Patent No. 5223425
561	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl	634	191	4.8	254	3	US-09-439-313-525	Sequence 525, App
562	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl	635	191	4.8	254	4	US-09-636-215-525	Sequence 525, App
563	198.5	5.0	223	2	US-08-487-167-9	Sequence 9, Appl	636	191	4.8	254	4	US-09-685-166A-525	Sequence 525, App
564	198.5	5.0	223	2	US-08-482-816-9	Sequence 9, Appl	637	191	4.8	254	4	US-09-679-426-525	Sequence 525, App
565	198.5	5.0	223	2	US-08-296-149-9	Sequence 9, Appl	638	191	4.8	254	4	US-09-759-143-525	Sequence 525, App
566	198.5	5.0	223	2	US-08-801-499-9	Sequence 9, Appl	639	191	4.8	254	4	US-09-651-236-525	Sequence 525, App
567	198.5	5.0	223	2	US-08-615-271-9	Sequence 9, Appl	640	191	4.8	455	3	US-09-261-416-2	Sequence 2, Appl
568	198.5	5.0	223	3	US-09-074-660-9	Sequence 9, Appl	641	190	4.8	284	4	US-09-386-642-54	Sequence 54, Appl
569	198.5	5.0	223	3	US-09-074-659-9	Sequence 9, Appl	642	189	4.8	220	3	US-09-439-313-327	Sequence 327, App
570	198.5	5.0	223	3	US-09-106-468-9	Sequence 9, Appl	643	189	4.8	220	3	US-09-352-616A-327	Sequence 327, App
571	198.5	5.0	223	3	US-09-106-466A-9	Sequence 9, Appl	644	189	4.8	220	4	US-09-232-149A-327	Sequence 327, App
572	198.5	5.0	223	3	US-09-106-467-9	Sequence 9, Appl	645	189	4.8	220	4	US-09-636-215-327	Sequence 327, App
573	198.5	5.0	223	3	US-09-601-318-2	Sequence 2, Appl	646	189	4.8	220	4	US-09-685-166A-327	Sequence 327, App
574	198.5	5.0	223	3	US-09-120-582-2	Sequence 2, Appl	647	189	4.8	220	4	US-09-688-489-327	Sequence 327, App
575	198.5	5.0	232	2	US-08-578-404B-45	Sequence 45, Appl	648	189	4.8	220	4	US-09-679-426-327	Sequence 327, App
576	198.5	5.0	242	4	US-09-949-016-10271	Sequence 10271, A	649	189	4.8	220	4	US-09-759-143-327	Sequence 327, App
577	198	5.0	849	3	US-08-944-483-57	Sequence 57, Appl	650	189	4.8	220	4	US-09-651-236-327	Sequence 327, App
578	197.5	5.0	221	3	US-08-944-483-54	Sequence 54, Appl	651	189	4.8	224	3	US-08-944-483-33	Sequence 33, Appl
579	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl	652	189	4.8	225	2	US-09-027-337-4	Sequence 4, Appl
580	197.5	5.0	222	1	US-08-266-407A-46	Sequence 46, Appl	653	189	4.8	225	4	US-09-644-600-4	Sequence 4, Appl
581	197.5	5.0	222	2	US-08-892-544-46	Sequence 46, Appl	654	189	4.8	225	4	US-09-654-600A-4	Sequence 4, Appl
582	197	5.0	338	4	US-08-991-761A-10	Sequence 10, Appl	655	189	4.8	238	6	5223425-5	Patent No. 5223425
583	196.5	5.0	241	3	US-08-944-483-60	Sequence 60, Appl	656	189	4.8	238	6	5223425-5	Patent No. 5223425
584	196.5	5.0	248	3	US-08-944-483-71	Sequence 71, Appl	657	189	4.8	238	6	5223425-5	Patent No. 5223425
585	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl	658	189	4.8	253	2	US-08-557-146-2	Sequence 2, Appl
586	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl	659	189	4.8	253	2	US-08-824-874-3	Sequence 2, Appl
587	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl	660	189	4.8	253	3	US-09-154-344-2	Sequence 2, Appl
588	196.5	5.0	2523	4	US-08-899-232-3	Sequence 3, Appl	661	189	4.8	253	3	US-08-930-188-2	Sequence 2, Appl
589	196.5	5.0	2523	4	US-09-121-457-3	Sequence 3, Appl	662	189	4.8	253	3	US-09-210-084-3	Sequence 3, Appl
590	195.5	5.0	232	3	US-08-944-483-45	Sequence 45, Appl	663	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appl
591	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl	664	189	4.8	265	4	US-09-949-016-7716	Sequence 7716, App
592	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl	665	189	4.8	312	4	US-09-023-942A-4	Sequence 4, Appl
593	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl	666	189	4.8	449	4	US-09-636-215-617	Sequence 617, App
594	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl	667	189	4.8	449	4	US-09-685-166A-617	Sequence 617, App
595	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl	668	189	4.8	449	4	US-09-426-617	Sequence 617, App
596	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl	669	189	4.8	449	4	US-09-759-143-617	Sequence 617, App
597	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl	670	189	4.8	449	4	US-09-651-236-617	Sequence 617, App
598	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl	671	188.5	4.8	290	4	US-09-386-653A-7	Sequence 7, Appl
599	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl	672	188	4.8	248	2	US-08-744-026-1	Sequence 1, Appl
600	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl	673	188	4.8	248	2	US-09-102-732-1	Sequence 1, Appl
601	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl	674	188	4.8	248	3	US-09-261-767-1	Sequence 1, Appl
602	195.5	5.0	306	1	US-08-774-592-1	Sequence 1, Appl	675	188	4.8	254	3	US-09-439-313-523	Sequence 523, App
603	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	676	188	4.8	254	4	US-09-636-215-523	Sequence 523, App
604	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl	677	188	4.8	254	4	US-09-685-166A-523	Sequence 523, App
605	195.5	5.0	2471	3	US-08-532-384-19	Sequence 19, Appl	678	188	4.8	254	4	US-09-679-426-523	Sequence 523, App
606	195.5	5.0	2471	4	US-08-899-232-1	Sequence 1, Appl	679	188	4.8	254	4	US-09-759-143-523	Sequence 523, App
607	195.5	5.0	2471	4	US-09-121-457-1	Sequence 1, Appl	680	188	4.8	254	4	US-09-651-236-523	Sequence 523, App
608	194.5	4.9	246	2	US-08-978-404B-44	Sequence 44, Appl	681	188	4.8	263	2	US-08-790-137-4	Sequence 4, Appl
609	194.5	4.9	415	3	US-09-032-523-2	Sequence 2, Appl	682	188	4.8	263	2	US-08-824-874-5	Sequence 5, Appl
610	194.5	4.9	415	4	US-09-802-633-2	Sequence 2, Appl	683	188	4.8	263	3	US-08-807-151-5	Sequence 5, Appl
611	194	4.9	113	4	US-09-438-046-20	Sequence 20, Appl	684	188	4.8	263	3	US-09-210-084-5	Sequence 5, Appl

685	188	4.8	263	3	US-09-478-957-5	Sequence 5, Appli	758	181.5	4.6	258	1	US-07-990-301A-2	Sequence 2, Appli
686	188	4.8	263	4	US-09-764-762-5	Sequence 5, Appli	759	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appli
687	188	4.8	333	4	US-08-591-761A-8	Sequence 8, Appli	760	181.5	4.6	299	2	US-08-628-198-8	Sequence 8, Appli
688	187.5	4.8	224	3	US-08-944-483-35	Sequence 35, Appli	761	181.5	4.6	299	3	US-09-201-038-8	Sequence 8, Appli
689	187.5	4.8	242	3	US-08-944-483-29	Sequence 29, Appli	762	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 86, Appli
690	187.5	4.8	255	3	US-08-906-769-83	Sequence 83, Appli	763	181	4.6	296	4	US-09-800-729-86	Sequence 6948, Ap
691	187.5	4.8	255	3	US-08-906-616-83	Sequence 83, Appli	764	180	4.6	254	4	US-09-949-016-6948	Patent No. 5223425
692	187.5	4.8	255	3	US-08-817-795-83	Sequence 83, Appli	765	180	4.6	260	6	5223425-10	Patent No. 5223425
693	187.5	4.8	255	3	US-08-639-075A-83	Sequence 83, Appli	766	180	4.6	260	6	5223425-10	Sequence 176, App
694	187.5	4.8	255	3	US-09-012-431-83	Sequence 83, Appli	767	179.5	4.6	205	3	US-09-020-956-176	Sequence 176, App
695	187.5	4.8	255	3	US-09-012-692-83	Sequence 83, Appli	768	179.5	4.6	205	3	US-09-030-607-176	Sequence 176, App
696	187.5	4.8	255	3	US-08-906-613-83	Sequence 83, Appli	769	179.5	4.6	205	3	US-09-439-313-176	Sequence 176, App
697	187.5	4.8	255	5	PCT-US95-14442A-83	Sequence 83, Appli	770	179.5	4.6	205	3	US-09-352-616A-176	Sequence 176, App
698	186	4.7	110	4	US-09-341-461-28	Sequence 28, Appli	771	179.5	4.6	205	4	US-09-232-149A-176	Sequence 176, App
699	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appli	772	179.5	4.6	205	4	US-09-159-812-176	Sequence 176, App
700	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appli	773	179.5	4.6	205	4	US-09-636-215-176	Sequence 176, App
701	186	4.7	230	2	US-08-892-544-47	Sequence 47, Appli	774	179.5	4.6	205	4	US-09-685-166A-176	Sequence 176, App
702	186	4.7	230	2	US-08-766-982-12	Sequence 12, Appli	775	179.5	4.6	205	4	US-09-115-453-176	Sequence 176, App
703	186	4.7	230	3	US-08-944-483-53	Sequence 53, Appli	776	179.5	4.6	205	4	US-09-688-489-176	Sequence 176, App
704	186	4.7	230	3	US-09-296-219-12	Sequence 12, Appli	777	179.5	4.6	205	4	US-09-679-426-176	Sequence 176, App
705	186	4.7	232	2	US-08-897-340-31	Sequence 31, Appli	778	179.5	4.6	205	4	US-09-759-143-176	Sequence 176, App
706	186	4.7	232	3	US-09-252-329-31	Sequence 31, Appli	779	179.5	4.6	205	4	US-09-651-236-176	Sequence 176, App
707	186	4.7	326	3	US-09-411-977-3	Sequence 3, Appli	780	179.5	4.6	259	6	5223425-2	Patent No. 5223425
708	186	4.7	326	4	US-10-057-951-3	Sequence 3, Appli	781	179.5	4.6	259	6	5223425-2	Patent No. 5223425
709	185.5	4.7	256	3	US-09-032-215-27	Sequence 27, Appli	782	179.5	4.6	728	3	US-08-981-392-2	Sequence 2, Appli
710	185.5	4.7	261	3	US-08-163-913A-2	Sequence 2, Appli	783	179.5	4.6	728	4	US-09-908-322-2	Sequence 2, Appli
711	185.5	4.7	261	4	US-08-462-515-2	Sequence 2, Appli	784	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appli
712	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appli	785	179	4.5	230	1	US-08-379-621-2	Sequence 2, Appli
713	185.5	4.7	306	4	US-09-386-642-53	Sequence 53, Appli	786	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appli
714	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appli	787	179	4.5	230	2	US-08-889-078-2	Sequence 2, Appli
715	185.5	4.7	711	1	US-08-334-177-2	Sequence 2, Appli	788	179	4.5	253	3	US-09-578-303-4	Sequence 22, Appli
716	185.5	4.7	711	2	US-08-666-082B-1	Sequence 1, Appli	789	179	4.5	384	3	US-09-032-215-22	Sequence 4, Appli
717	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 2, Appli	790	178.5	4.5	250	3	US-08-944-483-68	Sequence 68, Appli
718	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appli	791	178.5	4.5	315	4	US-09-386-653A-9	Sequence 9, Appli
719	185	4.7	247	3	US-08-944-483-49	Sequence 49, Appli	792	178.5	4.5	401	2	US-08-839-008-5	Sequence 9, Appli
720	185	4.7	258	1	US-09-102-732-3	Sequence 3, Appli	793	178.5	4.5	468	2	US-09-839-008-7	Sequence 7, Appli
721	185	4.7	258	2	US-09-102-732-3	Sequence 3, Appli	794	178.5	4.5	468	3	US-09-032-523-8	Sequence 8, Appli
722	185	4.7	258	3	US-09-261-767-3	Sequence 3, Appli	795	178.5	4.5	468	4	US-09-802-633-8	Sequence 8, Appli
723	185	4.7	314	4	US-09-023-942A-6	Sequence 6, Appli	796	178.5	4.5	922	4	US-09-116-473-4	Sequence 4, Appli
724	184	4.7	144	4	US-09-618-259-1	Sequence 1, Appli	797	178.5	4.5	923	3	US-08-936-135-6	Sequence 6, Appli
725	184	4.7	314	3	US-09-008-271A-3	Sequence 3, Appli	798	178.5	4.5	923	4	US-09-439-711C-6	Sequence 3, Appli
726	184	4.7	314	4	US-09-907-794A-257	Sequence 257, App	799	177.5	4.5	248	2	US-08-851-974-3	Sequence 3, Appli
727	184	4.7	314	4	US-09-905-125A-257	Sequence 257, App	800	177.5	4.5	248	3	US-09-213-390-3	Sequence 1, Appli
728	184	4.7	314	4	US-09-902-775A-257	Sequence 257, App	801	177.5	4.5	1964	2	US-09-467-997-1	Sequence 7, Appli
729	184	4.7	314	4	US-09-906-700-257	Sequence 257, App	802	177	4.5	1102	3	US-09-374-135-7	Sequence 29, Appli
730	184	4.7	314	4	US-09-903-603A-257	Sequence 257, App	803	177	4.5	110	4	US-09-341-461-29	Sequence 45768, A
731	184	4.7	314	4	US-09-904-920A-257	Sequence 257, App	804	177	4.5	223	4	US-09-270-767-45768	Sequence 11, Appl
732	184	4.7	314	4	US-09-909-064-257	Sequence 257, App	805	177	4.5	240	1	US-08-278-091-11	Sequence 11, Appl
733	184	4.7	314	4	US-09-905-381A-257	Sequence 257, App	806	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl
734	184	4.7	314	4	US-09-906-618-257	Sequence 257, App	807	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appl
735	183.5	4.7	711	2	US-08-766-982-2	Sequence 2, Appli	808	177	4.5	240	2	US-08-487-167-11	Sequence 11, Appl
736	183.5	4.7	711	3	US-09-296-219-2	Sequence 2, Appli	809	177	4.5	240	2	US-08-482-816-11	Sequence 11, Appl
737	183.5	4.7	711	4	US-09-600-991-20	Sequence 20, Appli	810	177	4.5	240	2	US-08-296-149-11	Sequence 11, Appl
738	183.5	4.7	711	4	US-09-601-040A-12	Sequence 12, Appli	811	177	4.5	240	2	US-08-801-499-11	Sequence 11, Appl
739	183.5	4.7	711	4	US-09-949-016-6981	Sequence 6981, Ap	812	177	4.5	240	3	US-08-615-271-11	Sequence 11, Appl
740	183.5	4.7	722	3	US-08-981-392-12	Sequence 12, Appli	813	177	4.5	240	3	US-09-074-660-11	Sequence 11, Appl
741	183.5	4.7	722	4	US-09-908-322-12	Sequence 12, Appli	814	177	4.5	240	3	US-09-074-659-11	Sequence 11, Appl
742	183	4.6	418	4	US-10-177-661-6	Sequence 6, Appli	815	177	4.5	240	3	US-09-106-468-11	Sequence 11, Appl
743	182.5	4.6	258	4	US-09-023-942A-8	Sequence 8, Appli	816	177	4.5	240	3	US-09-106-466A-11	Sequence 11, Appl
744	182.5	4.6	484	2	US-08-252-493C-9	Sequence 9, Appli	817	177	4.5	729	3	US-09-106-467-11	Sequence 8, Appli
745	182.5	4.6	484	3	US-09-276-197-9	Sequence 9, Appli	818	177	4.5	830	6	US-08-872-855-8	Sequence 8, Appli
746	182.5	4.6	720	3	US-08-872-855-4	Sequence 4, Appli	819	177	4.5	830	6	5378464-2	Patent No. 5378464
747	182	4.6	405	3	US-09-734-675-2	Sequence 2, Appli	820	177	4.5	830	6	5378464-2	Patent No. 5378464
748	182	4.6	721	3	US-08-872-855-7	Sequence 7, Appli	821	176.5	4.5	232	1	US-07-990-301A-4	Sequence 4, Appli
749	182	4.6	1055	3	US-09-214-278-2	Sequence 2, Appli	822	176.5	4.5	901	3	US-08-936-135-22	Sequence 22, Appl
750	182	4.6	1055	4	US-09-855-722-2	Sequence 2, Appli	823	176.5	4.5	901	4	US-09-439-711C-22	Sequence 22, Appl
751	182	4.6	1055	2	US-08-400-159-8	Sequence 8, Appli	824	176.5	4.5	906	3	US-08-936-135-24	Sequence 24, Appl
752	182	4.6	1212	3	US-09-214-278-3	Sequence 3, Appli	825	176.5	4.5	906	4	US-09-439-711C-24	Sequence 24, Appl
753	182	4.6	1212	4	US-09-855-722-3	Sequence 3, Appli	826	176.5	4.5	909	3	US-08-936-135-8	Sequence 8, Appli
754	182	4.6	1238	4	US-09-214-278-5	Sequence 5, Appli	827	176.5	4.5	909	4	US-08-936-135-10	Sequence 10, Appli
755	182	4.6	1238	4	US-09-855-722-5	Sequence 5, Appli	828	176.5	4.5	909	4	US-09-439-711C-8	Sequence 8, Appli
756	182	4.6	1257	3	US-08-611-729A-8	Sequence 8, Appli	829	176.5	4.5	909	4	US-09-439-711C-10	Sequence 10, Appl
757	182	4.6	1257	4	US-09-195-524-8	Sequence 8, Appli	830	176.5	4.5	914	3	US-08-936-135-12	Sequence 12, Appl

831	176.5	4.5	914	4	US-09-439-711C-12	Sequence 12, Appl	Sequence 12, Appl	904	170	4.3	213	3	US-08-906-769-149	Sequence 149, App
832	176.5	4.5	925	3	US-09-116-473-2	Sequence 2, Appl	Sequence 2, Appl	905	170	4.3	213	3	US-08-906-616-149	Sequence 149, App
833	176.5	4.5	926	3	US-08-936-135-14	Sequence 14, Appl	Sequence 14, Appl	906	170	4.3	213	3	US-08-936-075A-149	Sequence 149, App
834	176.5	4.5	926	3	US-09-439-711C-14	Sequence 14, Appl	Sequence 14, Appl	907	170	4.3	213	3	US-09-012-431-149	Sequence 149, App
835	176.5	4.5	931	3	US-08-936-135-16	Sequence 16, Appl	Sequence 16, Appl	908	170	4.3	213	3	US-09-012-692-149	Sequence 149, App
836	176.5	4.5	931	3	US-09-439-711C-16	Sequence 16, Appl	Sequence 16, Appl	909	170	4.3	213	3	US-08-906-613-149	Sequence 149, App
837	176	4.5	933	3	US-09-004-731-27	Sequence 27, Appl	Sequence 27, Appl	910	170	4.3	717	4	US-09-601-040A-8	Sequence 8, Appl
838	176	4.5	933	3	US-08-749-699-27	Sequence 27, Appl	Sequence 27, Appl	911	170	4.3	729	4	US-09-601-040A-4	Sequence 4, Appl
839	176	4.5	933	3	US-08-044-729-27	Sequence 27, Appl	Sequence 27, Appl	912	170	4.3	729	4	US-09-601-040A-4	Sequence 4, Appl
840	176	4.5	242	3	US-09-004-729-27	Sequence 27, Appl	Sequence 27, Appl	913	170	4.3	1148	3	US-08-882-046-4	Sequence 4, Appl
841	176	4.5	242	3	US-08-944-483-58	Sequence 58, Appl	Sequence 58, Appl	914	170	4.3	95	3	US-09-566-047-4	Sequence 8, Appl
842	176	4.5	266	3	US-09-004-731-24	Sequence 24, Appl	Sequence 24, Appl	915	169	4.3	95	3	US-09-341-135-8	Sequence 8, Appl
843	176	4.5	266	3	US-08-749-699-24	Sequence 24, Appl	Sequence 24, Appl	916	169	4.3	237	1	US-08-096-946-11	Sequence 11, Appl
844	176	4.5	266	4	US-09-004-729-24	Sequence 24, Appl	Sequence 24, Appl	917	169	4.3	237	1	US-08-096-946-11	Sequence 11, Appl
845	175.5	4.4	921	4	US-09-439-711C-4	Sequence 4, Appl	Sequence 4, Appl	918	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl
846	175	4.4	112	4	US-09-438-046-21	Sequence 21, Appl	Sequence 21, Appl	919	169	4.3	237	5	PCT-US95-06157-1	Sequence 11, Appl
847	175	4.4	909	3	US-08-936-135-18	Sequence 18, Appl	Sequence 18, Appl	920	169	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
848	175	4.4	926	3	US-09-439-711C-18	Sequence 18, Appl	Sequence 18, Appl	921	168.5	4.3	222	6	5223425-6	Patent No. 5223425
849	175	4.4	926	3	US-08-936-135-20	Sequence 20, Appl	Sequence 20, Appl	922	168.5	4.3	222	6	5223425-6	Patent No. 5223425
850	175	4.4	926	4	US-09-439-711C-20	Sequence 20, Appl	Sequence 20, Appl	923	168.5	4.3	222	6	5223425-6	Patent No. 5223425
851	174	4.4	931	4	US-09-583-638-4	Sequence 4, Appl	Sequence 4, Appl	924	168	4.3	383	4	US-09-142-027A-12	Sequence 12, Appl
852	174	4.4	265	2	US-08-177-109A-57	Sequence 57, Appl	Sequence 57, Appl	925	168	4.3	245	3	US-08-906-769-121	Sequence 121, App
853	174	4.4	265	2	US-08-687-706-57	Sequence 57, Appl	Sequence 57, Appl	926	168	4.3	245	3	US-08-906-616-121	Sequence 121, App
854	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl	Sequence 9, Appl	927	168	4.3	245	3	US-08-639-075A-121	Sequence 121, App
855	174	4.4	286	3	US-08-628-198-9	Sequence 9, Appl	Sequence 9, Appl	928	168	4.3	245	3	US-09-012-431-121	Sequence 121, App
856	174	4.4	286	3	US-09-201-038-9	Sequence 9, Appl	Sequence 9, Appl	929	167.5	4.2	261	1	US-09-012-692-121	Sequence 121, App
857	173.5	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl	Sequence 9, Appl	930	167.5	4.2	261	1	US-08-906-613-121	Sequence 121, App
858	173.5	4.4	294	4	US-09-800-729-146	Sequence 146, App	Sequence 146, App	931	167.5	4.2	261	1	US-08-744-026-5	Sequence 5, Appl
859	173.5	4.4	294	4	US-10-067-422-12	Sequence 12, Appl	Sequence 12, Appl	932	167.5	4.2	261	3	US-09-102-732-5	Sequence 5, Appl
860	173.5	4.4	414	4	US-09-270-767-46426	Sequence 46426, A	Sequence 46426, A	933	167.5	4.2	261	3	US-09-083-521-6	Sequence 6, Appl
861	173	4.4	717	3	US-08-872-855-9	Sequence 9, Appl	Sequence 9, Appl	934	167.5	4.2	261	3	US-09-261-767-5	Sequence 5, Appl
862	173	4.4	211	3	US-09-220-731-25	Sequence 25, Appl	Sequence 25, Appl	935	167.5	4.2	261	4	US-09-413-049-1	Sequence 1, Appl
863	172.5	4.4	449	2	US-08-839-008-2	Sequence 2, Appl	Sequence 2, Appl	936	167.5	4.2	261	4	US-09-907-402-1	Sequence 1, Appl
864	172.5	4.4	449	2	US-08-839-008-9	Sequence 9, Appl	Sequence 9, Appl	937	167.5	4.2	262	1	US-09-618-259-10	Sequence 10, Appl
865	172.5	4.4	449	4	US-09-919-497-89	Sequence 89, Appl	Sequence 89, Appl	938	167.5	4.2	262	2	US-08-744-026-4	Sequence 4, Appl
866	172.5	4.4	458	4	US-09-949-016-7238	Sequence 7238, Ap	Sequence 7238, Ap	939	167.5	4.2	262	2	US-09-102-732-4	Sequence 4, Appl
867	172.5	4.4	1248	3	US-08-882-046-6	Sequence 6, Appl	Sequence 6, Appl	940	167	4.2	262	3	US-09-261-767-4	Sequence 4, Appl
868	172.5	4.4	1248	4	US-09-566-047-6	Sequence 6, Appl	Sequence 6, Appl	941	166.5	4.2	262	3	US-09-583-638-2	Sequence 2, Appl
869	172	4.4	250	4	US-09-270-767-33709	Sequence 33709, A	Sequence 33709, A	942	166.5	4.2	520	3	US-09-374-135-5	Sequence 5, Appl
870	172	4.4	357	4	US-09-270-767-43564	Sequence 43564, A	Sequence 43564, A	943	166.5	4.2	702	3	US-09-068-740A-3	Sequence 3, Appl
871	172	4.4	357	4	US-09-270-767-58366	Sequence 58366, A	Sequence 58366, A	944	166.5	4.2	723	3	US-09-068-740A-9	Sequence 9, Appl
872	172	4.4	721	3	US-08-981-392-5	Sequence 5, Appl	Sequence 5, Appl	945	166.5	4.2	723	3	US-09-423-753-27	Sequence 27, Appl
873	172	4.4	721	3	US-09-908-322-5	Sequence 5, Appl	Sequence 5, Appl	946	166	4.2	723	3	US-09-641-612-6	Sequence 6, Appl
874	171.5	4.3	238	3	US-08-944-483-39	Sequence 39, Appl	Sequence 39, Appl	947	166	4.2	124	6	5514582-38	Patent No. 5514582
875	171.5	4.3	259	3	US-08-906-769-190	Sequence 190, App	Sequence 190, App	948	166	4.2	124	6	5514582-38	Patent No. 5514582
876	171.5	4.3	259	3	US-08-906-616-190	Sequence 190, App	Sequence 190, App	949	166	4.2	237	3	US-08-768-859A-1	Sequence 1, Appl
877	171.5	4.3	259	3	US-08-639-075A-190	Sequence 190, App	Sequence 190, App	950	166	4.2	237	3	US-08-767-820A-1	Sequence 1, Appl
878	171.5	4.3	259	3	US-09-004-731-85	Sequence 85, Appl	Sequence 85, Appl	951	166	4.2	237	3	US-08-622-046B-7	Sequence 7, Appl
879	171.5	4.3	259	3	US-09-012-431-190	Sequence 190, App	Sequence 190, App	952	166	4.2	237	3	US-08-944-483-38	Sequence 38, Appl
880	171.5	4.3	259	3	US-08-749-699-85	Sequence 85, Appl	Sequence 85, Appl	953	166	4.2	237	3	US-09-100-264-3	Sequence 3, Appl
881	171.5	4.3	259	3	US-09-012-692-190	Sequence 190, App	Sequence 190, App	954	166	4.2	237	4	US-09-303-339-2	Sequence 2, Appl
882	171.5	4.3	259	3	US-08-906-613-190	Sequence 190, App	Sequence 190, App	955	166	4.2	237	4	US-08-843-076D-7	Sequence 7, Appl
883	171.5	4.3	259	4	US-09-004-729-85	Sequence 85, Appl	Sequence 85, Appl	956	166	4.2	237	4	US-09-303-208-1	Sequence 1, Appl
884	171.5	4.3	262	2	US-08-790-137-1	Sequence 1, Appl	Sequence 1, Appl	957	166	4.2	243	3	US-08-944-483-70	Sequence 70, Appl
885	171.5	4.3	262	2	US-08-790-137-3	Sequence 3, Appl	Sequence 3, Appl	958	166	4.2	441	4	US-09-949-016-10792	Sequence 10792, A
886	171.5	4.3	262	2	US-08-681-151-4	Sequence 4, Appl	Sequence 4, Appl	959	165.5	4.2	923	4	US-09-439-711C-2	Sequence 2, Appl
887	171.5	4.3	262	2	US-08-824-874-4	Sequence 4, Appl	Sequence 4, Appl	960	165.5	4.2	240	1	US-08-472-228A-1	Sequence 1, Appl
888	171.5	4.3	262	3	US-08-807-151-4	Sequence 4, Appl	Sequence 4, Appl	961	165.5	4.2	240	5	PCT-US96-09303-1	Sequence 1, Appl
889	171.5	4.3	262	3	US-09-210-084-4	Sequence 4, Appl	Sequence 4, Appl	962	165.5	4.2	240	3	US-09-146-831-1	Sequence 1, Appl
890	171.5	4.3	262	3	US-09-478-957-4	Sequence 4, Appl	Sequence 4, Appl	963	165.5	4.2	383	1	US-08-597-545-2	Sequence 2, Appl
891	171.5	4.3	262	4	US-09-764-762-4	Sequence 4, Appl	Sequence 4, Appl	964	165	4.2	383	1	US-08-457-135-2	Sequence 2, Appl
892	171.5	4.3	262	4	US-09-618-259-9	Sequence 9, Appl	Sequence 9, Appl	965	164	4.2	101	3	US-09-374-135-4	Sequence 4, Appl
893	171.5	4.3	666	3	US-09-341-587-1	Sequence 1, Appl	Sequence 1, Appl	966	164	4.2	351	3	US-09-358-055B-11	Sequence 11, Appl
894	171.5	4.3	1785	3	US-09-341-587-3	Sequence 3, Appl	Sequence 3, Appl	967	164	4.2	351	4	US-09-893-238-11	Sequence 11, Appl
895	171	4.3	262	3	US-09-025-059-4	Sequence 4, Appl	Sequence 4, Appl	968	164	4.2	812	4	US-09-192-012-9	Sequence 9, Appl
896	171	4.3	262	4	US-09-755-100A-14	Sequence 14, Appl	Sequence 14, Appl	969	163	4.1	441	4	US-09-949-016-11196	Sequence 11196, A
897	171	4.3	287	4	US-09-270-767-33263	Sequence 33263, A	Sequence 33263, A	970	163	4.1	441	4	US-09-907-725A-190	Sequence 190, App
898	171	4.3	287	4	US-09-270-767-48480	Sequence 48480, A	Sequence 48480, A	971	163	4.1	607	4	US-09-905-125A-190	Sequence 190, App
899	171	4.3	290	4	US-09-949-016-8166	Sequence 8166, Ap	Sequence 8166, Ap	972	163	4.1	607	4	US-09-902-775A-190	Sequence 190, App
900	171	4.3	717	4	US-09-601-040A-6	Sequence 6, Appl	Sequence 6, Appl	973	163	4.1	607	4	US-09-906-700-190	Sequence 190, App
901	171	4.3	729	4	US-09-601-040A-2	Sequence 2, Appl	Sequence 2, Appl	974	163	4.1	607	4	US-09-903-603A-190	Sequence 190, App
902	171	4.3	737	4	US-09-866-028-15	Sequence 15, Appl	Sequence 15, Appl	975	163	4.1	607	4	US-09-904-920A-190	Sequence 190, App
903	171	4.3	737	4	US-09-944-457-15	Sequence 15, Appl	Sequence 15, Appl	976	163	4.1	607	4	US-09-909-064-190	Sequence 190, App

977	163	4.1	607	4	US-09-905-381A-190	Sequence 190, App	1050	156	4.0	238	5	PCT-US95-06157-8	Sequence 8, Appli
978	163	4.1	607	4	US-09-906-618-190	Sequence 190, App	1051	156	4.0	244	3	US-08-768-859A-10	Sequence 10, Appl
979	162.5	4.1	1290	1	US-08-470-3508-2	Sequence 2, Appli	1052	156	4.0	244	3	US-08-767-820A-10	Sequence 10, Appl
980	161.5	4.1	251	3	US-08-944-483-28	Sequence 28, Appli	1053	156	4.0	244	3	US-08-622-046B-5	Sequence 5, Appli
981	161.5	4.1	832	3	US-08-981-392-6	Sequence 6, Appli	1054	156	4.0	244	3	US-08-622-046B-16	Sequence 16, Appli
982	161.5	4.1	832	4	US-09-908-322-6	Sequence 6, Appli	1055	156	4.0	244	3	US-09-100-264-5	Sequence 5, Appli
983	161.5	4.1	1025	4	US-09-834-309-5	Sequence 5, Appli	1056	156	4.0	244	4	US-08-843-076D-5	Sequence 5, Appli
984	161	4.1	207	4	US-09-949-016-7712	Sequence 7712, Ap	1057	156	4.0	244	5	PCT-US95-06157-10	Sequence 10, Appl
985	161	4.1	293	4	US-09-509-908-2	Sequence 2, Appli	1058	156	4.0	261	3	US-08-768-859A-6	Sequence 6, Appli
986	160.5	4.1	238	4	US-09-664-595A-15	Sequence 15, Appli	1059	156	4.0	261	3	US-08-768-859A-19	Sequence 19, Appl
987	160.5	4.1	263	4	US-09-949-016-9072	Sequence 9072, Ap	1060	156	4.0	261	3	US-08-767-820A-6	Sequence 6, Appli
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990	160.5	4.1	665	4	US-09-949-016-10776	Sequence 10776, A	1063	156	4.0	261	3	US-08-622-046B-14	Sequence 14, Appl
991	160	4.1	207	4	US-10-000-489-54	Sequence 54, Appli	1064	156	4.0	261	3	US-09-100-264-7	Sequence 7, Appli
992	160	4.1	234	3	US-08-944-483-46	Sequence 46, Appli	1065	156	4.0	261	3	US-08-983-075D-7	Sequence 7, Appli
993	160	4.1	268	4	US-09-949-016-10712	Sequence 10712, A	1066	156	4.0	261	4	US-08-843-076D-3	Sequence 3, Appli
994	160	4.1	2871	4	US-09-538-092-1076	Sequence 1076, Ap	1067	156	4.0	261	5	PCT-US95-06157-6	Sequence 6, Appli
995	159.5	4.0	228	2	US-08-766-982-11	Sequence 11, Appli	1068	156	4.0	278	4	US-09-949-016-7711	Sequence 7711, Ap
996	159.5	4.0	228	3	US-09-296-219-11	Sequence 11, Appli	1069	155.5	3.9	247	2	US-08-851-974-1	Sequence 1, Appli
997	159.5	4.0	276	4	US-09-270-767-32048	Sequence 32048, A	1070	155.5	3.9	247	2	US-09-213-320-1	Sequence 1, Appli
998	159.5	4.0	276	4	US-09-270-767-47265	Sequence 47265, A	1071	155.5	3.9	830	3	US-08-872-855-11	Sequence 11, Appli
999	159	4.0	237	2	US-08-844-024-2	Sequence 2, Appli	1072	155	3.9	2489	4	US-09-911-842A-5	Sequence 5, Appli
1000	159	4.0	237	2	US-08-718-547-2	Sequence 2, Appli	1073	154.5	3.9	228	1	US-08-278-091-7	Sequence 7, Appli
1001	158.5	4.0	283	4	US-09-244-111-2	Sequence 2, Appli	1074	154.5	3.9	228	1	US-08-483-859-7	Sequence 7, Appli
1002	158.5	4.0	385	1	US-08-597-545-1	Sequence 1, Appli	1075	154.5	3.9	228	1	US-08-472-173-7	Sequence 7, Appli
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1004	158.5	4.0	385	1	US-09-142-027A-10	Sequence 10, Appli	1077	154.5	3.9	228	2	US-08-482-816-7	Sequence 7, Appli
1005	158.5	4.0	833	1	US-08-264-534-6	Sequence 6, Appli	1078	154.5	3.9	228	2	US-08-296-149-7	Sequence 7, Appli
1006	158.5	4.0	833	1	US-08-083-590A-2	Sequence 2, Appli	1079	154.5	3.9	228	2	US-08-801-499-7	Sequence 7, Appli
1007	158.5	4.0	833	1	US-08-465-500-6	Sequence 6, Appli	1080	154.5	3.9	228	2	US-08-615-271-7	Sequence 7, Appli
1008	158.5	4.0	833	2	US-08-346-128-6	Sequence 6, Appli	1081	154.5	3.9	228	3	US-09-074-660-7	Sequence 7, Appli
1009	158.5	4.0	833	2	US-08-532-384-2	Sequence 2, Appli	1082	154.5	3.9	228	3	US-09-074-659-7	Sequence 7, Appli
1010	158.5	4.0	833	3	US-08-893-828-6	Sequence 6, Appli	1083	154.5	3.9	228	3	US-09-106-468-7	Sequence 7, Appli
1011	158.5	4.0	156	3	US-09-261-416-6	Sequence 6, Appli	1084	154.5	3.9	228	3	US-09-106-468-7	Sequence 7, Appli
1012	158	4.0	190	2	US-08-845-998-4	Sequence 4, Appli	1085	154.5	3.9	228	3	US-09-374-135-6	Sequence 6, Appli
1013	157.5	4.0	190	3	US-09-206-537-4	Sequence 4, Appli	1086	154	3.9	224	1	US-08-553-516-2	Sequence 2, Appli
1014	157.5	4.0	190	3	US-09-430-854-4	Sequence 4, Appli	1087	154	3.9	227	1	US-08-944-483-40	Sequence 40, Appli
1015	157.5	4.0	226	4	US-09-601-040A-28	Sequence 28, Appli	1088	154	3.9	248	1	US-08-238-130-2	Sequence 2, Appli
1016	157.5	4.0	228	3	US-08-944-483-55	Sequence 55, Appli	1089	154	3.9	248	1	US-08-921-426-4	Sequence 4, Appli
1017	157.5	4.0	255	3	US-08-906-769-91	Sequence 91, Appli	1090	154	3.9	248	2	US-08-816-915-4	Sequence 4, Appli
1018	157.5	4.0	255	3	US-08-906-616-91	Sequence 91, Appli	1091	154	3.9	248	3	US-09-032-215-37	Sequence 37, Appli
1019	157.5	4.0	255	3	US-08-817-795-91	Sequence 91, Appli	1092	154	3.9	248	5	PCT-US95-07743-4	Sequence 4, Appli
1020	157.5	4.0	255	3	US-08-639-078A-91	Sequence 91, Appli	1093	154	3.9	268	2	US-08-824-874-1	Sequence 1, Appli
1021	157.5	4.0	255	3	US-09-012-431-91	Sequence 91, Appli	1094	154	3.9	268	3	US-09-210-084-1	Sequence 1, Appli
1022	157.5	4.0	255	3	US-08-906-613-91	Sequence 91, Appli	1095	154	3.9	268	4	US-09-764-762-1	Sequence 1, Appli
1023	157.5	4.0	255	3	US-08-906-613-91	Sequence 91, Appli	1096	154	3.9	321	4	US-09-270-767-33762	Sequence 33762, A
1024	157.5	4.0	255	5	PCT-US95-14442A-91	Sequence 91, Appli	1097	154	3.9	321	4	US-09-270-767-48979	Sequence 48979, A
1025	157.5	4.0	185	3	US-08-906-769-141	Sequence 141, App	1098	154	3.9	1466	6	5256642-6	Patent No. 5256642
1026	157	4.0	185	3	US-08-906-616-141	Sequence 141, App	1099	154	3.9	1466	6	5472939-6	Patent No. 5472939
1027	157	4.0	185	3	US-08-906-616-141	Sequence 141, App	1100	154	3.9	1466	6	5256642-6	Patent No. 5256642
1028	157	4.0	185	3	US-08-639-075A-141	Sequence 141, App	1101	154	3.9	1466	6	5472939-5	Patent No. 5472939
1029	157	4.0	185	3	US-09-012-431-141	Sequence 141, App	1102	154	3.9	1537	6	5256642-5	Patent No. 5256642
1030	157	4.0	185	3	US-09-012-692-141	Sequence 141, App	1103	154	3.9	1537	6	5472939-5	Patent No. 5472939
1031	157	4.0	185	3	US-08-906-613-141	Sequence 141, App	1104	154	3.9	1537	6	5256642-5	Patent No. 5256642
1032	157	4.0	610	6	5217870-2	Patent No. 5217870	1105	154	3.9	1537	6	5256642-5	Patent No. 5256642
1033	157	4.0	610	6	5217870-2	Patent No. 5217870	1106	154	3.9	1537	6	5472939-5	Patent No. 5472939
1034	157	4.0	647	4	US-09-949-016-10272	Sequence 10272, A	1107	154	3.9	1537	6	5256642-10	Patent No. 5256642
1035	156.5	4.0	312	4	US-09-636-382A-15	Sequence 15, Appli	1108	154	3.9	1847	6	5472939-10	Patent No. 5472939
1036	156.5	4.0	3635	4	US-09-845-583A-2	Sequence 2, Appli	1109	154	3.9	1847	6	5256642-10	Patent No. 5256642
1037	156	4.0	237	3	US-08-768-859A-16	Sequence 16, Appli	1110	154	3.9	1847	6	5472939-10	Patent No. 5472939
1038	156	4.0	237	3	US-08-768-859A-21	Sequence 21, Appli	1111	154	3.9	1947	6	US-09-612-314A-52	Sequence 52, Appli
1039	156	4.0	237	3	US-08-767-820A-16	Sequence 16, Appli	1112	154	3.9	2039	6	5472939-2	Patent No. 5472939
1040	156	4.0	237	3	US-08-767-820A-21	Sequence 21, Appli	1113	154	3.9	2039	6	5256642-2	Patent No. 5256642
1041	156	4.0	237	3	US-08-622-046B-1	Sequence 12, Appli	1114	154	3.9	2039	6	5472939-2	Patent No. 5472939
1042	156	4.0	237	3	US-08-622-046B-12	Sequence 12, Appli	1115	154	3.9	2039	6	5472939-2	Patent No. 5472939
1043	156	4.0	237	3	US-08-944-483-37	Sequence 37, Appli	1116	153.5	3.9	185	3	US-08-705-875A-5	Sequence 5, Appli
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1045	156	4.0	237	3	US-09-100-264-12	Sequence 12, Appli	1118	153.5	3.9	185	4	US-09-242-999-5	Sequence 5, Appli
1046	156	4.0	237	4	US-08-843-076D-1	Sequence 1, Appli	1119	153.5	3.9	190	2	US-08-845-998-6	Sequence 6, Appli
1047	156	4.0	237	4	US-08-843-076D-8	Sequence 8, Appli	1120	153.5	3.9	190	3	US-09-206-537-6	Sequence 6, Appli
1048	156	4.0	238	3	US-08-768-859A-8	Sequence 8, Appli	1121	153.5	3.9	190	3	US-09-430-854-6	Sequence 6, Appli
1049	156	4.0	238	3	US-08-767-820A-8	Sequence 8, Appli	1122	153.5	3.9	352	4	US-09-902-540-9796	Sequence 9796, Ap

1123	153.5	3.9	610	1	US-08-365-470-3	Sequence 3, Appli	1196	148.5	3.8	111	4	US-09-341-461-30	Sequence 30, Appl
1124	153.5	3.9	610	3	US-09-209-668-19	Sequence 19, Appl	1197	148	3.8	113	4	US-09-438-046-23	Sequence 23, Appl
1125	153.5	3.9	610	3	US-09-009-490A-89	Sequence 89, Appl	1198	148	3.8	218	3	US-09-578-303-3	Sequence 3, Appli
1126	153.5	3.9	610	4	US-09-949-016-5942	Sequence 5942, Ap	1199	148	3.8	242	3	US-09-032-215-47	Sequence 47, Appl
1127	153.5	3.9	1725	4	US-09-562-702A-20	Sequence 20, Appl	1200	148	3.8	657	4	US-09-949-016-11365	Sequence 11365, A
1128	153.5	3.9	1725	4	US-09-561-818A-20	Sequence 20, Appl	1201	148	3.8	657	4	US-09-949-016-11366	Sequence 11366, A
1129	153.5	3.9	1786	4	US-09-562-702A-18	Sequence 18, Appl	1202	148	3.8	657	4	US-09-949-016-11367	Sequence 11367, A
1130	153.5	3.9	1786	4	US-09-561-818A-18	Sequence 18, Appl	1203	148	3.8	657	4	US-09-949-016-11368	Sequence 11368, A
1131	153	3.9	158	3	US-09-374-135-2	Sequence 2, Appli	1204	148	3.8	1480	3	US-09-191-647-7	Sequence 7, Appli
1132	153	3.9	248	3	US-08-906-769-111	Sequence 111, App	1205	148	3.8	1480	3	US-09-540-245A-7	Sequence 7, Appli
1133	153	3.9	248	3	US-08-906-616-111	Sequence 111, App	1206	148	3.8	1480	3	US-09-540-153-7	Sequence 7, Appli
1134	153	3.9	248	3	US-08-817-795-111	Sequence 111, App	1207	148	3.8	1480	3	PCT-US91-09055-2	Sequence 2, Appli
1135	153	3.9	248	3	US-08-639-075A-111	Sequence 111, App	1208	147.5	3.7	197	1	US-08-456-840-48	Sequence 48, Appl
1136	153	3.9	248	3	US-09-012-431-111	Sequence 111, App	1209	147.5	3.7	197	1	US-08-266-407A-48	Sequence 48, Appl
1137	153	3.9	248	3	US-09-012-692-111	Sequence 111, App	1210	147.5	3.7	197	2	US-08-892-544-48	Sequence 48, Appl
1138	153	3.9	248	3	US-08-906-613-111	Sequence 111, App	1211	147.5	3.7	246	3	US-08-906-769-127	Sequence 127, App
1139	153	3.9	248	5	PCT-US95-14442A-111	Sequence 111, App	1212	147.5	3.7	246	3	US-08-906-616-127	Sequence 127, App
1140	153	3.9	254	3	US-09-578-303-5	Sequence 5, Appli	1213	147.5	3.7	246	3	US-08-639-075A-127	Sequence 127, App
1141	153	3.9	286	4	US-09-270-767-45162	Sequence 45162, A	1214	147.5	3.7	246	3	US-09-012-431-127	Sequence 127, App
1142	152.5	3.9	267	4	US-09-949-016-10711	Sequence 10711, A	1215	147.5	3.7	246	3	US-09-012-692-127	Sequence 127, App
1143	152.5	3.9	642	3	US-08-872-855-10	Sequence 10, Appl	1216	147.5	3.7	246	3	US-08-906-613-127	Sequence 127, App
1144	152	3.9	247	2	US-08-851-974-4	Sequence 4, Appli	1217	147.5	3.7	574	6	5378464-3	Patent No. 5378464
1145	152	3.9	247	2	US-09-213-390-4	Sequence 4, Appli	1218	147.5	3.7	574	6	5378464-3	Patent No. 5378464
1146	152	3.9	247	4	US-09-949-016-6457	Sequence 6457, Ap	1219	147.5	3.7	1765	4	US-09-562-702A-16	Sequence 16, Appl
1147	152	3.9	237	1	US-08-096-946-10	Sequence 10661, A	1220	147.5	3.7	1765	4	US-09-561-818A-16	Sequence 16, Appl
1148	152	3.9	1033	4	US-09-834-309-1	Sequence 1, Appli	1221	147.5	3.7	1786	4	US-09-562-702A-14	Sequence 14, Appl
1149	151.5	3.8	259	4	US-09-949-016-10954	Sequence 10954, A	1222	147.5	3.7	1786	4	US-09-561-818A-14	Sequence 14, Appl
1150	151.5	3.8	716	2	US-08-766-982-1	Sequence 1, Appli	1223	147.5	3.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
1151	151.5	3.8	716	3	US-09-296-219-1	Sequence 1, Appli	1224	147.5	3.7	1786	4	US-09-538-092-869	Sequence 869, App
1152	151	3.8	110	4	US-09-341-461-27	Sequence 27, Appl	1225	147.5	3.7	4391	4	US-10-006-011A-2	Sequence 2, Appli
1153	151	3.8	237	1	US-08-096-946-10	Sequence 10, Appl	1226	147	3.7	239	3	US-09-004-731-44	Sequence 44, Appl
1154	151	3.8	237	5	PCT-US94-0732B-10	Sequence 10, Appl	1227	147	3.7	239	3	US-08-749-699-44	Sequence 44, Appl
1155	151	3.8	237	5	PCT-US95-06157-16	Sequence 16, Appl	1228	147	3.7	239	3	US-09-004-729-44	Sequence 44, Appl
1156	150.5	3.8	277	1	US-08-024-868-2	Sequence 2, Appli	1229	147	3.7	242	3	US-09-004-731-41	Sequence 41, Appl
1157	150.5	3.8	277	2	US-08-242-097-2	Sequence 2, Appli	1230	147	3.7	242	3	US-08-749-699-41	Sequence 41, Appl
1158	150.5	3.8	277	3	US-09-206-695-2	Sequence 2, Appli	1231	147	3.7	242	3	US-09-004-729-41	Sequence 41, Appl
1159	150.5	3.8	277	3	US-09-000-179-1	Sequence 1, Appli	1232	147	3.7	476	4	US-09-949-016-11726	Sequence 11726, A
1160	150.5	3.8	277	5	PCT-US96-11995-1	Sequence 2, Appli	1233	146.5	3.7	223	1	US-08-278-091-13	Sequence 13, Appl
1161	150.5	3.8	277	5	PCT-US96-11995-1	Sequence 2, Appli	1234	146.5	3.7	223	1	US-08-483-859-13	Sequence 13, Appl
1162	150.5	3.8	500	4	US-09-423-753-2	Sequence 2, Appli	1235	146.5	3.7	223	2	US-08-472-173-13	Sequence 13, Appl
1163	150.5	3.8	659	4	US-09-423-753-3	Sequence 3, Appli	1236	146.5	3.7	223	2	US-08-487-167-13	Sequence 13, Appl
1164	150.5	3.8	685	3	US-08-872-855-2	Sequence 2, Appli	1237	146.5	3.7	223	2	US-08-482-816-13	Sequence 13, Appl
1165	150.5	3.8	685	4	US-09-423-753-25	Sequence 25, Appl	1238	146.5	3.7	223	2	US-08-296-149-13	Sequence 13, Appl
1166	150.5	3.8	685	4	US-09-641-612-7	Sequence 7, Appli	1239	146.5	3.7	223	2	US-08-801-499-13	Sequence 13, Appl
1167	150.5	3.8	1064	1	US-08-537-210A-3	Sequence 3, Appli	1240	146.5	3.7	223	2	US-08-615-271-13	Sequence 13, Appl
1168	150.5	3.8	1064	3	US-09-113-825-3	Sequence 3, Appli	1241	146.5	3.7	223	3	US-09-074-660-13	Sequence 13, Appl
1169	150	3.8	113	3	US-09-438-046-22	Sequence 22, Appl	1242	146.5	3.7	223	3	US-09-074-659-13	Sequence 13, Appl
1170	150	3.8	238	3	US-08-344-483-31	Sequence 31, Appl	1243	146.5	3.7	223	3	US-09-106-468-13	Sequence 13, Appl
1171	150	3.8	238	6	5180819-4	Patent No. 5180819	1244	146.5	3.7	223	3	US-09-106-466A-13	Sequence 13, Appl
1172	150	3.8	238	6	5180819-4	Patent No. 5180819	1245	146.5	3.7	223	3	US-09-106-467-13	Sequence 13, Appl
1173	150	3.8	263	4	US-09-653-813-2	Sequence 2, Appli	1246	146	3.7	143	4	US-10-067-422-32	Sequence 32, Appl
1174	150	3.8	267	2	US-08-378-404B-46	Sequence 46, Appl	1247	146	3.7	157	3	US-09-518-046-23	Sequence 23, Appl
1175	150	3.8	276	1	US-08-467-155A-1	Sequence 1, Appli	1248	146	3.7	263	4	US-09-653-813-4	Sequence 4, Appli
1176	150	3.8	276	2	US-08-628-198-1	Sequence 1, Appli	1249	146	3.7	263	4	US-09-653-813-6	Sequence 6, Appli
1177	150	3.8	276	3	US-09-201-038-1	Sequence 1, Appli	1250	145.5	3.7	108	4	US-09-341-461-22	Sequence 22, Appl
1178	150	3.8	276	5	PCT-US96-07343-1	Sequence 1, Appli	1251	145.5	3.7	252	3	US-08-906-769-103	Sequence 103, App
1179	150	3.8	677	4	US-09-949-016-11369	Sequence 11369, A	1252	145.5	3.7	252	3	US-08-906-616-103	Sequence 103, App
1180	150	3.8	677	4	US-09-949-016-11370	Sequence 11370, A	1253	145.5	3.7	252	3	US-08-817-795-103	Sequence 103, App
1181	150	3.8	677	4	US-09-949-016-11371	Sequence 11371, A	1254	145.5	3.7	252	3	US-08-639-075A-103	Sequence 103, App
1182	150	3.8	677	4	US-09-949-016-11372	Sequence 11372, A	1255	145.5	3.7	252	3	US-09-012-431-103	Sequence 103, App
1183	149.5	3.8	46	4	US-10-067-422-17	Sequence 17, Appl	1256	145.5	3.7	252	3	US-09-012-692-103	Sequence 103, App
1184	149.5	3.8	385	1	US-08-340-539A-2	Sequence 2, Appli	1257	145.5	3.7	252	3	US-08-906-613-103	Sequence 103, App
1185	149.5	3.8	385	2	US-08-461-592B-2	Sequence 2, Appli	1258	145.5	3.7	252	5	PCT-US95-14442A-103	Sequence 103, App
1186	149.5	3.8	1925	4	US-09-949-016-10403	Sequence 10403, A	1259	145	3.7	110	4	US-09-341-461-21	Sequence 21, Appl
1187	149	3.8	263	1	US-07-306-983-2	Sequence 2, Appli	1260	145	3.7	232	3	US-08-906-769-81	Sequence 81, Appl
1188	149	3.8	575	4	US-09-949-016-11264	Sequence 11264, A	1261	145	3.7	232	3	US-08-906-616-81	Sequence 81, Appl
1189	149	3.8	575	4	US-09-949-016-11265	Sequence 11265, A	1262	145	3.7	232	3	US-08-817-795-81	Sequence 81, Appl
1190	149	3.8	575	4	US-09-949-016-11266	Sequence 11266, A	1263	145	3.7	232	3	US-08-639-075A-81	Sequence 81, Appl
1191	149	3.8	575	4	US-09-949-016-11267	Sequence 11267, A	1264	145	3.7	232	3	US-09-012-431-81	Sequence 81, Appl
1192	149	3.8	806	4	US-09-949-016-7248	Sequence 7248, Ap	1265	145	3.7	232	3	US-09-012-692-81	Sequence 81, Appl
1193	149	3.8	1404	2	US-08-400-159-2	Sequence 2, Appli	1266	145	3.7	232	3	US-08-906-613-81	Sequence 81, Appl
1194	149	3.8	1404	3	US-08-611-729A-2	Sequence 2, Appli	1267	145	3.7	232	5	PCT-US95-14442A-81	Sequence 81, Appl
1195	149	3.8	1404	4	US-09-195-524-2	Sequence 2, Appli	1268	145	3.7	372	2	US-08-513-278-4	Sequence 4, Appli



1269	145	3.7	372	6	5514582-4	Patent No. 5514582	1342	136.5	3.5	224	1	US-08-483-859-12	Sequence 12, Appl
1270	145	3.7	272	6	5514582-4	Patent No. 5514582	1343	136.5	3.5	224	1	US-08-472-173-12	Sequence 12, Appl
1271	144.5	3.7	258	3	US-09-004-731-16	Sequence 16, Appl	1344	136.5	3.5	224	2	US-08-487-167-12	Sequence 12, Appl
1272	144.5	3.7	258	3	US-09-004-731-19	Sequence 19, Appl	1345	136.5	3.5	224	2	US-08-482-816-12	Sequence 12, Appl
1273	144.5	3.7	258	3	US-08-749-699-16	Sequence 16, Appl	1346	136.5	3.5	224	2	US-08-296-149-12	Sequence 12, Appl
1274	144.5	3.7	258	3	US-08-749-699-19	Sequence 19, Appl	1347	136.5	3.5	224	2	US-08-801-499-12	Sequence 12, Appl
1275	144.5	3.7	258	4	US-09-004-729-16	Sequence 16, Appl	1348	136.5	3.5	224	2	US-08-615-271-12	Sequence 12, Appl
1276	144.5	3.7	258	4	US-09-004-729-19	Sequence 19, Appl	1349	136.5	3.5	224	2	US-09-074-660-12	Sequence 12, Appl
1277	144	3.7	163	4	US-09-270-767-60652	Sequence 60652, A	1350	136.5	3.5	224	3	US-09-074-659-12	Sequence 12, Appl
1278	143	3.6	237	3	US-09-004-731-22	Sequence 22, Appl	1351	136.5	3.5	224	3	US-09-106-468-12	Sequence 12, Appl
1279	143	3.6	237	3	US-08-749-699-22	Sequence 22, Appl	1352	136.5	3.5	224	3	US-09-106-468A-12	Sequence 12, Appl
1280	143	3.6	237	4	US-09-004-729-22	Sequence 22, Appl	1353	136.5	3.5	224	3	US-09-106-467-12	Sequence 12, Appl
1281	143	3.6	549	3	US-09-245-041-9	Sequence 9, Appl	1354	136.5	3.5	226	1	US-07-929-198-4	Sequence 4, Appl
1282	143	3.6	549	4	US-09-358-055B-9	Sequence 9, Appl	1355	136.5	3.5	247	2	US-08-978-404B-47	Sequence 47, Appl
1283	143	3.6	549	4	US-09-893-238-9	Sequence 9, Appl	1356	136	3.4	326	2	US-08-640-977-1	Sequence 1, Appl
1284	143	3.6	1260	3	US-09-245-041-2	Sequence 2, Appl	1357	136	3.4	345	4	US-09-976-594-458	Sequence 458, App
1285	143	3.6	1260	4	US-09-358-055B-2	Sequence 2, Appl	1358	135.5	3.4	256	3	US-08-906-763-89	Sequence 89, Appl
1286	143	3.6	1260	4	US-09-893-238-2	Sequence 2, Appl	1359	135.5	3.4	256	3	US-08-906-616-89	Sequence 89, Appl
1287	143	3.6	3075	2	US-08-460-309-5	Sequence 5, Appl	1360	135.5	3.4	256	3	US-08-817-795-89	Sequence 89, Appl
1288	143	3.6	3075	2	US-08-125-077-5	Sequence 5, Appl	1361	135.5	3.4	256	3	US-08-639-075A-89	Sequence 89, Appl
1289	142.5	3.6	226	1	US-07-929-198-6	Sequence 6, Appl	1362	135.5	3.4	256	3	US-09-012-431-89	Sequence 89, Appl
1290	142	3.6	240	3	US-08-824-692-23	Sequence 23, Appl	1363	135.5	3.4	256	3	US-09-012-692-89	Sequence 89, Appl
1291	142	3.6	577	2	US-08-435-149-3	Sequence 3, Appl	1364	135.5	3.4	256	3	US-08-906-613-89	Sequence 89, Appl
1292	142	3.6	611	3	US-09-475-460A-32	Sequence 32, Appl	1365	135.5	3.4	313	5	PCT-US95-1442A-89	Sequence 89, Appl
1293	142	3.6	611	4	US-09-748-061A-32	Sequence 32, Appl	1366	135.5	3.4	372	4	US-09-270-767-44375	Sequence 44375, A
1294	142	3.6	1068	1	US-08-537-210A-2	Sequence 2, Appl	1367	135.5	3.4	372	6	US-08-513-278-2	Sequence 2, Appl
1295	142	3.6	1068	3	US-09-113-825-2	Sequence 2, Appl	1368	135.5	3.4	372	6	5514582-2	Patent No. 5514582
1296	142	3.6	1480	3	US-09-182-024A-5	Sequence 5, Appl	1369	135.5	3.4	372	6	5514582-2	Patent No. 5514582
1297	141	3.5	226	3	US-08-944-483-41	Sequence 41, Appl	1370	135	3.4	233	2	US-08-738-413B-9	Sequence 9, Appl
1298	140	3.5	148	4	US-09-618-259-2	Sequence 2, Appl	1371	135	3.4	735	3	US-09-191-647-9	Sequence 9, Appl
1299	140	3.5	154	3	US-09-261-416-7	Sequence 7, Appl	1372	135	3.4	735	3	US-09-540-153-9	Sequence 9, Appl
1300	140	3.5	578	3	US-08-981-392-13	Sequence 13, Appl	1373	135	3.4	735	3	US-09-540-153-9	Sequence 9, Appl
1301	140	3.5	578	4	US-09-908-392-13	Sequence 13, Appl	1374	134.5	3.4	113	4	US-09-341-461-24	Sequence 24, Appl
1302	140	3.5	597	4	US-09-747-371-3	Sequence 3, Appl	1375	134.5	3.4	223	1	US-07-956-848A-41	Sequence 41, Appl
1303	139.5	3.5	207	4	US-09-244-111-4	Sequence 4, Appl	1376	134.5	3.4	223	1	US-08-471-956-41	Sequence 41, Appl
1304	139.5	3.5	214	4	US-09-380-682-57	Sequence 57, Appl	1377	134.5	3.4	304	3	US-09-088-651-2	Sequence 2, Appl
1305	139.5	3.5	256	3	US-09-012-215-32	Sequence 32, Appl	1378	134.5	3.4	1525	3	US-09-191-647-2	Sequence 2, Appl
1306	139	3.5	267	3	US-08-906-769-145	Sequence 145, App	1379	134.5	3.4	1525	3	US-09-540-153-2	Sequence 2, Appl
1307	139	3.5	267	3	US-08-906-616-145	Sequence 145, App	1380	134.5	3.4	1525	3	US-09-540-153-2	Sequence 2, Appl
1308	139	3.5	267	3	US-08-639-075A-145	Sequence 145, App	1381	134	3.4	286	2	US-08-640-977-4	Sequence 4, Appl
1309	139	3.5	267	3	US-09-004-731-67	Sequence 67, Appl	1382	134	3.4	1656	4	US-09-949-016-7247	Sequence 7247, App
1310	139	3.5	267	3	US-09-012-431-145	Sequence 145, App	1383	134	3.4	1821	4	US-09-949-016-5938	Sequence 5938, App
1311	139	3.5	267	3	US-08-749-699-67	Sequence 67, Appl	1384	133.5	3.4	290	3	US-08-824-692-29	Sequence 29, Appl
1312	139	3.5	267	3	US-09-012-692-145	Sequence 145, App	1385	133	3.4	240	3	US-08-640-977-2	Sequence 2, Appl
1313	139	3.5	267	3	US-08-906-613-145	Sequence 145, App	1386	132	3.3	110	4	US-09-341-461-26	Sequence 26, Appl
1314	139	3.5	267	4	US-09-004-729-67	Sequence 67, Appl	1387	132	3.3	112	4	US-09-341-461-34	Sequence 34, Appl
1315	139	3.5	495	4	US-10-006-011A-4	Sequence 4, Appl	1388	132	3.3	119	4	US-09-438-046-24	Sequence 24, Appl
1316	139	3.5	705	4	US-10-006-011A-3	Sequence 3, Appl	1389	132	3.3	159	3	US-09-020-956-172	Sequence 172, App
1317	139	3.5	1139	1	US-08-537-210A-4	Sequence 4, Appl	1390	132	3.3	159	3	US-09-030-607-172	Sequence 172, App
1318	139	3.5	1139	3	US-09-113-825-4	Sequence 4, Appl	1391	132	3.3	159	3	US-09-439-313-172	Sequence 172, App
1319	138.5	3.5	158	3	US-09-518-046-22	Sequence 22, Appl	1392	132	3.3	159	4	US-09-352-616A-172	Sequence 172, App
1320	138.5	3.5	226	1	US-07-929-198-2	Sequence 2, Appl	1393	132	3.3	159	4	US-09-232-149A-172	Sequence 172, App
1321	138.5	3.5	226	2	US-08-557-146-15	Sequence 15, Appl	1394	132	3.3	159	4	US-09-159-812-172	Sequence 172, App
1322	138.5	3.5	226	2	US-09-154-344-15	Sequence 15, Appl	1395	132	3.3	159	4	US-09-636-215-172	Sequence 172, App
1323	138.5	3.5	226	3	US-08-944-483-43	Sequence 43, Appl	1396	132	3.3	159	4	US-09-685-166A-172	Sequence 172, App
1324	138.5	3.5	226	3	US-08-983-075D-9	Sequence 9, Appl	1397	132	3.3	159	4	US-09-115-453-172	Sequence 172, App
1325	138	3.5	182	4	US-09-328-925-12	Sequence 12, Appl	1398	132	3.3	159	4	US-09-688-489-172	Sequence 172, App
1326	138	3.5	216	3	US-08-824-692-24	Sequence 24, Appl	1399	132	3.3	159	4	US-09-679-426-172	Sequence 172, App
1327	138	3.5	249	3	US-09-578-303-2	Sequence 2, Appl	1400	132	3.3	159	4	US-09-759-143-172	Sequence 172, App
1328	138	3.5	253	3	US-08-906-769-131	Sequence 131, App	1401	132	3.3	159	4	US-09-651-236-172	Sequence 172, App
1329	138	3.5	253	3	US-08-906-616-131	Sequence 131, App	1402	132	3.3	166	4	US-09-636-215-838	Sequence 838, App
1330	138	3.5	253	3	US-08-639-075A-131	Sequence 131, App	1403	132	3.3	166	4	US-09-685-166A-838	Sequence 838, App
1331	138	3.5	253	3	US-09-012-431-131	Sequence 131, App	1404	132	3.3	166	4	US-09-679-426-838	Sequence 838, App
1332	138	3.5	253	3	US-09-012-692-131	Sequence 131, App	1405	132	3.3	166	4	US-09-759-143-838	Sequence 838, App
1333	138	3.5	253	3	US-08-906-613-131	Sequence 131, App	1406	132	3.3	166	4	US-09-651-236-838	Sequence 838, App
1334	138	3.5	291	1	US-08-467-155A-11	Sequence 11, Appl	1407	131.5	3.3	215	4	US-09-612-314A-33	Sequence 33, Appl
1335	138	3.5	291	2	US-08-628-198-11	Sequence 11, Appl	1408	131.5	3.3	810	2	US-08-820-170A-34	Sequence 34, Appl
1336	138	3.5	291	3	US-09-301-038-11	Sequence 11, Appl	1409	131.5	3.3	810	3	US-09-055-699-34	Sequence 34, Appl
1337	138	3.5	291	5	PCT-US96-07343-11	Sequence 11, Appl	1410	131.5	3.3	810	3	US-09-273-565-34	Sequence 34, Appl
1338	138	3.5	345	4	US-10-000-489-106	Sequence 106, App	1411	131.5	3.3	810	3	US-09-565-538-34	Sequence 34, Appl
1339	138	3.5	583	4	US-09-641-612-2	Sequence 2, Appl	1412	131.5	3.3	810	3	US-09-661-468-34	Sequence 34, Appl
1340	136.5	3.5	109	4	US-09-341-461-33	Sequence 33, Appl	1413	131.5	3.3	810	4	US-09-976-165-34	Sequence 34, Appl
1341	136.5	3.5	224	1	US-08-278-091-12	Sequence 12, Appl	1414	131	3.3	219	2	US-08-925-708-2	Sequence 2, Appl

1415	131	3.3	274	2	US-08-177-109A-58	Sequence 58, Appl
1416	131	3.3	274	2	US-08-687-706-58	Sequence 58, Appl
1417	131	3.3	3647	4	US-09-949-016-10932	Sequence 10932, A
1418	130.5	3.3	324	1	US-08-310-416A-14	Sequence 14, Appl
1419	130.5	3.3	324	1	US-08-888-171-14	Sequence 14, Appl
1420	130.5	3.3	376	4	US-09-844-311-2	Sequence 2, Appl
1421	130.5	3.3	1257	1	US-08-340-428B-49	Sequence 49, Appl
1422	130.5	3.3	1572	4	US-09-562-702A-32	Sequence 32, Appl
1423	130.5	3.3	1572	4	US-09-561-818A-28	Sequence 28, Appl
1424	130.5	3.3	1605	4	US-09-562-702A-30	Sequence 30, Appl
1425	130.5	3.3	1605	4	US-09-561-818A-26	Sequence 26, Appl
1426	130	3.3	144	3	US-08-906-769-153	Sequence 153, App
1427	130	3.3	144	3	US-08-906-616-153	Sequence 153, App
1428	130	3.3	144	3	US-08-639-075A-153	Sequence 153, App
1429	130	3.3	144	3	US-09-004-731-81	Sequence 81, Appl
1430	130	3.3	144	3	US-09-012-431-153	Sequence 153, App
1431	130	3.3	144	3	US-08-749-699-81	Sequence 81, Appl
1432	130	3.3	144	3	US-09-012-692-153	Sequence 153, App
1433	130	3.3	144	3	US-08-906-613-153	Sequence 153, App
1434	130	3.3	144	3	US-09-004-729-81	Sequence 81, Appl
1435	130	3.3	490	4	US-09-907-794A-132	Sequence 132, App
1436	130	3.3	490	4	US-09-905-125A-132	Sequence 132, App
1437	130	3.3	490	4	US-09-902-775A-132	Sequence 132, App
1438	130	3.3	490	4	US-09-906-700-132	Sequence 132, App
1439	130	3.3	490	4	US-09-903-603A-132	Sequence 132, App
1440	130	3.3	490	4	US-09-904-920A-132	Sequence 132, App
1441	130	3.3	490	4	US-09-909-064-132	Sequence 132, App
1442	130	3.3	490	4	US-09-905-381A-132	Sequence 132, App
1443	130	3.3	490	4	US-09-906-618-132	Sequence 132, App
1444	129.5	3.3	274	4	US-09-612-314A-47	Sequence 47, Appl
1445	129.5	3.3	323	2	US-08-435-149-2	Sequence 2, Appl
1446	129.5	3.3	381	4	US-09-014-240-2	Sequence 2, Appl
1447	129.5	3.3	381	4	US-09-844-311-4	Sequence 4, Appl
1448	129.5	3.3	440	4	US-09-014-240-4	Sequence 4, Appl
1449	129.5	3.3	652	2	US-08-751-305-2	Sequence 2, Appl
1450	129.5	3.3	716	4	US-09-312-283C-183	Sequence 183, App
1451	129.5	3.3	771	3	US-09-188-930-183	Sequence 183, App
1452	128.5	3.3	235	2	US-08-557-146-14	Sequence 14, Appl
1453	128.5	3.3	235	2	US-09-154-344-14	Sequence 14, Appl
1454	128.5	3.3	235	3	US-08-944-483-42	Sequence 42, Appl
1455	128.5	3.3	255	1	US-08-208-007A-14	Sequence 14, Appl
1456	128.5	3.3	255	3	US-08-315-095A-14	Sequence 14, Appl
1457	128.5	3.3	255	3	US-08-798-096-14	Sequence 14, Appl
1458	128.5	3.3	255	4	US-08-798-095A-14	Sequence 14, Appl
1459	128.5	3.3	255	4	US-09-953-956-14	Sequence 14, Appl
1460	128.5	3.3	255	4	US-08-553-125A-14	Sequence 14, Appl
1461	128.5	3.3	255	4	US-10-114-464-14	Sequence 14, Appl
1462	128.5	3.3	257	4	US-09-349-016-10662	Sequence 10662, A
1463	128	3.2	222	4	US-09-270-767-62005	Sequence 62005, A
1464	128	3.2	236	1	US-08-684-862-4	Sequence 4, Appl
1465	128	3.2	477	4	US-09-380-682-59	Sequence 59, Appl
1466	128	3.2	585	4	US-09-641-612-5	Sequence 5, Appl
1467	127	3.2	105	4	US-09-270-767-32654	Sequence 32654, A
1468	127	3.2	197	4	US-09-380-682-1	Sequence 1, Appl
1469	127	3.2	197	4	US-09-380-682-9	Sequence 9, Appl
1470	127	3.2	197	4	US-09-380-682-15	Sequence 15, Appl
1471	127	3.2	198	4	US-09-380-682-31	Sequence 31, Appl
1472	127	3.2	211	4	US-09-380-682-54	Sequence 54, Appl
1473	127	3.2	215	4	US-09-380-682-34	Sequence 34, Appl
1474	127	3.2	234	1	US-08-684-862-6	Sequence 6, Appl
1475	127	3.2	260	3	US-08-906-769-139	Sequence 139, App
1476	127	3.2	260	3	US-08-906-616-139	Sequence 139, App
1477	127	3.2	260	3	US-08-639-075A-139	Sequence 139, App
1478	127	3.2	260	3	US-09-012-431-139	Sequence 139, App
1479	127	3.2	260	3	US-09-012-692-139	Sequence 139, App
1480	127	3.2	260	3	US-08-906-613-139	Sequence 139, App
1481	127	3.2	1576	4	US-09-562-702A-24	Sequence 24, Appl
1482	127	3.2	1576	4	US-09-561-818A-24	Sequence 24, Appl
1483	127	3.2	1584	4	US-09-562-702A-28	Sequence 28, Appl
1484	127	3.2	1609	4	US-09-562-702A-22	Sequence 22, Appl
1485	127	3.2	1609	4	US-09-561-818A-22	Sequence 22, Appl
1486	127	3.2	1609	4	US-09-538-092-900	Sequence 900, App
1487	127	3.2	1617	4	US-09-562-702A-26	Sequence 26, Appl

1488	127	3.2	2123	4	US-09-949-016-7517	Sequence 7517, Ap
1489	127	3.2	3070	4	US-09-961-403-7	Sequence 7, Appl
1490	127	3.2	3084	4	US-09-562-702A-12	Sequence 12, Appl
1491	127	3.2	3088	4	US-09-562-702A-8	Sequence 8, Appl
1492	127	3.2	3089	4	US-09-562-702A-4	Sequence 4, Appl
1493	127	3.2	3106	4	US-09-562-702A-10	Sequence 10, Appl
1494	127	3.2	3110	4	US-09-562-702A-2	Sequence 2, Appl
1495	127	3.2	3110	4	US-09-562-702A-6	Sequence 6, Appl
1496	127	3.2	3110	4	US-09-561-709B-7	Sequence 7, Appl
1497	127	3.2	3110	4	US-09-917-254-86	Sequence 86, Appl
1498	127	3.2	3110	4	US-09-949-016-5937	Sequence 5937, Ap
1499	127	3.2	3111	2	US-08-460-309-4	Sequence 4, Appl
1500	127	3.2	3111	2	US-08-125-077-4	Sequence 4, Appl
ALIGNMENTS						
RESULT 1						
US-10-067-422-9						
; Sequence 9, Application US/10067422						
; Patent No. 6743613						
; GENERAL INFORMATION:						
; APPLICANT: NI et al.						
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, an						
; FILE REFERENCE: PT004P1						
; CURRENT APPLICATION NUMBER: US/10/067,422						
; CURRENT FILING DATE: 2002-02-07						
; PRIOR APPLICATION NUMBER: 09/685,899						
; PRIOR FILING DATE: 2000-10-11						
; PRIOR APPLICATION NUMBER: PCT/US00/09028						
; PRIOR FILING DATE: 2000-04-06						
; PRIOR APPLICATION NUMBER: 60/152,933						
; PRIOR FILING DATE: 1999-09-09						
; PRIOR APPLICATION NUMBER: 60/147,020						
; PRIOR FILING DATE: 1999-08-03						
; PRIOR APPLICATION NUMBER: 60/131,672						
; PRIOR FILING DATE: 1999-04-29						
; PRIOR APPLICATION NUMBER: 60/130,693						
; PRIOR FILING DATE: 1999-04-23						
; NUMBER OF SEQ ID NOS: 32						
; SOFTWARE: Patent in Ver. 2.0						
; SEQ ID NO 9						
; LENGTH: 570						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-10-067-422-9						
Query Match 74.7%; Score 2946.5; DB 4; Length 570;						
Best Local Similarity 96.8%; Pred. No. 9.5e-237;						
Matches 552; Conservative 0; Mismatches 1; Indels 17; Gaps 1;						
Qy	168	MLSLFDMYQDYVEVRDGNRDQIIKRVCGNERPAPIQISGSLHLVLFHSDGSKNFD	227			
Db	1	MLSLFDMYQDYVEVRDGNRDQIIKRVCGNERPAPIQISGSLHLVLFHSDGSKNFD	60			
Qy	228	GPHAIYEETACSSPCFHDGTCVLDKAGSYKACACLAGYTGRCENL-----	274			
Db	61	GPHAIYEETACSSPCFHDGTCVLDKAGSYKACACLAGYTGRCENLLEAGSKIKASED	120			
Qy	275	----LEERNCSDPGPGVNGYQKITGGPGLNGRHAKIGTVGVSFFCNNSYVLSGNEKRTQ	330			
Db	121	SLSVLEERNCSDPGPGVNGYQKITGGPGLNGRHAKIGTVGVSFFCNNSYVLSGNEKRTQ	180			
Qy	331	QNGWSGKQPICIKACREPKISDLVRRVRLPMQVQSRETPHLQLYSAASQKQLQAPTK	390			
Db	181	QNGWSGKQPICIKACREPKISDLVRRVRLPMQVQSRETPHLQLYSAASQKQLQAPTK	240			
Qy	391	KPALPFGDLPWGMQVHQLTQYECISPFYRRLLGSSRRRTCLRTGKWSGRAPSCIPICGKIE	450			
Db	241	KPALPFGDLPWGMQVHQLTQYECISPFYRRLLGSSRRRTCLRTGKWSGRAPSCIPICGKIE	300			



Qy	451	NITAPKTOGLRWPQAAIYRRTSGVHDGSLGHKGAWFLVCSGALVNERTVVVAACHCVTDILG	510
Db	301	NITAPKTOGLRWPQAAIYRRTSGVHDGSLGHKGAWFLVCSGALVNERTVVVAACHCVTDILG	360
Qy	511	KVTMIKTADLKVVILGKFYRDDDRDEKTTQSLQISAIILHPNYDPTILLDADIAILKLLDKA	570
Db	361	KVTMIKTADLKVVILGKFYRDDDRDEKTTQSLQISAIILHPNYDPTILLDADIAILKLLDKA	420
Qy	571	RISTRVOPICLAASRDLSSTFQESHITVAGWNVLADVRSPGPKNDTLRSGVVVVDLSLIC	630
Db	421	RISTRVOPICLAASRDLSSTFQESHITVAGWNVLADVRSPGPKNDTLRSGVVVVDLSLR	480
Qy	631	EEQEHEDHGIPVSVTDNNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVS	690
Db	481	EEQEHEDHGIPVSVTDNNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVS	540
Qy	691	WSYDKTCSHRLSTAFTKVLPFKDWTIERNNK	720
Db	541	WSYDKTCSHRLSTAFTKVLPFKDWTIERNNK	570

## RESULT 2

```

US-08-296-014A-4
; Sequence 4, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-014A-4

Query Match      16.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred.No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37

Qy      34   PGAENWIMCRCEYDQLTECVCGKRE-----VVGTIPCCRNEECDSCLIH 82
          :|:|:|
Db      194  PNGOWSNFPFKCIR---ECAMVSPHEGKVNALSGDMTIGATL-----RFSCDS---- 229
          :|:|:|
Ov      93   PGCTIFENCCKSCR-NGSWGCTL-----

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ZIP: 22042  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/596,405  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1781-105P  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1019 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-596-405-4

Query Match 16.9%; Score 665; DB 2; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 1.7e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAENIMRCCEVDQIECVCPGKRE-----VGVYIPCCRNENECDCLIH 82  
DB 184 PNGQSNFPKICR-----ECAMVSPFEGKVNALSGDMIEGATL-----RFSCHS----- 229  
QY 83 PCTIFENCKSCR-NGSWGTL----- 103  
DB 230 PYLLIGQETLTCGNGQWNGQIPQCKNLVFCPLDLPVNHAEHKVIGVEKYGQFPFGTE 289  
QY 104 -----DDFYVKGFGCAEACR--AGWYGG--DCWR-----CGQVLR-- 133  
DB 290 VYTCGNYFLMGFTLCKNPDGWSGQSCVKVADREVDCDSKAVDFLDDVGSPVRIH 349  
QY 134 APKGQILLES-----YPLNAHCETIHA-----KPGFVI----- 162  
DB 350 CPAGCSLTAGTGWGTATVHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDPLGSLNGI 409  
QY 163 ---QLRFVWLSLEEDYM-----CQDYVEVRD-----GDNRDQIIRKVCN--E 202  
DB 410 KSEELKSLARSPFYVRSSTAGKSGCPDGWFEVDENCYVYTSKORAMERAGQVCTNMAA 469  
QY 203 RPAPIQS--IGSSLHVLPHSDG-SKNFDGFH-----AIYBEITACSS 241  
DB 470 RLAVLDKQVIPNSLTETLKGKLTWTWGLHLRLDAEKFIFELMDRSNVVNDNLTFWAS 529  
QY 242 SPCPHDGTCL-----DKAGS--YKACLAGYTCQRCENLLEERN---CSDPGGPVNGYQKI 293  
DB 530 GEPGNETNCVYMDIQDLQSVKTKSCFQPSFACWMLSDRNKAKCDDPGSLENGHATL 589  
QY 294 TCGPGLINGRHAKIGTIVSFFCNSVYLSGNKPKCQNGEWSGKQPICIK--ACREPKI 351  
DB 590 HQQS--IDGFYA--GSSIRYSCEVLHLYSGTETVCTTGTWSPAPKRCIKVITCNPPV 645  
QY 352 SDLVRRRLVPMQVQSRRETPHLYSAAPSKQKQ-----SAPTKKPAKLPFGD----- 398  
DB 646 PSYGVEIKP---PRTNISIRVGPFPLPLPLPLPLPLPLPLPLPLPLPLPLPLPLPL 702  
QY 399 --LPMGYQHLHTQLOYECISPPYRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455  
DB 703 VKLPEGHYRVGSRAIYTCESRYELLGSGRRCDSDNGNWSGRPASCIPVCGRSDSPSPF 762  
QY 456 -----KTQGLRWPQAAIYRRTSGVHDGSLHKGAMFLVCSGALVNERTVVAHCVTDIG 510  
DB 763 IWNNGNSTGQWPQWQAGISRWLA-----DHNMMFLOCGGSLLEKRWITVAHCVTYS 815

QY 511 KVTMIKTADLVKVLGKYRDDRRDEKTIQSLQISAIILHPNYDPILLDDADIALKLDKA 570  
DB 816 TAEIIDPNQFKMYLGGYRDDSRDDYVQVREALRIHVNPNTDPGNLFDIALIQLKTPV 875  
QY 571 RISTRVQPICLAASRDLSFQESH-----TVAGNVVLADVRSPGPKNDTLRSQVSV 624  
DB 876 TLTRVQPICLPT--DITT---REHLKEGTLAVVWTG---LNENNTYSETIQQAVLPV 926  
QY 625 VDSLLCEEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGIAAIVSPFGRASPEPRWH 684  
DB 927 VAASTCEEGYKADLPLVTENNFCAGYK-KGRYDACSDSG--PLVFADDSRTERRWV 983  
QY 685 LMGLVSWSYDKTCSH-RLSTAFKVLPPFKDWIER 717  
DB 984 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017

## RESULT 4

US-08-877-620-4  
Sequence 4, Application US/08877620  
Patent No. 5985590  
GENERAL INFORMATION:  
APPLICANT: Ding, Jeak Ling  
APPLICANT: HO, Bow  
TITLE OF INVENTION: The Cloned Factor C cDNA of the  
TITLE OF INVENTION: Singapore Horshoe Crab, Carinoscorpius  
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Birch, Stewart, Kolasch & Birch  
STREET: 8110 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22042

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/877,620  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/596,405  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1781-105P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1019 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-877-620-4

Query Match 16.9%; Score 665; DB 2; Length 1019;

Best Local Similarity 25.4%; Pred. No. 1.7e-46;

Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAENIMRCCEVDQIECVCPGKRE-----VGVYIPCCRNENECDCLIH 82  
DB 184 PNGQSNFPKICR-----ECAMVSPFEGKVNALSGDMIEGATL-----RFSCHS----- 229  
QY 83 PCTIFENCKSCR-NGSWGTL----- 103



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Db      984 LEGIVSWGSPSCGKXANQYGGFTKXNVFLSWIRQ 1017

RESULT 6
US-09-626-795-4
; Sequence 4, Application US/09626795
; Patent No. 6719973
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
; FILE REFERENCE: 4810-61737
; CURRENT APPLICATION NUMBER: US/09/626,795
; CURRENT FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Carcinoscopus rotundicauda
US-09-626-795-4

Query Match          16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY      34 PGEAWNIMRECCEYDQIEVCVPGKRE-----VVGTYIPCCRNEECDSCLIH 82
DB      184 PNGQSNPPPKCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS----- 229
QY      83 PCTIFENCKSCR-NGSWGCTL----- 103
DB      230 PYLLIGQETLTCQGNQWNGQIPQCKNLVFCPLDPVNAHAEKVKIGVEQKYQFPQGTGTE 289
QY      104 -----DDPYVKGFCYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB      290 VTYTCGNYFLMGFTLKNPDGSGSQSPCKVADREVDCDSKAVDFLDDVGPVRIH 349
QY      134 APKGOILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
DB      350 CPAGCSLTAGTGWGTATYHIELSSVCRAAHAGKLPNSGGAHVHVNNGPVSDFLGSDLNGI 409
QY      163 ----QLRFVWLSLEFDYM-----CQDYVEVRD-----GDRDQGIKRVCGN--E 202
DB      410 KSEELKSLARSFRFYVRSSTAGSKGCPDGFWEVDENVYVTSKQRAWERAQGVCTNMAA 469
QY      203 RPAPIQS--IGSSLHVLPHSDG-SKNFDGFH-----AIVEEILTACSS 241
DB      470 RLAVLDKDVIPNSLTETLKGGLTTTWIGLHLRLDAEKPIWELMDRSNVVLDNLTFFWAS 529
QY      242 SPCHFHDGTCVL-----DKAGS-YKCACLAGYTCQRCENLLEERN-----CSDPGGPFVNGYQKI 293
DB      530 GEPGNETCVYNDIQDQLQSVKTKSCFPQSPSFACWMDLSDRNKAKCDDPGSLENGHATL 589
QY      294 TGGPGLNGRHAKIGTVVSFFCNNSVLSGNEKRTCOQNGEWSGKQICIK--ACREPKI 351
DB      590 HQQS--IDGFYA--GSSIRYSEVLHLSGTETVCTTNGTWSAPKPRCIVKVIITCQNPV 645
QY      352 SLDVRRRLPMQVQSRREPLHOLYSAPSKQKLQ--SAPTKKPALPFGD----- 398
DB      646 PSYGVEIKP---PRTSISVSGPFLLRLPLPLPLARAAKPPKPRSSQBSTVDLASK 702
QY      399 --LPMGYOHLHTQLOECISPPYRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
DB      703 VKLPGHYRVGSRAIYTCESRYELLGSGRCDCSNGENWSGRPASCIPVCGRSDSPRPF 762
QY      456 -----KTQGLRWPWQAAIYRRTSGVHDSGLHGAMFLVCSGALVNERTVVAACHCVTDLG 510
DB      763 IWNNGNSTEIGWPWQAGISRWLA-----DHNMFLOCGGSLNLEKWLVTAAHCVTISA 815
QY      511 KVTMIKTADLKVLGKFFRDDDRDEKTIQSLQISAILLHPNYDPIILLADIALKLLDKA 570
DB      816 TABIIIDPNQFMKGLKYRRDDSRDDYVQVREALEIHVNPNDPGLNFDIALIQKTPV 875

QY      571 RISTRVQPICLAASRDLSSTFSQESH-----TVAGWNVLADVRSPGFKNDLTRSGVSV 624
DB      876 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGWMG---LNENNTYSETIQAVLPV 926
QY      625 VDSLLCESQEHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPGRASPEPRWH 684
DB      927 VAASTCEGKYKEADLPLTVTENMFCAGYK-KGRYDACSGDSGG--PLVFADDSRTERRW 983
QY      685 LMGLVSWSYDKTCSH-RLSTAFTKVLPFKDWIER 717
DB      984 LEGIVSWGSPSCGKXANQYGGFTKXNVFLSWIRQ 1017

RESULT 7
US-08-296-014A-2
; Sequence 2, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horsehoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-014A-2

Query Match          16.9%; Score 665; DB 1; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY      34 PGEAWNIMRECCEYDQIEVCVPGKRE-----VVGTYIPCCRNEECDSCLIH 82
DB      248 PNGQSNPPPKCIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS----- 293
QY      83 PCTIFENCKSCR-NGSWGCTL----- 103
DB      294 PYLLIGQETLTCQGNQWNGQIPQCKNLVFCPLDPVNAHAEKVKIGVEQKYQFPQGTGTE 353
QY      104 -----DDPYVKGFCYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB      354 VTYTCGNYFLMGFTLKNPDGSGSQSPCKVADREVDCDSKAVDFLDDVGPVRIH 413
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Qy'	134	APKQIILS-----YPLNAHEWTIHA-----KPGFVI-----	162
Db	414	CPAGCSLTAGTVMGTATYIHELSSVCRAAIHAGKLPNSGGAVHVVNNGPYSDFLGSLNGI	473
Qy	163	---OLRFVWLSLEFDY-----CQDYVEVRD-----GDNRDQIHKVCGN--E	202
Db	474	KSELKSARSFRFDYVSSSTAGKSGCPDGMFEVDENCVVVTSKORAWERAQGVCTNMAA	533
Qy	203	RPAPIQS--IGSSLVHLFHS DG-SKNP DGFH-----AIYEITACSS	241
Db	534	RLAVLDKDVIPNSLTETRLRGKGLTTTWIGLHRLDAEKPFIWELMDRSNVVNLNLTFWAS	593
Qy	242	SPCFHDGTCVL---DKAGS-YKACACLAGYTGORCENLLEERN---CSDPGGVNGYQKI	293
Db	594	GEFGNETCYVMDIQDOLQSVWTKSCFQSSFACWMDLSDRNKA KCDDPGSLENGHATL	653
Qy	294	TGPGFLINGHAKIGTVVSPFCNNYSVLSGNEKRTCOONGEWGSKOPICIK--ACREPKI	351
Db	654	HGQS--IDGFWA--GSSIRYSCEVHLYSGTETVCTTNGTWSAPKPRCIKVITCQNPVP	709
Qy	352	SDLVRRRLVPMQVSRETPLHQLYSAAFSKQKLO--SAPTKPALPFGD-----	398
Db	710	PSYGSVEIKP---PSRTNSISRGVSPFLRLPLPLARAAKPPKPRSQPSTVDLASK	766
Qy	399	--LPMGYOHLHTOLQYECISPFYRRLGSSRRTCIRTGKWSGRAPSCIPICGKIENITAP-	455
Db	767	VKLPEGHYRGSRATYTCESRYVELLGSQGRCDNSGNWSGRPASCIPVCGRSDSPSPF	826
Qy	456	-----KTQGLRWPMQAAIYRRTSGVHDGSLHGAWFLVCSGALVNERTVVVAACHVTDLG	510
Db	827	INWGNSTEIGQVPMQAGISRWLA-----DHNWVFLQCGSLLNKWI VTAACHVTYSA	879
Qy	511	KVTMIKTADILKVLGKPYRDRDRDEKTIQSLQISA IILHNPYDPIILDADIALKLKLDKA	570
Db	880	TAEIIDNPQKVLGKYTRDSDRDDYVQVREALEIHVNPENYFGNLFNFDIALQKTVP	939
Qy	571	RISPRVOPICLAASRDLSSTFSQESH1-----TVAGNVLADVRS PGFKNDTLRSGVVSV	624
Db	940	TLTTRVOPICLPT--DITT---REHLKEGTLAVVTGMG-----LNENYTSETIQQAVLP	990
Qy	625	VDLSLLCEQEHEDHGIPVSYVDNNPFCASWEPTAPSDICTAETGTGGIAA VSPFCRASPEPRWH	684
Db	991	VAASTCEGYKEADPLTVTENMECAGYK-KGRYDACS GDSGG--PLVFADDSTRTERRW	1047
Qy	685	LMGLVWSWSYDKTCSH-RLSTAFTKVLFPFKOWIER	717
Db	1048	LEGTVSGSPGCGKANQOYGFTKVNVFLSWIRO	1081

## RESULT 8

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US-08-596-405-2
? Sequence 2, Application US/08596405
? Patent No. 5858706
? GENERAL INFORMATION:
? APPLICANT: Ding, Jeak Ling
? APPLICANT: Ho, Bow
? TITLE OF INVENTION: The Cloned Factor C cDNA of the
? TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
? TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
? NUMBER OF SEQUENCES: 4
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Birch, Stewart, Kolasch & Birch
? STREET: 8110 Gatehouse Road, Suite 500 East
? CITY: Falls Church
? STATE: Virginia
? COUNTRY: USA
? ZIP: 22042
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:

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Db 940 TLTRVQPICLPT--DITT--REHLKEGTAVVTCWG-----LNENNTYSETIQQAVLPV 990  
QY 625 VDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPFGRASPEPRWH 684  
Db 991 VAASTCEEGYKEADPLTLVTENMFCAGYK-KGRYDACSDDSG--PLVFADDSRTERRVW 1047  
QY 685 LMLVSWSYDKTCSH-RLSTAFKVLPPFKDWIER 717  
Db 1048 LEGIVSWGSPSCGKQANQYGGFTKVNFLSWIRQ 1081

RESULT 9  
US-08-877-620-2  
; Sequence 2, Application US/08877620  
; Patent No. 5985590  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolaach & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/877,620  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/596,405  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1781-105P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1083 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-877-620-2

Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1.8e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PCAEWNIMCRECEYDQIECVCGKRE-----VVGVTIPCCRNEECDSCLIH 82  
Db 248 PNGQNSNPPPKIR-----ECAMVSSPECHKVNAISGDMIEGATL-----RSCDS----- 293  
QY 83 PECTIFENCKSCR-NGSWGGLT----- 103  
Db 294 PYLLIGQETLTCCQNGWNGQIPQCKNLVFCPLDVPVNAHAKVIGVEKTYGQFPQGTG 353  
QY 104 -----DDFYKGYCAECR--AGWYGG--DCWR-----CGQVLR-- 133  
Db 354 VTYTCGNYFLMGFTLCKNCPGNSGSGQSPCKVADREVDCDSKAVDFLDDVGFPVRIH 413

QY 134 APKQIILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162  
Db 414 CPAGCSLTAGTVMGTATYHELSSVCRAAHAGKLPNSGAVHVNPNPYSDFLGSLNGI 473  
QY 163 ---QLRFVWLSLEFDYM-----CQDYVVEVRD-----GDNRDGOIKRVCGN--E 202  
Db 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGWEVDENCYVYTSKQRAWERAQVCCTNMAA 533  
QY 203 RPAPIQS--IGSSLHVLPHSDG-SKNFDGPH-----AIYEETACSS 241  
Db 534 RLAVLDKDVIPNSLTETLRGKGLTTTWIGLHRLDAEKPFIEWELMDRSNVVLDNLTFWAS 593  
QY 242 SPCFHDGTCVL-----DKAGS-YKACLAGYTCQRCENLEERN-----CSPGPGFVNGYQKI 293  
Db 594 GEPGNETNCVYMDIQDLQSVNMTKSCFCQSPSSFACMMDLSRDKAKACDPPGSLNGHATL 653  
QY 294 TGGPGLINGRAHAKIGTVVSVFFCNVSVLGSNGKRTCOQNGEWSGKQPICIK--ACREPKI 351  
Db 654 HQQS--IDGYA--GSSRYSCVHLHLSGTVTCTTNGTWSAPKPRCIKIVTCQNPV 709  
QY 352 SDLVRRRLPMQVQSRRETPHLQLYSAAFSKQLQ---SAPTKKPALPFGD----- 398  
Db 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLPLABAAPPPKPRSSQSPSTVDLASK 766  
QY 399 ---LPMGYOHLHTQLOECISPPYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP-- 455  
Db 767 VKLPEGHYRVGSRATYTCESRYEYELGSGRRCDNSGNMWSGRPASCPVCGRSDSPSPF 826  
QY 456 ----KTQGLRWPQAAIYRRTSGVHDGSLHKGANFLVCSGALVNERTVVVAHCVTDLG 510  
Db 827 IWNGNSTEIGQMPWQAGISWLA-----DHNMFLOCGGSLLEKWIIVTAHCHVTYSA 879  
QY 511 KVTMIKTADLVKLVKRYDDDRDEKTIQSLQISAIILHPNYDPIILLDDIALIKLLDKA 570  
Db 880 TAEIIDPNQFKMYLGYRDDSDDDYVQVREALSHVNPVNDPGLNFDIALIQLKTPV 939  
QY 571 RISTRVQPICLAAASRDLSTSFQESHI-----TVAGNVLAADVRSFGKNDTLRSQVSV 624  
Db 940 TLTRVQPICLPT--DITT--REHLKEGTAVVTCWG-----LNENNTYSETIQQAVLPV 990  
QY 625 VDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPFGRASPEPRWH 684  
Db 991 VAASTCEEGYKEADPLTLVTENMFCAGYK-KGRYDACSDDSG--PLVFADDSRTERRVW 1047  
QY 685 LMLVSWSYDKTCSH-RLSTAFKVLPPFKDWIER 717  
Db 1048 LEGIVSWGSPSCGKQANQYGGFTKVNFLSWIRQ 1081

RESULT 10  
US-09-287-368-2  
; Sequence 2, Application US/09287368A  
; Patent No. 6645724  
; GENERAL INFORMATION:  
; APPLICANT: DING, Jeak Ling  
; APPLICANT: HO, Bow  
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin  
; TITLE OF INVENTION: from a Sample Using Recombinant Factor C  
; FILE REFERENCE: 1781-016SP  
; CURRENT APPLICATION NUMBER: US/09/287,368A  
; CURRENT FILING DATE: 1999-04-07  
; EARLIER APPLICATION NUMBER: 09/201,786  
; EARLIER FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/081,767  
; EARLIER FILING DATE: 1998-05-21  
; EARLIER APPLICATION NUMBER: 60/058,816  
; EARLIER FILING DATE: 1997-09-19  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1083  
; TYPE: PRT  
; ORGANISM: Carinoscorpius rotundicauda





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Db 991 VAASCTCEGKADLPLVTENMFCAGYK-KGRYDACSDDSG--PLVFADDSRTERRW 1047
Qy 685 LMLGVSWSYDKTCSH-RLSTAFTKVLFPKDWIER 717
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 12
US-09-949-016-6138
; Sequence 6138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6138
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6138

Query Match 12.2%; Score 482; DB 4; Length 699;
Best Local Similarity 24.9%; Pred. No. 1.7e-31;
Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

Qy 69 CRNEECDSLIHPGCTIFENCKSCRNCSWGGLDDFVYKGYCAECRAGWY----GGD 124
Db 143 CREREDEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 180
Qy 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWTTHAKPGFVIQLRFVWLSLEFDY-- 176
Db 181 CRVCSNDLFTORTGVITSPDPNYPKSECLYIELEGFWNLQFEDI---PDIQH 237
Qy 177 ----COYDYVEVDGDNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAI 232
Db 238 PEVPCPYDIKIKVGP----KVLGPFCEGKAPEPISTQSHSVLLIFHSDNSAENRGWRL- 292
Qy 233 YEEITACSSSPCFHDGTCVLDKAGSYKACLAGYTCQRCENLEERNCSDDPGPVNGYQK 292
Db 293 -----SYRAA-----GNECPEL-----QP--PVH----- 309
Qy 293 ITGGPGLINGRAHAKIGTVVSFF-----CNNSY-VLSGNEKR-----TCQNGEWSGKQ 339
Db 310 -----GKIEPSQAKY-----FFKQVLSVCDTGYKVLKDNVEMDTFOIELCKDGTWSNKI 359
Qy 340 PIC-IKACREPKISDLVRRRLVPMQVQSRETPHLQLYSAAFSKQKLSAPTCKKPALPFGD 398
Db 360 PTKCIVDCRAP----- 372
Qy 399 LPMGQVHLHT-----OLOYECISPPYRRLGSSR--RTCLRTGKWS-----GRA-PSC 442
Db 373 LEHGLITFTSRNLATYKSEIKYSCQEPYKMLNNNTGIYTCSAQWMMNKVLRSLPTC 432
Qy 443 IPICG-----KIENTAPKTQGLRWPMQAAIYRTSGVHDSGLHKGAWFLVCSGA 492
Db 433 LPVCGLPKPSRKLMAIRFN-GRPAQKGT-PMIAML-----SHLNGQPF--CGGS 478
Qy 493 LVNERTVVAACHV---TDLGKVT-----MIKADLKVVLGKFYRDDDKETIOSLOIS 544
Db 479 LIGSSWIVTAACHLQSLDGPDPFTLRDLSDFSDFKILGKHW--LRSDNEHQHGVK 536
Qy 545 AIIHPNYPDPIILDADIAILKLDKARISTRVQPICLAASDLSTSFQE-SHITVAGMNV 603
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Db 537 HTTLHPQYDNTFENDVALVELLESPTVNAFVNPICLPEGPQ-----QEGAMVIVSGWK 591
Qy 604 LADVRSPGPKNDTLRSGVVSVVDSLLCEQHEHDHIGIPSVVTDNMFCASEPTAPSICTA 663
Db 592 QFLORFP-----ETLMEIEIPIVDHSTCQKAYAP--LKKKVTTRDMICAG-EKEGKDACAG 644
Qy 664 ETGGIAAASFPGRASPEPRWHLMLGVSWSYDKTCSHRLSTAFTKVLFPKDWIER 717
Db 645 DSGGPMVTLNRERG---QWYLVTGTVSGDDCGCKDRYG-VYSYIHHNKDWIOR 693

RESULT 13
US-09-949-016-11182
; Sequence 11182, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11182
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11182

Query Match 12.0%; Score 475; DB 4; Length 717;
Best Local Similarity 24.6%; Pred. No. 6.9e-31;
Matches 176; Conservative 93; Mismatches 217; Indels 228; Gaps 38;

Qy 69 CRNEECDSLIHPGCTIFENCKSCRNCSWGGLDDFVYKGYCAECRAGWY----GGD 124
Db 161 CREREDEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 198
Qy 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWTTHAKPGFVIQLRFVWLSLEFD--- 174
Db 199 CRVCSNDLFTORTGVITSPDPNYPKSECLYIELEGFWNLQFEDI---FJIEDH 255
Qy 175 --YMCQDYVEVDGDNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAI 232
Db 256 PEVPCPYDIKIKVGP----KVLGPFCEGKAPEPISTQSHSVLLIFHSDNSGENRGWRL- 310
Qy 233 YEEITACSSSPCFHDGTCVLDKAGSYKACLAGYTCQRCENLEERNCSDDPGPVNGYQK 292
Db 311 -----SYRAA-----GNECPEL-----QP--PVH----- 327
Qy 293 ITGGPGLINGRAHAKIGTVVSFF-----CNNSY-VLSGNEKR-----TCQNGEWSGKQ 339
Db 328 -----GKIEPSQAKY-----FFKQVLSVCDTGYKVLKDNVEMDTFOIELCKDGTWSNKI 377
Qy 340 PIC-IKACREPKISDLVRRRLVPMQVQSRETPHLQLYSAAFSKQKLSAPTCKKPALPFGD 398
Db 378 PTKCIVDCRAP----- 390
Qy 399 LPMGQVHLHT-----OLOYECISPPYRRLGSSR--RTCLRTGKWS-----GRA-PSC 442
Db 391 LEHGLITFTSRNLATYKSEIKYSCQEPYKMLNNNTGIYTCSAQWMMNKVLRSLPTC 450
Qy 443 IPICG-----KIENTAPKTQGLRWPMQAAIYRTSGVHDSGLHKGAWFLVCSGA 492
Db 451 LPVCGLPKPSRKLMAIRFN-GRPAQKGT-PMIAML-----SHLNGQPF--CGGS 496
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QY 493 LVNERTVVAAHCV-----TDLGKVTMIKTADLVVGLKGYRDDRDEKTIQSLOIS 544
Db 497 LIGSWIVTAACHLQSLDPEPTLSDLSLSPSFKIILGKHW--LRSDENEHLGVK 554
QY 545 AILHPNYPDILLDADIAILKLLDKARISTRVOPICLAASRDLS*SQB-SHITVAGMNV 603
Db 555 HTTLHPQYDNTFENDVALVELLESVPLNAFVMPICLPEGPQ-----QEGAMVIVSGWK 609
QY 604 LADVRSFGKNDTLRGVSVVDSLLCEQHEHEDHGIPVSTNNMFCASHEPTAPSDICTA 663
Db 610 QFLQRP-----ETLMEIEIPIVDHSTCQKAYAP--LKKKVTTRDMICAG-EKEGGKDACAG 662
QY 664 ETGGIAAVSFPGRASPEPWHLMGLVSWSYDKTCSHRLSTAFKVLPPFKDWIER 717
Db 663 DSGGPMVTLNRBG-----QWLVGVISWGGDCGKDKRYG-VYSYIHNKDWIQR 711

RESULT 14
US-09-949-016-7775
; Sequence 7775, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7775
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7775

Query Match 10.1%; Score 399.5; DB 4; Length 691;
Best Local Similarity 22.6%; Pred. No. 1.3e-24;
Matches 173; Conservative 79; Mismatches 243; Indels 269; Gaps 34;

QY 128 CGQVLR--APK-----GQILLESYP-----LNAHCETWTHAKPGFVIQLRFVMLSLEFDY 175
Db 16 CGSVATPLGPKWPEPVFGRSLASPGPGEVANDQERRWTLTAPGYRLRLYFTHFDLELSH 75
QY 176 MCQYDYVEVRDGDNRDQIIRKVCNE-----RPAP-----IQIGSSLHLVLFHSDGS--KN 225
Db 76 LCEYDFVKLSG-----AKVLATLCQGESTDTERAPGKDTFYSLGSLDITFRSDYSNEKP 131
QY 226 FDFGEHAIY--EETACSSSP-----CFHDGTCLVDKAGSVKACLAGYTGQR-----CENL 274
Db 132 FYGFEAFYAATEDIDECQVAPGEAPTCDHH---CHNHLGGFYCSCRAGYVLRHNRKTCAL 188
QY 275 -----LEE----- 277
Db 189 CSGQVFTQSGELSSPEYPRYPKLSCTSYISLEBGFVILDVFBESFDVETHPTLCYP 248
QY 278 -----RNCSDP 283
Db 249 DFLKIOTDREHGPFQCKTLPHRIETKSNVTVTITFTVDESQDHTGWKIHYTSTAQPCPY 308
QY 284 GGPVNGYQKITGPGGLNGRHAK--IGTVVSPFCNNYS-VLSG-----NEKRTCOQNGEW 335
Db 309 MAPPNHG-----VSPVQAKYILKDSFSLFCETGYELLQGHLPKLSFTAVCQXGDSW 359
QY 336 SGKQPTC-ICAKREPKISDLVRRVLP--QVOSRETPHLQLYSAAPSKLOSAPTKKPA 393
Db 360 DRMPACSI VDCGPPD-----YLPFSGRVEITGVTYTKAV----- 396
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QY 394 LPFGDLPMGYQHLHTOLOVEICISPFY-RRLGSSRRRTCLRTGKWSG-----RAPSCIPICG 447
Db 397 -----IOYSCEETFTYMKVNDGKVCCEADGFWTSSKGEKSLPVCEPVCG 440
QY 448 KIENITAPKTOGLR-----WPQAAIYRRRTSGVHDGSLHKGAMFLVCSGALVNERTVVV 501
Db 441 LSAITTTGRIYGGQAKPGDFEWQVLLGGTT-----AAGALLYNNWVLT 485
QY 502 AAHCYTDGLKVTMIKTADLVVGLKGYRDDRDEKTIQSLO-----ISAILLHPNY-D 553
Db 486 AAHAYVE-----QKHDASALDIRMG-----TLKRLSPHYTQAWSEAVFIHEGYTH 530
QY 554 PILLDADIAILKLLDKARISTRVOPICLAASRDLS*SQB-SHITVAGMNVLADVRSFGFK 613
Db 531 DAGFONDIALIKLNKKNVINSNITPICLPRKAESEFMRTDDIGTAGWG-----LTQGF 586
QY 614 NDTLRSGVSVVDSLLCEQHEHEDHGIP-VSVTDNNMFCASWEPTAPSDICTAETGGIAAVS 672
Db 587 AENLAMYVDIPIVDHOKCTAAAYEKPPYPRGSVTANMLCAGLE-SGGKDSCRGDSGG--ALV 643
QY 673 PPGRASPEPWHLMGLVSWSYDKTCSHRLSTAFKVLPPFKDWIE 716
Db 644 F--LDSETERWFGVGVISWGMNCGEAGQYGVYTKVINYPWIE 685

RESULT 15
US-09-027-337-2
; Sequence 2, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: Timothy J.
; APPLICANT: Tanimoto, Hirofushi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides
; OTHER INFORMATION: 23 to 2589 of Sequence 1
; Patent No. 5972616
US-09-027-337-2

Query Match 8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.8e-18;
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QY 235 EITACSSSPCFHDGTC-----VLDKAGSVKACLAGY----- 266
Db 445 -LSYDSSDPCPGQFTCRGTCIRKELRCGWDADCTDHSDELNCSDAGHQFTCKNFKCP 503
QY 267 -----TGQRCEENLLERNCSDPGGPVNGYQKITGPGGLNGRHAKIGTVVSPFCNNYSV 320
Db 504 LFWVCDSVNDGDNDSDEQSCSP-----AQTFRCNSGKC 537
QY 321 LSG-----NEKRTCOQNGEWSGKQICIKACREPKISDLVRRVLPVQVOSRETPHLQLYS 376
Db 538 LSKSQOCNCKDDCGDGSDEASCPKNVWTC----- 567
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QY 437 GRAPCIPICGKIENITAPKTQ-----GLR-----WPMQAAIYRRTS 473  
Db 585 -----PCDCGKEDCSGSDKDCDCGLRSTRQARVVGGTTADGEHPWQVSLHALGQ 637  
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QY 594 SH-ITVAGNVLADVRSFGKNDTLRSQVSVVDSLLCEEQEDHGI PVSVTDNMFCASW 652  
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QY 712 KDWIERN 718  
Db 846 RDWIKEN 852

Search completed: May 8, 2005, 16:06:10  
Job time : 40 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 9, 2005, 21:04:33 ; Search time 320 Seconds  
(without alignments)  
3681.623 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGCWTLGLTLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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8	665	16.9	3448	4	US-08-877-620-3
9	665	16.9	3448	4	US-09-287-368-3
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93	275.5	7.0	2422	2	US-08-860-289-1	Sequence 1, Appl	166	249.5	6.3	1212	4	US-09-880-503-15	Sequence 1, Appl
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98	275.5	7.0	2422	3	US-09-378-907-1	Sequence 1, Appl	171	248.5	6.3	1314	2	US-08-811-949-50	Sequence 50, Appl
99	275.5	7.0	2422	5	PCT-US94-05779-1	Sequence 1, Appl	172	248.5	6.3	1314	2	US-08-811-949-54	Sequence 54, Appl
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101	275	7.0	1683	4	US-09-912-559-2	Sequence 2, Appl	174	248.5	6.3	1314	2	US-08-811-949-56	Sequence 56, Appl
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105	267.5	6.8	1404	3	US-09-402-101-15	Sequence 15, Appl	178	246.5	6.2	1139	2	US-08-558-269-9	Sequence 9, Appl
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107	267	6.8	1437	3	US-08-487-427-26	Sequence 26, Appl	180	246.5	6.2	1947	1	US-08-952-967-7	Sequence 7, Appl
108	267	6.8	1437	3	US-08-479-727A-26	Sequence 26, Appl	181	246.5	6.2	1947	1	US-07-998-972A-2	Sequence 2, Appl
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117	263	6.7	1475	4	US-09-480-884A-122	Sequence 122, App	190	246.5	6.2	1988	3	US-08-651-472-15	Sequence 15, Appl
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123	263	6.7	1475	4	US-09-630-940B-122	Sequence 122, App	196	242.5	6.1	1605	2	US-08-427-640-7	Sequence 7, Appl
124	263	6.7	1475	4	US-09-285-479-122	Sequence 122, App	197	242.5	6.1	1605	2	US-09-000-846-1	Sequence 1, Appl
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138	262.5	6.7	1389	6	5521070-1	APPLICANT: MEU	211	238	6.0	2625	3	US-09-893-238-18	Sequence 18, Appl
139	262.5	6.7	1389	6	5521070-1	APPLICANT: MEU	212	238	6.0	4072	3	US-09-245-041-16	Sequence 16, Appl
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141	262.5	6.7	1548	4	US-09-150-811-6	Sequence 6, Appl	214	238	6.0	4072	4	US-09-893-238-16	Sequence 16, Appl
142	262.5	6.7	1610	1	US-08-209-816A-6	Sequence 6, Appl	215	238	6.0	8589	3	US-09-245-041-14	Sequence 14, Appl
143	262.5	6.7	1610	2	US-08-472-809B-6	Sequence 6, Appl	216	238	6.0	8589	4	US-09-358-055B-14	Sequence 14, Appl
144	262.5	6.7	1610	3	US-08-438-265-6	Sequence 6, Appl	217	238	6.0	8589	4	US-09-893-238-18	Sequence 18, Appl
145	262.5	6.7	2775	3	US-09-053-871A-22	Sequence 22, Appl	218	237	6.0	4771	2	US-09-021-287-2	Sequence 2, Appl
146	262.5	6.7	2802	3	US-08-742-877-1	Sequence 1, Appl	219	237	6.0	4771	2	US-08-866-650-2	Sequence 2, Appl
147	262.5	6.7	2804	4	US-10-133-307-2	Sequence 2, Appl	220	237	6.0	4771	3	US-09-420-473-2	Sequence 2, Appl
148	262.5	6.7	2833	4	US-09-949-016-5252	Sequence 5252, App	221	236.5	6.0	1065	1	US-08-427-640-5	Sequence 5, Appl
149	262.5	6.7	4933	4	US-09-959-392-1	Sequence 1, Appl	222	236.5	6.0	1065	1	US-08-427-640-5	Sequence 5, Appl
150	261.5	6.6	2792	4	US-09-118-748-1	Sequence 1, Appl	223	236.5	6.0	1068	1	US-08-137-116-2	Sequence 2, Appl
151	259	6.6	2505	4	US-09-799-451-179	Sequence 179, App	224	236.5	6.0	1068	2	US-08-427-640-3	Sequence 3, Appl
152	258.5	6.6	1236	1	US-07-957-039A-7	Sequence 7, Appl	225	236.5	6.0	1068	2	US-08-811-949-44	Sequence 44, Appl
153	258.5	6.6	1236	1	US-08-153-799-17	Sequence 17, Appl	226	236.5	6.0	1068	2	US-08-811-949-46	Sequence 46, Appl
154	258.5	6.6	1236	4	US-09-023-655-927	Sequence 927, App	227	236.5	6.0	1068	2	US-08-811-949-58	Sequence 58, Appl
155	258.5	6.6	1236	4	US-09-880-503-12	Sequence 12, Appl	228	236.5	6.0	1137	3	US-08-978-404B-4	Sequence 4, Appl
156	258.5	6.6	1548	1	US-08-106-078-15	Sequence 15, Appl	229	236.5	6.0	1137	3	US-09-553-498-9	Sequence 9, Appl
157	258.5	6.6	1548	1	US-08-591-492-21	Sequence 21, Appl	230	236.5	6.0	1137	3	US-09-618-869-9	Sequence 9, Appl
158	256.5	6.5	1335	1	US-07-942-157A-2	Sequence 2, Appl	231	236.5	6.0	1724	6	5200340-5	Patent No. 5200340

232	236.5	6.0	1724	5	5200340-5	Patent No. 5200340	305	224	5-7	2440	4	US-09-949-016-5212	Sequence 5212, Ap
233	236	6.0	1068	2	US-08-811-949-52	Sequence 52, Appl	306	223.5	5.7	1042	4	US-09-949-016-3129	Sequence 3129, Ap
234	235.5	6.0	1103	2	US-09-016-366A-24	Sequence 24, Appl	307	222.5	5.6	1783	3	US-09-510-738A-188	Sequence 188, App
235	235.5	6.0	2730	3	US-08-936-135-17	Sequence 17, Appl	308	222.5	5.6	1783	4	US-09-861-966-188	Sequence 188, App
236	235.5	6.0	2730	4	US-09-439-711C-17	Sequence 17, Appl	309	222.5	5.6	1783	4	US-09-919-048-188	Sequence 188, App
237	235.5	6.0	2781	3	US-08-936-135-19	Sequence 19, Appl	310	222.5	5.6	1783	4	US-09-949-016-1311	Sequence 1311, Ap
238	235.5	6.0	2781	4	US-09-439-711C-19	Sequence 19, Appl	311	222	5.6	1128	2	US-09-016-366A-20	Sequence 20, Appl
239	235.5	6.0	3404	4	US-09-583-638-3	Sequence 3, Appl	312	222	5.6	1128	2	US-08-978-404B-15	Sequence 15, Appl
240	235	6.0	1219	2	US-08-978-404B-7	Sequence 7, Appl	313	222	5.6	1615	3	US-09-820-002-1	Sequence 1, Appl
241	233.5	5.9	1163	2	US-08-558-269-5	Sequence 5, Appl	314	221.5	5.6	2413	3	US-09-518-046-1	Sequence 1, Appl
242	233.5	5.9	1163	3	US-09-410-882-5	Sequence 5, Appl	315	221	5.6	943	3	US-08-705-875A-3	Sequence 3, Appl
243	233.5	5.9	2363	3	US-09-742-703-3	Sequence 3, Appl	316	221	5.6	943	3	US-09-242-999-3	Sequence 3, Appl
244	233	5.9	1077	4	US-08-949-016-1108	Sequence 1108, Ap	317	220.5	5.6	1169	3	US-09-386-642-7	Sequence 7, Appl
245	232.5	5.9	1507	1	US-08-487-037-4	Sequence 4, Appl	318	220.5	5.6	11725	2	US-08-756-506-1	Sequence 1, Appl
246	232.5	5.9	3919	2	US-08-866-650-4	Sequence 4, Appl	319	220.5	5.6	11725	4	US-09-328-925-50	Sequence 50, Appl
247	232.5	5.9	3919	2	US-09-021-287-4	Sequence 4, Appl	320	220.5	5.6	11725	4	US-09-054-272-31	Sequence 31, Appl
248	232.5	5.9	3919	3	US-09-240-473-4	Sequence 4, Appl	321	220	5.6	1137	2	US-09-016-366A-18	Sequence 18, Appl
249	232.5	5.9	5145	3	US-08-991-408-1	Sequence 1, Appl	322	220	5.6	1137	2	US-08-978-404B-13	Sequence 13, Appl
250	232.5	5.9	5145	3	US-09-432-473-1	Sequence 1, Appl	323	218.5	5.5	735	3	US-09-079-970A-1	Sequence 1, Appl
251	231.5	5.9	1170	2	US-08-811-949-64	Sequence 64, Appl	324	218.5	5.5	771	3	US-09-079-970A-4	Sequence 4, Appl
252	231	5.9	4661	4	US-09-285-385C-3	Sequence 3, Appl	325	218.5	5.5	1189	4	US-09-607-745-8	Sequence 8, Appl
253	230.5	5.8	780	4	US-10-165-442-6	Sequence 6, Appl	326	218	5.5	2430	4	US-09-192-012-4	Sequence 4, Appl
254	230.5	5.8	888	4	US-10-165-442-5	Sequence 5, Appl	327	218	5.5	2679	6	5200340-7	Patent No. 5200340
255	230.5	5.8	967	4	US-09-242-999-21	Sequence 21, Appl	328	218	5.5	2679	6	5200340-7	Patent No. 5200340
256	230	5.8	1161	3	US-09-032-215-9	Sequence 9, Appl	329	218	5.5	2753	1	US-07-854-603-1	Sequence 1, Appl
c 257	230	5.8	1161	3	US-09-032-215-10	Sequence 10, Appl	330	217.5	5.5	1142	3	US-09-386-642-8	Sequence 8, Appl
258	230	5.8	1161	3	US-09-032-215-15	Sequence 15, Appl	331	217.5	5.5	8091	4	US-09-230-652-1	Sequence 1, Appl
c 259	230	5.8	1161	3	US-09-032-215-16	Sequence 16, Appl	332	217.5	5.5	8957	3	US-09-484-970B-65	Sequence 65, Appl
260	230	5.8	1175	3	US-09-032-215-12	Sequence 12, Appl	333	217	5.5	807	2	US-08-270-584A-1	Sequence 1, Appl
c 261	230	5.8	1175	3	US-09-032-215-14	Sequence 14, Appl	334	217	5.5	807	2	US-08-765-192-1	Sequence 1, Appl
262	230	5.8	1373	3	US-09-032-215-6	Sequence 6, Appl	335	217	5.5	807	3	US-09-199-793-1	Sequence 1, Appl
c 263	230	5.8	1373	3	US-09-032-215-7	Sequence 7, Appl	336	217	5.5	807	4	US-09-613-822B-1	Sequence 1, Appl
264	230	5.8	1434	4	US-10-177-661-1	Sequence 11, Appl	337	217	5.5	1031	2	US-08-978-404B-1	Sequence 1, Appl
265	230	5.8	1748	4	US-09-879-792-11	Sequence 11, Appl	338	217	5.5	1378	4	US-09-907-794A-262	Sequence 262, App
266	229	5.8	726	3	US-09-004-731-35	Sequence 35, Appl	339	217	5.5	1378	4	US-09-905-125A-262	Sequence 262, App
267	229	5.8	726	3	US-08-749-699-35	Sequence 35, Appl	340	217	5.5	1378	4	US-09-902-775A-262	Sequence 262, App
268	229	5.8	726	3	US-09-004-729-35	Sequence 35, Appl	341	217	5.5	1378	4	US-09-906-700-262	Sequence 262, App
269	229	5.8	1200	3	US-09-004-731-32	Sequence 32, Appl	342	217	5.5	1378	4	US-09-903-603A-262	Sequence 262, App
c 270	229	5.8	1200	3	US-09-004-731-34	Sequence 34, Appl	343	217	5.5	1378	4	US-09-904-920A-262	Sequence 262, App
c 271	229	5.8	1200	3	US-08-749-699-32	Sequence 32, Appl	344	217	5.5	1378	4	US-09-909-064-262	Sequence 262, App
c 272	229	5.8	1200	3	US-08-749-699-34	Sequence 34, Appl	345	217	5.5	1378	4	US-09-905-181A-262	Sequence 262, App
273	229	5.8	1200	3	US-09-004-729-32	Sequence 32, Appl	346	217	5.5	1378	4	US-09-906-618-262	Sequence 262, App
c 274	229	5.8	1200	3	US-09-004-729-34	Sequence 34, Appl	347	217	5.5	1430	3	US-09-386-629-1	Sequence 1, Appl
275	229	5.8	1894	3	US-09-004-731-29	Sequence 29, Appl	348	217	5.5	2497	1	US-08-643-219-12	Sequence 12, Appl
c 276	229	5.8	1894	3	US-09-004-731-31	Sequence 31, Appl	349	217	5.5	2497	2	US-09-131-995-12	Sequence 12, Appl
c 277	229	5.8	1894	3	US-09-032-215-3	Sequence 3, Appl	350	217	5.5	2497	2	US-08-832-087B-12	Sequence 12, Appl
278	229	5.8	1894	3	US-08-749-699-29	Sequence 29, Appl	351	217	5.5	2497	3	US-08-851-350-12	Sequence 12, Appl
c 279	229	5.8	1894	3	US-08-749-699-31	Sequence 31, Appl	352	217	5.5	2497	3	US-09-132-154-12	Sequence 12, Appl
280	229	5.8	1894	3	US-09-004-729-29	Sequence 29, Appl	353	217	5.5	2497	4	US-08-924-287A-12	Sequence 12, Appl
c 281	229	5.8	1894	3	US-09-004-729-31	Sequence 31, Appl	354	217	5.5	2732	4	US-09-949-016-4112	Sequence 4112, Ap
282	228	5.8	3690	3	US-08-991-408-3	Sequence 3, Appl	355	216.5	5.5	1292	4	US-09-205-258-189	Sequence 189, App
283	228	5.8	3690	3	US-09-432-473-3	Sequence 3, Appl	356	216	5.5	833	2	US-08-790-137-2	Sequence 2, Appl
284	227	5.8	726	4	US-09-657-986B-1	Sequence 1, Appl	357	216	5.5	959	1	US-08-568-031-1	Sequence 1, Appl
285	227	5.8	959	4	US-09-023-942A-25	Sequence 25, Appl	358	216	5.5	959	2	US-08-966-319-1	Sequence 1, Appl
286	227	5.8	968	3	US-08-705-875A-9	Sequence 9, Appl	359	216	5.5	959	3	US-09-153-304-1	Sequence 1, Appl
287	227	5.8	968	4	US-09-242-999-9	Sequence 9, Appl	360	216	5.5	1081	2	US-09-016-366A-22	Sequence 22, Appl
288	226.5	5.7	3579	4	US-09-949-016-4627	Sequence 4627, Ap	361	216	5.5	1081	2	US-08-978-404B-17	Sequence 17, Appl
289	226	5.7	2038	4	US-09-008-271A-18	Sequence 18, Appl	362	216	5.5	1081	4	US-09-917-254-50	Sequence 50, Appl
290	226	5.7	2057	4	US-09-949-016-3367	Sequence 3367, Ap	363	216	5.5	1130	4	US-09-387-375-8	Sequence 8, Appl
291	226	5.7	2057	4	US-09-949-016-3368	Sequence 3368, Ap	364	216	5.5	1130	4	US-10-041-400A-8	Sequence 8, Appl
292	226	5.7	2079	3	US-09-656-002-1	Sequence 1, Appl	365	216	5.5	1130	4	US-10-042-091A-8	Sequence 8, Appl
293	226	5.7	2079	4	US-09-851-588-5	Sequence 5, Appl	366	215	5.4	1166	3	US-09-386-629-2	Sequence 2, Appl
294	226	5.7	2091	4	US-09-851-588-7	Sequence 7, Appl	367	215	5.4	2296	1	US-07-750-080A-18	Sequence 18, Appl
295	226	5.7	2217	4	US-09-949-016-5667	Sequence 5667, Ap	368	215	5.4	2296	3	US-08-651-472-18	Sequence 18, Appl
296	226	5.7	2217	4	US-09-949-016-5668	Sequence 5668, Ap	369	215	5.4	2296	3	US-08-358-928-18	Sequence 18, Appl
297	225	5.7	24735	4	US-09-949-016-12850	Sequence 12850, A	370	215	5.4	14802	4	US-09-949-016-16753	Sequence 16753, A
298	224	5.7	831	4	US-09-880-503-14	Sequence 14, Appl	371	214	5.4	1314	3	US-09-025-059-2	Sequence 2, Appl
299	224	5.7	972	4	US-09-880-503-16	Sequence 16, Appl	372	212.5	5.4	1052	3	US-09-386-642-10	Sequence 10, Appl
300	224	5.7	1154	2	US-09-016-366A-16	Sequence 16, Appl	373	212.5	5.4	1192	3	US-08-944-483-8	Sequence 8, Appl
301	224	5.7	1154	2	US-08-978-404B-11	Sequence 11, Appl	374	211.5	5.4	696	1	US-08-508-448C-24	Sequence 24, Appl
302	224	5.7	2121	4	US-09-607-745-1	Sequence 1, Appl	375	211.5	5.4	901	1	US-08-508-448C-9	Sequence 9, Appl
303	224	5.7	2440	4	US-09-949-016-5210	Sequence 5210, Ap	376	211.5	5.4	1166	3	US-08-944-483-7	Sequence 7, Appl
304	224	5.7	2440	4	US-09-949-016-5211	Sequence 5211, Ap	377	211.5	5.4	1166	3	US-09-370-838-80	Sequence 80, Appl

378	211.5	5.4	1460	4	US-09-854-133-80	Sequence 80, Appl	451	203.5	5.2	802	4	US-09-949-016-2899	Sequence 2899, Ap
379	211.5	5.4	1517	1	US-08-508-448C-15	Sequence 15, Appl	452	203.5	5.2	1979	1	US-08-392-828C-3	Sequence 3, Appli
380	211.5	5.4	2790	3	US-09-370-838-79	Sequence 79, Appl	453	203.5	5.2	1979	3	US-09-330-945-3	Sequence 1, Appli
381	211.5	5.4	2790	4	US-09-854-133-79	Sequence 79, Appl	454	203.5	5.2	11272	4	US-09-341-461-1	Sequence 1, Appli
382	211	5.3	943	3	US-08-705-875A-1	Sequence 1, Appli	455	203	5.1	933	4	US-09-023-942A-29	Sequence 431, App
383	211	5.3	943	4	US-09-242-899-1	Sequence 1, Appli	456	203	5.1	1212	4	US-09-620-312D-43	Sequence 7, Appli
384	211	5.3	1108	2	US-09-016-366A-14	Sequence 14, Appl	457	203	5.1	3539	3	US-08-936-135-7	Sequence 7, Appli
385	211	5.3	1108	2	US-08-978-404B-20	Sequence 10, Appl	458	203	5.1	3539	3	US-09-439-711C-7	Sequence 7, Appli
386	211	5.3	1553	3	US-09-480-116-10	Sequence 10, Appl	459	203	5.1	3846	4	US-09-755-100A-3	Sequence 3, Appli
387	211	5.3	1605	3	US-09-949-016-2349	Sequence 17, Appl	460	203	5.1	4718	3	US-08-936-135-9	Sequence 9, Appli
388	211	5.3	3201	4	US-09-579-536C-17	Sequence 2349, Ap	461	203	5.1	4718	3	US-09-439-711C-9	Sequence 9, Appli
389	211	5.3	3657	4	US-09-579-536C-2	Sequence 2, Appli	462	203	5.1	4733	3	US-08-936-135-11	Sequence 11, Appl
390	211	5.3	4208	3	US-09-214-278-6	Sequence 6, Appli	463	203	5.1	4733	3	US-09-439-711C-11	Sequence 11, Appl
391	211	5.3	4208	3	US-09-068-740A-10	Sequence 10, Appl	464	203	5.1	4765	4	US-08-936-135-21	Sequence 21, Appl
392	211	5.3	4208	4	US-09-855-722-6	Sequence 6, Appli	465	203	5.1	4765	4	US-09-439-711C-21	Sequence 21, Appl
393	211	5.3	4855	4	US-09-917-254-34	Sequence 34, Appl	466	203	5.1	4769	3	US-08-936-135-13	Sequence 13, Appl
394	211	5.3	5458	3	US-09-199-865-2	Sequence 2, Appli	467	203	5.1	4769	3	US-09-439-711C-13	Sequence 13, Appl
395	211	5.3	5458	4	US-10-213-329-2	Sequence 2, Appli	468	203	5.1	4780	3	US-08-936-135-23	Sequence 23, Appl
396	211	5.3	5590	3	US-08-882-046-1	Sequence 1, Appli	469	203	5.1	4780	4	US-09-439-711C-23	Sequence 23, Appl
397	211	5.3	5590	4	US-09-566-047-1	Sequence 1, Appli	470	203	5.1	4784	3	US-08-936-135-15	Sequence 15, Appl
398	211	5.3	5885	4	US-09-949-016-4426	Sequence 4426, Ap	471	203	5.1	4784	4	US-09-439-711C-15	Sequence 15, Appl
399	211	5.3	5896	4	US-09-949-016-31	Sequence 31, Appl	472	203	5.1	16520	4	US-09-949-016-14710	Sequence 14710, A
400	211	5.3	6464	2	US-08-400-159-5	Sequence 5, Appli	473	203	5.1	16520	4	US-09-949-016-15394	Sequence 15394, A
401	211	5.3	6464	3	US-08-611-729A-5	Sequence 5, Appli	474	202	5.1	2544	3	US-09-518-046-3	Sequence 3, Appli
402	211	5.3	6464	4	US-09-195-524-5	Sequence 5, Appli	475	202	5.1	23640	4	US-09-949-016-13646	Sequence 13646, A
403	211	5.3	7191	4	US-09-949-016-14871	Sequence 14871, A	476	200.5	5.1	734	1	US-08-650-129-1	Sequence 1, Appli
404	210.5	5.3	866	1	US-08-650-129-3	Sequence 3, Appli	477	200.5	5.1	734	1	US-08-984-417-1	Sequence 1, Appli
405	210.5	5.3	866	3	US-08-984-417-3	Sequence 3, Appli	478	200.5	5.1	897	2	US-08-956-267A-1	Sequence 1, Appli
406	210.5	5.3	1462	3	US-09-370-838-55	Sequence 55, Appl	479	200.5	5.1	1154	3	US-09-636-382A-1	Sequence 1, Appli
407	210.5	5.3	1462	4	US-09-854-133-55	Sequence 55, Appl	480	200	5.1	1154	3	US-09-163-951-15	Sequence 15, Appl
408	210	5.3	1341	4	US-10-177-661-3	Sequence 3, Appli	481	200	5.1	1155	4	US-09-345-881-15	Sequence 15, Appl
409	210	5.3	2771	4	US-09-949-016-5148	Sequence 5148, Ap	482	200	5.1	1240	3	US-09-163-951-14	Sequence 14, Appl
410	210	5.3	2821	4	US-09-620-312D-179	Sequence 179, App	483	200	5.1	1240	4	US-09-345-881-14	Sequence 14, Appl
411	209.5	5.3	1479	3	US-09-342-749-1	Sequence 1, Appli	484	200	5.1	9723	1	US-08-083-590A-21	Sequence 21, Appl
412	209.5	5.3	1479	3	US-09-691-840-1	Sequence 1, Appli	485	200	5.1	9723	1	US-08-532-384-21	Sequence 21, Appl
413	209	5.3	1230	4	US-09-879-792-35	Sequence 35, Appl	486	199	5.0	994	3	US-09-008-271A-19	Sequence 19, Appl
414	208.5	5.3	2479	3	US-09-342-749-29	Sequence 29, Appl	487	199	5.0	1068	4	US-09-949-016-2280	Sequence 2280, Ap
415	208.5	5.3	2479	3	US-09-691-840-29	Sequence 29, Appl	488	198.5	5.0	825	3	US-09-120-582-1	Sequence 1, Appli
416	208.5	5.3	2479	4	US-09-685-166A-894	Sequence 894, App	489	198.5	5.0	3199	4	US-09-949-016-4400	Sequence 4400, Ap
417	208.5	5.3	2479	4	US-09-679-426-894	Sequence 894, App	490	198	5.0	1126	2	US-08-479-733A-27	Sequence 27, Appl
418	208.5	5.3	2479	4	US-09-759-143-894	Sequence 894, App	491	198	5.0	1126	3	US-08-487-427-27	Sequence 27, Appl
419	207.5	5.3	1077	3	US-08-807-151-2	Sequence 2, Appli	492	198	5.0	1126	3	US-08-479-727A-27	Sequence 27, Appl
420	207.5	5.3	1077	3	US-09-478-957-2	Sequence 2, Appli	493	198	5.0	1126	3	US-08-482-369A-27	Sequence 27, Appl
421	207.5	5.3	1146	4	US-08-205-258-247	Sequence 247, App	494	198	5.0	1126	5	PCT-US95-07439-27	Sequence 27, Appl
422	207.5	5.3	1476	4	US-09-759-143-931	Sequence 931, App	495	197.5	5.0	871	1	US-08-744-026-2	Sequence 2, Appli
423	207.5	5.3	1479	4	US-09-759-143-930	Sequence 930, App	496	197.5	5.0	871	2	US-09-102-732-2	Sequence 2, Appli
424	207.5	5.3	2026	4	US-09-907-794A-103	Sequence 103, App	497	197.5	5.0	871	3	US-09-261-767-2	Sequence 7, Appli
425	207.5	5.3	2026	4	US-09-905-125A-103	Sequence 103, App	498	197.5	5.0	871	3	US-08-969-987-7	Sequence 7, Appli
426	207.5	5.3	2026	4	US-09-902-775A-103	Sequence 103, App	499	197.5	5.0	1074	4	US-09-949-016-1077	Sequence 1077, Ap
427	207.5	5.3	2026	4	US-09-906-700-103	Sequence 103, App	500	196.5	5.0	970	1	US-08-148-910-3	Sequence 3, Appli
428	207.5	5.3	2026	4	US-09-903-603A-103	Sequence 103, App	501	196.5	5.0	970	1	US-08-448-937A-3	Sequence 3, Appli
429	207.5	5.3	2026	4	US-09-904-920A-103	Sequence 103, App	502	195.5	5.0	2340	3	US-08-742-877-3	Sequence 3, Appli
430	207.5	5.3	2026	4	US-09-909-064-103	Sequence 103, App	503	195.5	5.0	6677	3	US-08-939-366-27	Sequence 27, Appl
431	207.5	5.3	2026	4	US-09-905-381A-103	Sequence 103, App	504	195.5	5.0	6677	3	US-09-467-997-6	Sequence 6, Appli
432	207.5	5.3	2026	4	US-09-906-618-103	Sequence 103, App	505	194.5	4.9	1802	3	US-09-032-523-5	Sequence 5, Appli
433	207.5	5.3	2448	4	US-09-949-016-5203	Sequence 5203, Ap	506	194.5	4.9	1802	4	US-09-802-633-5	Sequence 5, Appli
434	207.5	5.3	3245	4	US-09-759-143-929	Sequence 929, App	507	194	4.9	1093	6	5223425-3	Patent No. 5223425
435	206.5	5.2	821	1	US-08-650-129-2	Sequence 2, Appli	508	194	4.9	1093	6	5223425-3	Patent No. 5223425
436	206.5	5.2	821	3	US-08-984-417-2	Sequence 2, Appli	509	194	4.9	1167	3	US-09-020-956-175	Sequence 175, App
437	206.5	5.2	1613	4	US-09-387-375-1	Sequence 1, Appli	510	194	4.9	1167	3	US-09-030-607-175	Sequence 175, App
438	206.5	5.2	1613	4	US-10-041-400A-1	Sequence 1, Appli	511	194	4.9	1167	3	US-09-439-313-175	Sequence 175, App
439	206.5	5.2	1613	3	US-10-042-091A-1	Sequence 1, Appli	512	194	4.9	1167	3	US-09-352-616A-175	Sequence 175, App
440	205.5	5.2	1049	3	US-09-386-642-9	Sequence 9, Appli	513	194	4.9	1167	3	US-09-232-149A-175	Sequence 175, App
441	205.5	5.2	1095	2	US-08-978-404B-9	Sequence 9, Appli	514	194	4.9	1167	4	US-09-159-812-175	Sequence 175, App
442	205.5	5.2	1165	4	US-09-023-942A-28	Sequence 28, Appl	515	194	4.9	1167	4	US-09-636-215-175	Sequence 175, App
443	204.5	5.2	1332	4	US-09-949-016-3389	Sequence 3389, Ap	516	194	4.9	1167	4	US-09-685-166A-175	Sequence 175, App
444	204.5	5.2	3582	2	US-08-400-159-9	Sequence 9, Appli	517	194	4.9	1167	4	US-09-115-453-175	Sequence 175, App
445	204.5	5.2	3582	3	US-08-611-729A-9	Sequence 9, Appli	518	194	4.9	1167	4	US-09-688-489-175	Sequence 175, App
446	204.5	5.2	3582	4	US-09-195-524-9	Sequence 9, Appli	519	194	4.9	1167	4	US-09-679-426-175	Sequence 175, App
447	204	5.2	944	3	US-09-070-526-1	Sequence 1, Appli	520	194	4.9	1167	4	US-09-759-143-175	Sequence 175, App
448	204	5.2	1343	4	US-09-618-259-72	Sequence 72, Appl	521	194	4.9	1167	4	US-09-651-236-175	Sequence 175, App
449	204	5.2	1360	4	US-09-618-259-6	Sequence 6, Appli	522	193.5	4.9	1806	4	US-09-800-729-75	Sequence 75, Appl
450	204	5.2	7244	4	US-09-774-528-143	Sequence 143, App	523	193.5	4.9	1806	4	US-10-067-422-5	Sequence 5, Appli

524	193	4.9	804	3	US-09-032-215-44	Sequence 44, Appl	597	186.5	4.7	796	3	US-09-380-116-107	Sequence 107, App
525	193	4.9	804	3	US-09-032-215-45	Sequence 45, Appl	598	186	4.7	1130	3	US-09-386-653A-8	Sequence 8, Appl
526	193	4.9	835	6	5223425-7	Patent No. 5223425	599	186	4.7	2508	3	US-08-981-392-1	Sequence 1, Appl
527	193	4.9	835	6	5223425-7	Patent No. 5223425	600	186	4.7	2508	3	US-09-908-322-1	Sequence 1, Appl
528	193	4.9	933	3	US-09-032-215-41	Sequence 41, Appl	601	186	4.7	2883	3	US-08-981-392-3	Sequence 3, Appl
529	193	4.9	933	3	US-09-032-215-43	Sequence 43, Appl	602	186	4.7	2883	3	US-09-908-322-3	Sequence 3, Appl
530	193	4.9	1266	4	US-09-800-729-15	Sequence 15, Appl	603	186	4.7	3471	3	US-09-116-473-3	Sequence 3, Appl
531	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	604	185.5	4.7	768	3	US-09-032-215-29	Sequence 29, Appl
532	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	605	185.5	4.7	768	3	US-09-032-215-30	Sequence 30, Appl
533	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	606	185.5	4.7	1059	3	US-08-163-919A-1	Sequence 1, Appl
534	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	607	185.5	4.7	1059	3	US-08-462-515-1	Sequence 1, Appl
535	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	608	185.5	4.7	1059	3	PCT-US94-14073-1	Sequence 1, Appl
536	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	609	185.5	4.7	1103	3	US-09-386-642-59	Sequence 59, Appl
537	192	4.9	944	3	US-08-906-769-82	Sequence 82, Appl	610	185.5	4.7	2216	2	US-08-666-082B-2	Sequence 2, Appl
538	192	4.9	944	3	PCT-US95-1442A-82	Sequence 82, Appl	611	185.5	4.7	2219	1	US-07-882-925A-1	Sequence 1, Appl
539	192	4.9	2419	3	US-09-245-041-8	Sequence 8, Appl	612	185.5	4.7	2219	1	US-08-184-012C-1	Sequence 1, Appl
540	192	4.9	2419	3	US-09-245-041-8	Sequence 8, Appl	613	185.5	4.7	2232	1	US-08-334-177-1	Sequence 1, Appl
541	192	4.9	2419	3	US-09-245-041-8	Sequence 8, Appl	614	185.5	4.7	2232	1	PCT-US95-13830-1	Sequence 1, Appl
542	192	4.9	8827	3	US-09-893-238-8	Sequence 8, Appl	615	185.5	4.7	2262	1	US-07-882-925A-7	Sequence 7, Appl
543	192	4.9	8827	3	US-09-893-238-8	Sequence 8, Appl	616	185.5	4.7	2262	1	US-08-184-012C-7	Sequence 7, Appl
544	192	4.9	8827	3	US-09-893-238-8	Sequence 8, Appl	617	185	4.7	1100	4	US-09-023-942A-5	Sequence 5, Appl
545	191.5	4.9	3142	1	US-08-110-158-3	Sequence 3, Appl	618	184.5	4.7	992	1	US-08-358-782D-13	Sequence 13, Appl
546	191.5	4.9	3142	1	US-09-023-655-1090	Sequence 1090, Ap	619	184.5	4.7	992	2	US-08-764-527A-13	Sequence 13, Appl
547	191.5	4.9	3144	5	PCT-US91-05059-1	Sequence 1, Appl	620	184	4.7	1081	2	US-09-008-271A-15	Sequence 15, Appl
548	191	4.8	765	3	US-09-439-313-524	Sequence 524, App	621	184	4.7	1100	4	US-09-907-794A-256	Sequence 256, App
549	191	4.8	765	4	US-09-636-215-524	Sequence 524, App	622	184	4.7	1100	4	US-09-905-125A-256	Sequence 256, App
550	191	4.8	765	4	US-09-685-166A-524	Sequence 524, App	623	184	4.7	1100	4	US-09-902-775A-256	Sequence 256, App
551	191	4.8	765	4	US-09-679-426-524	Sequence 524, App	624	184	4.7	1100	4	US-09-906-700-256	Sequence 256, App
552	191	4.8	765	4	US-09-759-143-524	Sequence 524, App	625	184	4.7	1100	4	US-09-903-603A-256	Sequence 256, App
553	191	4.8	765	4	US-09-651-236-524	Sequence 524, App	626	184	4.7	1100	4	US-09-904-920A-256	Sequence 256, App
554	191	4.8	2416	3	US-09-261-416-1	Sequence 1, Appl	627	184	4.7	1100	4	US-09-909-064-256	Sequence 256, App
555	191	4.8	3371	3	US-09-116-473-1	Sequence 1, Appl	628	184	4.7	1100	4	US-09-905-381A-256	Sequence 256, App
556	190	4.8	945	3	US-09-032-215-26	Sequence 26, Appl	629	184	4.7	1100	4	US-09-906-618-256	Sequence 256, App
557	190	4.8	945	3	US-09-032-215-28	Sequence 28, Appl	630	184	4.7	1248	3	US-09-020-956-171	Sequence 171, App
558	190	4.8	1037	3	US-09-386-642-60	Sequence 60, Appl	631	184	4.7	1248	3	US-09-030-607-171	Sequence 171, App
559	190	4.8	2185	4	US-09-270-767-12720	Sequence 12720, A	632	184	4.7	1248	3	US-09-439-313-171	Sequence 171, App
560	189.5	4.8	1110	3	US-09-386-653A-1	Sequence 1, Appl	633	184	4.7	1248	3	US-09-352-616A-171	Sequence 171, App
561	189	4.8	969	3	US-09-502-600-30	Sequence 30, Appl	634	184	4.7	1248	3	US-09-232-149A-171	Sequence 171, App
562	189	4.8	969	3	US-09-918-243-30	Sequence 30, Appl	635	184	4.7	1248	4	US-09-159-812-171	Sequence 171, App
563	189	4.8	986	2	US-08-557-146-1	Sequence 1, Appl	636	184	4.7	1248	4	US-09-636-215-171	Sequence 171, App
564	189	4.8	986	2	US-09-154-344-1	Sequence 1, Appl	637	184	4.7	1248	4	US-09-685-166A-171	Sequence 171, App
565	189	4.8	980	4	US-09-949-016-1845	Sequence 1845, Ap	638	184	4.7	1248	4	US-09-115-453-171	Sequence 171, App
566	189	4.8	1089	3	US-08-930-188-1	Sequence 3, Appl	639	184	4.7	1248	4	US-09-688-489-171	Sequence 171, App
567	189	4.8	1089	3	US-08-930-188-3	Sequence 3, Appl	640	184	4.7	1248	4	US-09-679-426-171	Sequence 171, App
568	189	4.8	1089	5	PCT-US96-04294-1	Sequence 1, Appl	641	184	4.7	1248	4	US-09-759-143-171	Sequence 171, App
569	189	4.8	1089	5	PCT-US96-04294-3	Sequence 3, Appl	642	184	4.7	1248	4	US-09-651-236-171	Sequence 171, App
570	189	4.8	1094	4	US-09-023-942A-3	Sequence 3, Appl	643	184	4.7	3955	3	US-09-214-278-4	Sequence 4, Appl
571	189	4.8	1214	3	US-09-439-313-225	Sequence 225, App	644	184	4.7	3955	4	US-09-855-722-4	Sequence 4, Appl
572	189	4.8	1214	3	US-09-352-616A-225	Sequence 225, App	645	184	4.7	4464	2	US-08-400-159-7	Sequence 7, Appl
573	189	4.8	1214	3	US-09-232-149A-225	Sequence 225, App	646	184	4.7	4483	3	US-08-611-729A-7	Sequence 7, Appl
574	189	4.8	1214	4	US-09-159-812-225	Sequence 225, App	647	184	4.7	4483	4	US-09-195-524-7	Sequence 7, Appl
575	189	4.8	1214	4	US-09-636-215-225	Sequence 225, App	648	183.5	4.7	2136	4	US-09-600-991-19	Sequence 19, Appl
576	189	4.8	1214	4	US-09-685-166A-225	Sequence 225, App	649	183.5	4.7	2136	4	US-09-601-040A-11	Sequence 11, Appl
577	189	4.8	1214	4	US-09-115-453-225	Sequence 225, App	650	183.5	4.7	2219	4	US-09-949-016-1110	Sequence 1110, Ap
578	189	4.8	1214	4	US-09-688-489-225	Sequence 225, App	651	183.5	4.7	2692	3	US-08-981-392-11	Sequence 11, Appl
579	189	4.8	1214	4	US-09-679-426-225	Sequence 225, App	652	183.5	4.7	2692	4	US-09-908-322-11	Sequence 11, Appl
580	189	4.8	1214	4	US-09-759-143-225	Sequence 225, App	653	183.5	4.7	3652	3	US-08-936-135-5	Sequence 5, Appl
581	189	4.8	1214	4	US-09-651-236-225	Sequence 225, App	654	183.5	4.7	3652	4	US-09-439-711C-5	Sequence 5, Appl
582	189	4.8	1215	3	US-09-439-313-326	Sequence 326, App	655	182.5	4.6	799	4	US-09-023-942A-7	Sequence 7, Appl
583	189	4.8	1215	3	US-09-352-616A-326	Sequence 326, App	656	182.5	4.6	980	4	US-09-023-942A-30	Sequence 30, Appl
584	189	4.8	1215	3	US-09-232-149A-326	Sequence 326, App	657	182.5	4.6	1592	2	US-08-252-493C-1	Sequence 1, Appl
585	189	4.8	1215	4	US-09-636-215-326	Sequence 326, App	658	182.5	4.6	1592	3	US-09-276-197-1	Sequence 1, Appl
586	189	4.8	1215	4	US-09-685-166A-326	Sequence 326, App	659	182	4.6	1225	3	US-09-734-675-1	Sequence 1, Appl
587	189	4.8	1215	4	US-09-688-489-326	Sequence 326, App	660	182	4.6	1386	2	US-08-897-340-1	Sequence 1, Appl
588	189	4.8	1215	4	US-09-679-426-326	Sequence 326, App	661	182	4.6	1386	3	US-09-252-329-1	Sequence 1, Appl
589	189	4.8	1215	4	US-09-759-143-326	Sequence 326, App	662	181.5	4.6	867	1	US-07-590-301A-1	Sequence 1, Appl
590	189	4.8	1215	4	US-09-651-236-326	Sequence 326, App	663	181.5	4.6	1556	1	US-08-597-545-3	Sequence 3, Appl
591	189	4.8	1350	4	US-09-636-215-616	Sequence 616, App	664	181.5	4.6	1556	1	US-08-457-135-3	Sequence 3, Appl
592	189	4.8	1350	4	US-09-685-166A-616	Sequence 616, App	665	181.5	4.6	3231	4	US-09-866-028-14	Sequence 14, Appl
593	189	4.8	1350	4	US-09-679-426-616	Sequence 616, App	666	181.5	4.6	3231	4	US-09-944-457-14	Sequence 14, Appl
594	189	4.8	1350	4	US-09-759-143-616	Sequence 616, App	667	181.5	4.6	3757	2	US-09-016-366A-13	Sequence 13, Appl
595	189	4.8	1350	4	US-09-651-236-616	Sequence 616, App	668	181.5	4.6	3757	2	US-08-978-404B-19	Sequence 19, Appl
596	188	4.8	855	4	US-09-044-604-1	Sequence 1, Appl	669	180.5	4.6	917	4	US-09-669-751-101	Sequence 101, App



670	180.5	4.6	2219	1	US-07-882-925A-2	Sequence 2, Appli	743	170	4.3	641	3	US-08-306-616-148	Sequence 148, App
671	180.5	4.6	2219	1	US-08-184-012C-2	Sequence 2, Appli	744	170	4.3	641	3	US-08-639-075A-148	Sequence 148, App
672	179.5	4.6	863	6	5223425-9	Sequence 2, Appli	745	170	4.3	641	3	US-09-012-431-148	Sequence 148, App
673	179.5	4.6	863	6	5223425-9	Patent No. 5223425	746	170	4.3	641	3	US-09-012-692-148	Sequence 148, App
674	179.5	4.6	925	1	US-07-990-301A-3	Sequence 3, Appli	747	170	4.3	641	3	US-08-906-613-148	Sequence 148, App
675	179	4.5	690	1	US-08-379-621-1	Sequence 1, Appli	748	170	4.3	1051	3	US-09-245-041-10	Sequence 10, Appl
676	179	4.5	690	2	US-08-889-078-1	Sequence 1, Appli	749	170	4.3	1051	4	US-09-358-055B-10	Sequence 10, Appl
677	179	4.5	1152	2	US-09-032-215-24	Sequence 24, Appl	750	170	4.3	1051	4	US-09-893-238-10	Sequence 10, Appl
c 678	179	4.5	1152	3	US-09-032-215-25	Sequence 25, Appl	751	170	4.3	2154	4	US-09-601-040A-7	Sequence 7, Appli
679	179	4.5	1303	3	US-09-032-215-21	Sequence 21, Appl	752	170	4.3	2190	4	US-09-601-040A-3	Sequence 3, Appli
c 680	179	4.5	1303	3	US-09-032-215-23	Sequence 23, Appl	753	170	4.3	2772	3	US-08-936-135-1	Sequence 1, Appli
681	179	4.5	1828	3	US-09-280-116-108	Sequence 108, App	754	170	4.3	2772	4	US-09-439-711C-1	Sequence 1, Appli
682	178.5	4.5	1504	2	US-08-839-008-4	Sequence 4, Appli	755	169.5	4.3	11009	4	US-09-845-583A-1	Sequence 11, Appl
683	178.5	4.5	1506	2	US-08-839-008-6	Sequence 6, Appli	756	169.5	4.3	25621	4	US-09-902-540-1253	Sequence 1253, Ap
684	178.5	4.5	2786	3	US-08-936-135-3	Sequence 3, Appli	757	169	4.3	1158	4	US-09-142-027A-13	Sequence 13, Appl
685	178.5	4.5	2786	3	US-09-439-711C-3	Sequence 3, Appli	758	169	4.3	1158	4	US-09-142-027A-13	Sequence 13, Appl
686	178	4.5	700	4	US-09-270-767-14199	Sequence 14199, A	759	169	4.3	1573	1	US-08-597-545-4	Sequence 4, Appli
687	178	4.5	13863	4	US-09-814-915A-83	Sequence 83, Appl	760	169	4.3	1573	1	US-08-457-135-4	Sequence 4, Appli
688	176.5	4.5	859	3	US-09-044-604-2	Sequence 2, Appli	761	169	4.3	3423	4	US-09-755-100A-5	Sequence 5, Appli
c 689	176	4.5	699	3	US-09-004-731-26	Sequence 26, Appl	762	168.5	4.3	3423	4	US-09-229-151C-13	Sequence 13, Appl
c 690	176	4.5	699	3	US-09-004-731-28	Sequence 28, Appl	763	168.5	4.3	4661	4	US-09-755-100A-2	Sequence 2, Appli
691	176	4.5	699	3	US-08-749-699-26	Sequence 26, Appl	764	168.5	4.3	4661	4	US-09-755-100A-2	Sequence 2, Appli
c 692	176	4.5	699	3	US-08-749-699-28	Sequence 28, Appl	765	168	4.3	806	3	US-08-906-769-120	Sequence 120, App
693	176	4.5	699	3	US-09-004-729-26	Sequence 26, Appl	766	168	4.3	806	3	US-08-906-616-120	Sequence 120, App
c 694	176	4.5	699	3	US-09-004-729-28	Sequence 28, Appl	767	168	4.3	806	3	US-08-639-075A-120	Sequence 120, App
695	176	4.5	924	3	US-09-004-731-23	Sequence 23, Appl	768	168	4.3	806	3	US-09-012-431-120	Sequence 120, App
c 696	176	4.5	924	3	US-09-004-731-25	Sequence 25, Appl	769	168	4.3	806	3	US-09-012-692-120	Sequence 120, App
697	176	4.5	924	3	US-08-749-699-23	Sequence 23, Appl	770	168	4.3	806	3	US-08-906-613-120	Sequence 120, App
c 698	176	4.5	924	3	US-08-749-699-25	Sequence 25, Appl	771	167.5	4.2	1462	1	US-08-358-782D-14	Sequence 14, Appl
699	176	4.5	924	3	US-09-004-729-23	Sequence 23, Appl	772	167.5	4.2	1462	1	US-08-764-527A-14	Sequence 14, Appl
c 700	176	4.5	924	3	US-09-004-729-25	Sequence 25, Appl	773	167	4.2	2183	4	US-09-641-612-9	Sequence 9, Appli
701	175.5	4.4	1491	4	US-09-495-050A-249	Sequence 249, App	774	167	4.2	2989	6	5378464-1	Patent No. 5378464
702	174.5	4.4	4315	3	US-08-882-046-3	Sequence 3, Appli	775	167	4.2	2989	6	5378464-1	Patent No. 5378464
703	174.5	4.4	4315	3	US-09-566-047-3	Sequence 3, Appli	776	167	4.2	2989	6	5378464-1	Patent No. 5378464
704	174	4.4	2001	3	US-09-341-587-2	Sequence 2, Appli	c 777	166	4.2	14844	4	US-09-902-540-1108	Sequence 1108, Ap
705	174	4.4	2663	3	US-09-068-740A-8	Sequence 8, Appli	778	166	4.2	711	3	US-09-100-264-4	Sequence 4, Appli
706	174	4.4	2663	3	US-09-423-753-8	Sequence 8, Appli	779	165	4.2	1454	1	US-08-467-155A-23	Sequence 23, Appl
707	174	4.4	5802	3	US-09-341-587-4	Sequence 4, Appli	780	165	4.2	1454	1	US-08-467-155A-23	Sequence 23, Appl
708	174	4.4	5943	4	US-09-976-594-272	Sequence 272, App	781	165	4.2	1454	2	US-08-628-198-2	Sequence 2, Appli
709	173.5	4.4	1245	4	US-09-270-767-14860	Sequence 14860, A	782	165	4.2	1454	2	US-08-628-198-2	Sequence 2, Appli
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711	172.5	4.4	863	6	5223425-1	Patent No. 5223425	784	165	4.2	1454	4	US-09-771-357-94	Sequence 94, Appl
712	172.5	4.4	863	6	5223425-1	Patent No. 5223425	785	164.5	4.2	903	4	US-10-059-579A-94	Sequence 94, Appl
713	172.5	4.4	1480	2	US-08-839-008-8	Sequence 8, Appli	786	164.5	4.2	916	4	US-09-902-540-2069	Sequence 2, Appli
714	172.5	4.4	1480	2	US-09-919-497-39	Sequence 39, Appli	787	164.5	4.2	916	4	US-09-774-528-420	Sequence 420, App
715	172.5	4.4	1508	4	US-09-949-016-1367	Sequence 1367, Ap	788	164.5	4.2	9668	4	US-09-949-016-4532	Sequence 4532, Ap
716	172.5	4.4	1537	2	US-08-839-008-1	Sequence 1, Appli	789	164	4.2	696	3	US-09-280-116-180	Sequence 180, App
717	172.5	4.4	1820	4	US-09-799-451-885	Sequence 885, App	790	163.5	4.1	12270	4	US-09-229-151C-14	Sequence 14, Appl
c 718	172	4.4	828	4	US-09-270-767-2080	Sequence 2080, Ap	c 791	163.5	4.1	12270	4	US-09-949-016-16891	Sequence 16891, A
c 719	172	4.4	828	4	US-09-270-767-17362	Sequence 17362, A	792	163.5	4.1	22089	4	US-09-949-016-16890	Sequence 16890, A
720	172	4.4	1452	4	US-09-270-767-27664	Sequence 27664, A	793	163	4.1	1752	4	US-09-641-612-1	Sequence 1, Appli
721	172	4.4	2039	4	US-09-270-767-11981	Sequence 11981, A	794	163	4.1	2917	4	US-08-907-794A-189	Sequence 189, App
722	172	4.4	5653	4	US-09-583-638-1	Sequence 1, Appli	795	163	4.1	2917	4	US-09-905-125A-189	Sequence 189, App
723	172	4.4	8374	4	US-09-639-207-11	Sequence 11, Appl	796	163	4.1	2917	4	US-09-902-775A-189	Sequence 189, App
724	171.5	4.3	682	3	US-09-163-951-13	Sequence 13, Appl	797	163	4.1	2917	4	US-09-906-700-189	Sequence 189, App
725	171.5	4.3	682	3	US-09-345-881-13	Sequence 13, Appl	798	163	4.1	2917	4	US-09-903-603A-189	Sequence 189, App
726	171.5	4.3	778	3	US-08-906-769-189	Sequence 189, App	799	163	4.1	2917	4	US-09-904-920A-189	Sequence 189, App
727	171.5	4.3	778	3	US-08-906-616-189	Sequence 189, App	800	163	4.1	2917	4	US-09-909-064-189	Sequence 189, App
728	171.5	4.3	778	3	US-08-639-075A-189	Sequence 189, App	801	163	4.1	2917	4	US-09-905-381A-189	Sequence 189, App
729	171.5	4.3	778	3	US-09-004-731-84	Sequence 84, Appl	802	163	4.1	2917	4	US-09-906-618-189	Sequence 189, App
730	171.5	4.3	778	3	US-09-012-431-189	Sequence 189, App	803	162.5	4.1	873	4	US-09-949-016-3201	Sequence 3201, Ap
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732	171.5	4.3	778	3	US-09-012-692-189	Sequence 189, App	805	162	4.1	2055	3	US-08-872-855-3	Sequence 3, Appli
733	171.5	4.3	778	3	US-08-906-612-189	Sequence 189, App	806	162	4.1	2055	4	US-09-641-612-10	Sequence 10, Appl
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737	171	4.3	864	4	US-09-270-767-16916	Sequence 16916, A	810	161.5	4.1	884	2	US-09-213-390-2	Sequence 2, Appli
738	171	4.3	1253	3	US-09-949-016-2295	Sequence 2295, Ap	811	161.5	4.1	1265	3	US-09-020-956-173	Sequence 173, App
739	171	4.3	1406	4	US-09-949-016-5325	Sequence 5325, Ap	812	161.5	4.1	1265	3	US-09-030-607-173	Sequence 173, App
740	171	4.3	2154	4	US-09-601-040A-5	Sequence 5, Appli	813	161.5	4.1	1285	3	US-09-439-313-173	Sequence 173, App
741	171	4.3	2190	4	US-09-601-040A-1	Sequence 1, Appli	814	161.5	4.1	1265	3	US-09-352-616A-173	Sequence 173, App
742	170	4.3	641	3	US-08-906-769-148	Sequence 148, App	815	161.5	4.1	1265	3	US-09-232-149A-173	Sequence 173, App

816	161.5	4.1	1265	4	US-09-159-812-173	Sequence 173, App	889	157	4.0	610	3	US-09-012-692-140	Sequence 140, App
817	161.5	4.1	1265	4	US-09-636-215-173	Sequence 173, App	890	157	4.0	610	3	US-08-906-613-140	Sequence 140, App
818	161.5	4.1	1265	4	US-09-685-166A-173	Sequence 173, App	891	157	4.0	1148	4	US-09-270-767-13591	Sequence 13591, A
819	161.5	4.1	1265	4	US-09-115-453-173	Sequence 173, App	892	157	4.0	3862	4	US-09-949-016-4401	Sequence 4401, App
820	161.5	4.1	1265	4	US-09-688-489-173	Sequence 173, App	893	157	4.0	3863	4	US-08-482-073-1	Sequence 1, Appli
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832	160.5	4.1	725	3	US-09-664-595A-12	Sequence 12, Appli	905	156	4.0	711	3	US-09-100-264-2	Sequence 2, Appli
833	160.5	4.1	2186	4	US-09-949-016-4905	Sequence 4905, Ap	906	156	4.0	711	4	US-08-843-076D-2	Sequence 2, Appli
834	160.5	4.1	2186	4	US-09-949-016-286	Sequence 286, App	907	156	4.0	760	3	US-08-768-859A-7	Sequence 7, Appli
835	160.5	4.1	3042	4	US-09-919-039-100	Sequence 100, App	908	156	4.0	760	3	US-08-767-820A-7	Sequence 7, Appli
836	160	4.1	900	4	US-09-949-016-4841	Sequence 4841, App	909	156	4.0	760	5	PCT-US95-06157-7	Sequence 7, Appli
837	159.5	4.0	875	4	US-09-270-767-419	Sequence 419, App	910	156	4.0	766	3	US-08-768-859A-9	Sequence 9, Appli
838	159.5	4.0	875	4	US-09-270-767-15701	Sequence 15701, A	911	156	4.0	766	3	US-08-767-820A-9	Sequence 9, Appli
839	159.5	4.0	12183	4	US-09-902-540-1066	Sequence 1066, Ap	912	156	4.0	766	3	US-08-622-046B-6	Sequence 6, Appli
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841	159	4.0	1507	4	US-09-949-016-1840	Sequence 1840, Ap	914	156	4.0	766	3	US-09-100-264-6	Sequence 6, Appli
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847	159	4.0	2857	4	US-09-908-322-4	Sequence 4, Appli	920	155.5	3.9	6951	4	US-09-023-655-1265	Sequence 1265, Ap
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849	159	4.0	2892	1	US-08-083-590A-1	Sequence 1, Appli	922	154.5	3.9	998	1	US-08-553-516-1	Sequence 1, Appli
850	159	4.0	2892	1	US-08-465-500-5	Sequence 5, Appli	923	154.5	3.9	998	2	US-08-238-130-1	Sequence 1, Appli
851	159	4.0	2892	2	US-08-346-126-5	Sequence 5, Appli	924	154.5	3.9	998	3	US-08-821-926-3	Sequence 3, Appli
852	159	4.0	2892	2	US-08-346-128-5	Sequence 5, Appli	925	154.5	3.9	998	3	US-08-816-915-3	Sequence 3, Appli
853	159	4.0	2892	3	US-08-532-384-1	Sequence 1, Appli	926	154.5	3.9	998	5	PCT-US95-07743-3	Sequence 3, Appli
854	159	4.0	2892	3	US-08-893-828-5	Sequence 5, Appli	927	154.5	3.9	1498	4	US-09-919-039-99	Sequence 99, Appli
855	158	4.0	832	3	US-09-100-264-8	Sequence 8, Appli	928	154.5	3.9	6951	6	5256642-1	Patent No. 5256642
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859	158	4.0	832	3	US-08-767-820A-20	Sequence 20, Appli	932	154	3.9	744	3	US-09-032-215-39	Sequence 39, Appli
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861	158	4.0	832	3	US-08-622-046B-15	Sequence 15, Appli	934	154	3.9	782	4	US-09-229-151C-9	Sequence 9, Appli
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863	158	4.0	832	5	PCT-US95-06157-5	Sequence 5, Appli	936	154	3.9	839	4	US-09-229-151C-8	Sequence 8, Appli
864	158	4.0	1341	3	US-08-983-075D-6	Sequence 6, Appli	937	154	3.9	841	3	US-09-032-215-36	Sequence 36, Appli
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866	158	4.0	5329	4	US-09-562-702A-19	Sequence 19, Appli	939	154	3.9	896	4	US-09-023-655-1309	Sequence 1309, Ap
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871	157.5	4.0	894	3	US-08-906-616-90	Sequence 90, Appli	944	154	3.9	1476	3	US-09-210-084-2	Sequence 2, Appli
872	157.5	4.0	894	3	US-08-817-795-90	Sequence 90, Appli	945	153.5	3.9	599	3	US-08-705-875A-2	Sequence 2, Appli
873	157.5	4.0	894	3	US-08-639-075A-90	Sequence 90, Appli	946	153.5	3.9	599	3	US-09-242-999-2	Sequence 2, Appli
874	157.5	4.0	894	3	US-09-012-431-90	Sequence 90, Appli	947	153.5	3.9	1059	4	US-09-902-540-2450	Sequence 2450, Ap
875	157.5	4.0	894	3	US-09-012-692-90	Sequence 90, Appli	948	153.5	3.9	1364	3	US-09-280-116-20	Sequence 20, Appli
876	157.5	4.0	894	3	US-08-906-613-90	Sequence 90, Appli	949	153.5	3.9	1833	1	US-08-365-470-2	Sequence 2, Appli
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880	157.5	4.0	2259	3	US-09-430-854-3	Sequence 3, Appli	953	153.5	3.9	3834	4	US-09-209-668-18	Sequence 18, Appli
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882	157.5	4.0	5420	6	5472939-3	Patent No. 5472939	955	153.5	3.9	3854	1	US-08-365-470-1	Sequence 1, Appli
883	157.5	4.0	5420	6	5256642-3	Patent No. 5256642	956	153.5	3.9	3858	4	US-08-344-155C-98	Sequence 98, Appli
884	157.5	4.0	5420	6	5472939-3	Patent No. 5472939	957	153.5	3.9	3858	4	US-09-009-490A-88	Sequence 88, Appli
885	157	4.0	610	3	US-08-906-769-140	Sequence 140, App	958	153.5	3.9	30371	4	US-09-949-016-15395	Sequence 15395, A
886	157	4.0	610	3	US-08-906-616-140	Sequence 140, App	959	153	3.9	1358	3	US-08-983-075D-8	Sequence 8, Appli
887	157	4.0	610	3	US-08-639-075A-140	Sequence 140, App	960	153	3.9	5561	1	US-08-400-159-1	Sequence 1, Appli
888	157	4.0	610	3	US-09-012-431-140	Sequence 140, App	961	153	3.9	5561	3	US-08-611-729A-1	Sequence 1, Appli

962	153	3.9	5561	4	US-09-195-524-1	Sequence 1, Appli	1035	147.5	3.7	758	3	US-09-012-692-126	Sequence 126, App
963	152.5	3.9	1040	4	US-09-023-655-1487	Sequence 1487, Ap	1036	147.5	3.7	758	3	US-08-906-613-126	Sequence 126, App
964	152.5	3.9	1040	4	US-09-949-016-4840	Sequence 4840, Ap	1037	147.5	3.7	493	3	US-09-392-184-20	Sequence 20, Appl
965	152.5	3.9	2272	4	US-09-949-016-5498	Sequence 5498, Ap	1038	147.5	3.7	1361	3	US-09-578-303-1	Sequence 1, Appl1
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967	152.5	3.9	2272	4	US-09-949-016-5500	Sequence 5500, Ap	1040	147.5	3.7	11220	4	US-09-949-016-5061	Sequence 5061, Ap
968	152.5	3.9	2272	4	US-09-949-016-5501	Sequence 5501, Ap	1041	146.5	3.7	1734	3	US-09-484-970B-63	Sequence 63, Appl
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970	152	3.9	841	3	US-08-906-616-110	Sequence 110, App	1043	146	3.7	779	3	US-08-906-616-80	Sequence 80, Appl
971	152	3.9	841	3	US-08-817-795-110	Sequence 110, App	1044	146	3.7	779	3	US-08-817-795-80	Sequence 80, Appl
972	152	3.9	841	3	US-08-639-075A-110	Sequence 110, App	1045	146	3.7	779	3	US-08-639-075A-80	Sequence 80, Appl
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974	152	3.9	841	3	US-09-012-692-110	Sequence 110, App	1047	146	3.7	779	3	US-09-012-692-80	Sequence 80, Appl
975	152	3.9	841	3	US-08-906-613-110	Sequence 110, App	1048	146	3.7	779	3	US-08-906-613-80	Sequence 80, Appl
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977	152	3.9	882	4	US-09-949-016-4790	Sequence 4790, Ap	1050	146	3.7	789	4	US-09-653-813-3	Sequence 5, Appl1
978	152	3.9	882	4	US-09-023-655-1150	Sequence 1150, Ap	1051	146	3.7	789	4	US-09-653-813-5	Sequence 5, Appl1
979	152	3.9	920	4	US-09-949-016-586	Sequence 586, App	1052	145.5	3.7	850	3	US-08-906-769-102	Sequence 102, App
980	152	3.9	3934	4	US-09-023-655-1066	Sequence 1066, Ap	1053	145.5	3.7	850	3	US-08-906-616-102	Sequence 102, App
981	151.5	3.8	781	4	US-09-949-016-5083	Sequence 5083, Ap	1054	145.5	3.7	850	3	US-08-817-795-102	Sequence 102, App
982	151.5	3.8	5433	4	US-09-562-702A-15	Sequence 15, Appl	1055	145.5	3.7	850	3	US-08-639-075A-102	Sequence 102, App
983	151.5	3.8	5433	4	US-09-561-818A-15	Sequence 15, Appl	1056	145.5	3.7	850	3	US-09-012-431-102	Sequence 102, App
984	151.5	3.8	5613	4	US-09-562-702A-13	Sequence 13, Appl	1057	145.5	3.7	850	3	US-09-012-692-102	Sequence 102, App
985	151.5	3.8	5613	4	US-09-561-818A-13	Sequence 13, Appl	1058	145.5	3.7	850	3	US-08-906-613-102	Sequence 102, App
986	151.5	3.8	5613	4	US-09-561-709B-10	Sequence 10, Appl	1059	145.5	3.7	850	5	PCT-US95-14442A-102	Sequence 102, App
987	151	3.8	2330	1	US-08-481-803-1	Sequence 1, Appli	1060	145	3.7	36755	4	US-09-949-016-16994	Sequence 16994, A
988	151	3.8	2330	1	US-08-215-366A-1	Sequence 1, Appli	1061	145	3.7	38059	4	US-09-328-925-4	Sequence 4, Appli
989	151	3.8	2330	1	US-08-340-539A-1	Sequence 1, Appli	1062	144.5	3.7	769	3	US-09-331-709-1	Sequence 1, Appl1
990	151	3.8	2330	2	US-08-461-592B-1	Sequence 1, Appli	1063	144.5	3.7	774	3	US-09-004-731-18	Sequence 18, Appl
991	150.5	3.8	1414	1	US-08-024-868-1	Sequence 1, Appli	1064	144.5	3.7	774	3	US-09-004-731-20	Sequence 20, Appl
992	150.5	3.8	1414	2	US-08-242-097-1	Sequence 1, Appli	1065	144.5	3.7	774	3	US-08-749-699-18	Sequence 18, Appl
993	150.5	3.8	1414	3	US-09-206-695-1	Sequence 1, Appli	1066	144.5	3.7	774	3	US-08-749-699-20	Sequence 20, Appl
994	150.5	3.8	1414	4	US-09-799-118-1	Sequence 1, Appli	1067	144.5	3.7	774	3	US-09-004-729-18	Sequence 18, Appl
995	150.5	3.8	2214	6	US-08-513-278-3	Sequence 3, Appli	1068	144.5	3.7	774	3	US-09-004-729-20	Sequence 20, Appl
996	150.5	3.8	2214	6	5514582-3	Patent No. 5514582	1069	144.5	3.7	1089	3	US-09-004-731-15	Sequence 15, Appl
997	150.5	3.8	2214	6	5514582-3	Patent No. 5514582	1070	144.5	3.7	1089	3	US-09-004-731-17	Sequence 17, Appl
998	150	3.8	789	4	US-09-653-813-1	Sequence 1, Appli	1071	144.5	3.7	1089	3	US-08-749-699-15	Sequence 15, Appl
999	150	3.8	2021	1	US-07-882-325A-3	Sequence 3, Appli	1072	144.5	3.7	1089	3	US-08-749-699-17	Sequence 17, Appl
1000	150	3.8	2021	1	US-08-184-012C-3	Sequence 3, Appli	1073	144.5	3.7	1089	3	US-09-004-729-15	Sequence 15, Appl
1001	149.5	3.8	726	3	US-09-032-215-49	Sequence 49, Appl	1074	144.5	3.7	1089	3	US-09-004-729-17	Sequence 17, Appl
1002	149.5	3.8	726	3	US-09-032-215-50	Sequence 50, Appl	1075	144.5	3.7	1109	3	US-09-088-651-1	Sequence 1, Appl1
1003	149.5	3.8	841	3	US-09-032-215-46	Sequence 46, Appl	1076	144.5	3.7	17098	4	US-09-949-016-13119	Sequence 13119, A
1004	149.5	3.8	841	3	US-09-032-215-48	Sequence 48, Appl	1077	144	3.7	490	4	US-09-370-767-29595	Sequence 29595, A
1005	149.5	3.8	881	4	US-09-669-751-112	Sequence 112, App	1078	143.5	3.6	601	4	US-09-949-016-121483	Sequence 121483, A
1006	149.5	3.8	19253	4	US-09-949-016-15131	Sequence 15131, A	1079	143.5	3.6	6101	4	US-09-949-016-1376	Sequence 1376, Ap
1007	149	3.8	840	1	US-07-906-983-1	Sequence 1, Appli	1080	143.5	3.6	7017	4	US-09-949-016-67	Sequence 67, Appl
1008	149	3.8	917	4	US-09-799-451-516	Sequence 516, App	1081	143	3.6	711	3	US-09-004-731-21	Sequence 21, Appl
1009	149	3.8	2385	4	US-09-495-050A-292	Sequence 292, App	1082	143	3.6	711	3	US-08-749-699-21	Sequence 21, Appl
1010	149	3.8	2621	4	US-09-949-016-1377	Sequence 1377, Ap	1083	143	3.6	711	3	US-09-004-729-21	Sequence 21, Appl
1011	148.5	3.8	717	3	US-09-004-731-43	Sequence 43, Appl	1084	143	3.6	2354	4	US-09-023-655-1154	Sequence 1154, Ap
1012	148.5	3.8	717	3	US-09-004-731-45	Sequence 45, Appl	1085	143	3.6	3737	4	US-09-747-371-1	Sequence 1, Appli
1013	148.5	3.8	717	3	US-08-749-699-43	Sequence 43, Appl	1086	142.5	3.6	681	1	US-07-529-198-5	Sequence 5, Appli
1014	148.5	3.8	717	3	US-08-749-699-45	Sequence 45, Appl	1087	142.5	3.6	942	4	US-09-636-382A-3	Sequence 3, Appl1
1015	148.5	3.8	717	3	US-09-004-729-43	Sequence 43, Appl	1088	142.5	3.6	1980	1	US-08-278-630A-12	Sequence 12, Appl
1016	148.5	3.8	717	3	US-09-004-729-45	Sequence 45, Appl	1089	142	3.6	649	3	US-08-824-692-21	Sequence 21, Appl
1017	148.5	3.8	841	3	US-09-004-731-40	Sequence 40, Appl	1090	142	3.6	1848	3	US-09-475-460A-31	Sequence 31, Appl
1018	148.5	3.8	841	3	US-09-004-731-42	Sequence 42, Appl	1091	142	3.6	1848	3	US-09-748-061A-31	Sequence 31, Appl
1019	148.5	3.8	841	3	US-08-749-699-40	Sequence 40, Appl	1092	142	3.6	2397	2	US-08-978-404B-2	Sequence 2, Appli
1020	148.5	3.8	841	3	US-08-749-699-42	Sequence 42, Appl	1093	142	3.6	3173	4	US-09-799-451-428	Sequence 428, App
1021	148.5	3.8	841	3	US-09-004-729-40	Sequence 40, Appl	1094	141.5	3.6	1464	3	US-09-188-930-255	Sequence 255, App
1022	148.5	3.8	841	3	US-09-004-729-42	Sequence 42, Appl	1095	141.5	3.6	1464	3	US-09-312-283C-255	Sequence 255, App
1023	148.5	3.8	921	4	US-09-902-540-1978	Sequence 1978, Ap	1096	141.5	3.6	1633	3	US-09-188-930-73	Sequence 73, Appl
1024	148.5	3.8	15572	4	US-09-902-540-1131	Sequence 1131, Ap	1097	141.5	3.6	1635	4	US-09-012-283C-73	Sequence 73, Appl
1025	148	3.8	1878	2	US-08-435-149-17	Sequence 17, Appl	1098	141	3.6	1119	3	US-09-020-956-177	Sequence 177, App
1026	148	3.8	2070	4	US-09-949-016-5494	Sequence 5494, Ap	1099	141	3.6	1119	3	US-09-030-607-177	Sequence 177, App
1027	148	3.8	2070	4	US-09-949-016-5495	Sequence 5495, Ap	1100	141	3.6	1119	3	US-09-439-313-177	Sequence 177, App
1028	148	3.8	2070	4	US-09-949-016-5496	Sequence 5496, Ap	1101	141	3.6	1119	3	US-09-352-616A-177	Sequence 177, App
1029	148	3.8	2070	4	US-09-949-016-5497	Sequence 5497, Ap	1102	141	3.6	1119	3	US-09-232-149A-177	Sequence 177, App
1030	148	3.8	8378	5	PCT-US91-09055-1	Sequence 1, Appli	1103	141	3.6	1119	4	US-09-159-812-177	Sequence 177, App
1031	147.5	3.7	758	3	US-08-906-769-126	Sequence 126, App	1104	141	3.6	1119	4	US-09-636-215-177	Sequence 177, App
1032	147.5	3.7	758	3	US-08-906-616-126	Sequence 126, App	1105	141	3.6	1119	4	US-09-685-166A-177	Sequence 177, App
1033	147.5	3.7	758	3	US-08-639-075A-126	Sequence 126, App	1106	141	3.6	1119	4	US-09-115-453-177	Sequence 177, App
1034	147.5	3.7	758	3	US-09-012-431-126	Sequence 126, App	1107	141	3.6	1119	4	US-09-688-489-177	Sequence 177, App

1108	141	3.6	1119	4	US-09-679-426-177	Sequence 177, App	1181	135.5	3.4	80161	3	US-09-370-700-1	Sequence 1, Appli
1109	141	3.6	1119	4	US-09-759-443-177	Sequence 177, App	1182	135.5	3.4	80161	4	US-09-603-207-1	Sequence 1, Appli
1110	141	3.6	1119	4	US-09-651-236-177	Sequence 177, App	1183	135	3.4	716	4	US-09-423-753-11	Sequence 11, Appl
1111	141	3.6	1129	4	US-09-799-451-471	Sequence 471, App	1184	134.5	3.4	4758	3	US-09-191-647-1	Sequence 1, Appli
1112	141	3.6	1187	4	US-10-000-489-105	Sequence 105, App	1185	134.5	3.4	4758	3	US-09-540-245A-1	Sequence 1, Appli
1113	140	3.5	857	4	US-09-023-655-1046	Sequence 1046, Ap	1186	134.5	3.4	4758	4	US-09-540-153-1	Sequence 1, Appli
1114	140	3.5	857	4	US-09-949-016-4791	Sequence 4791, Ap	1187	134.5	3.4	5933	4	US-09-919-172-23	Sequence 23, Appl
1115	139.5	3.5	768	3	US-09-032-215-34	Sequence 34, Appl	1188	134.5	3.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
1116	139.5	3.5	792	3	US-09-244-111-31	Sequence 31, Appli	1189	134.5	3.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
1117	139.5	3.5	932	3	US-09-032-215-31	Sequence 31, Appl	1190	134	3.4	1638	1	US-08-253-155A-1	Sequence 1, Appli
1118	139.5	3.5	3448	4	US-09-799-451-34	Sequence 34, Appl	1191	134	3.4	1785	4	US-09-148-545-112	Sequence 112, App
1119	139	3.5	923	3	US-08-906-769-144	Sequence 144, App	1192	134	3.4	2430	2	US-08-820-170A-35	Sequence 35, Appl
1120	139	3.5	923	3	US-08-906-616-144	Sequence 144, App	1193	134	3.4	2430	3	US-09-055-699-35	Sequence 35, Appl
1121	139	3.5	923	3	US-08-639-075A-144	Sequence 144, App	1194	134	3.4	2430	3	US-09-273-565-35	Sequence 35, Appl
1122	139	3.5	923	3	US-09-004-731-66	Sequence 66, Appl	1195	134	3.4	2430	3	US-09-565-538-35	Sequence 35, Appl
1123	139	3.5	923	3	US-09-012-431-144	Sequence 144, App	1196	134	3.4	2430	3	US-09-661-468-35	Sequence 35, Appl
1124	139	3.5	923	3	US-08-749-699-66	Sequence 66, Appl	1197	134	3.4	2430	4	US-09-976-165-35	Sequence 35, Appl
1125	139	3.5	923	3	US-09-012-692-144	Sequence 144, App	1198	134	3.4	2977	2	US-08-820-170A-36	Sequence 36, Appl
1126	139	3.5	923	3	US-08-906-613-144	Sequence 144, App	1199	134	3.4	2977	3	US-09-055-699-36	Sequence 36, Appl
1127	139	3.5	923	3	US-09-004-729-66	Sequence 66, Appl	1200	134	3.4	2977	3	US-09-273-565-36	Sequence 36, Appl
1128	139	3.5	1205	4	US-09-976-594-457	Sequence 457, App	1201	134	3.4	2977	3	US-09-565-538-36	Sequence 36, Appl
1129	139	3.5	1333	1	US-08-684-862-9	Sequence 9, Appli	1202	134	3.4	2977	3	US-09-661-468-36	Sequence 36, Appl
1130	138.5	3.5	681	1	US-07-929-198-1	Sequence 1, Appli	1203	134	3.4	2977	4	US-09-976-165-36	Sequence 36, Appl
1131	138.5	3.5	769	4	US-09-023-655-1039	Sequence 1039, Ap	1204	133.5	3.4	654	3	US-09-380-116-57	Sequence 57, Appl
1132	138.5	3.5	4080	4	US-09-016-434-1326	Sequence 1326, Ap	1205	133.5	3.4	767	3	US-08-824-692-25	Sequence 25, Appl
1133	138.5	3.5	5645	4	US-09-023-655-1319	Sequence 1319, Ap	1206	133.5	3.4	5499	3	US-08-479-722B-1	Sequence 1, Appli
1134	138.5	3.5	5681	4	US-09-919-172-58	Sequence 58, Appl	1207	133.5	3.4	5499	4	US-09-592-685-1	Sequence 1, Appli
1135	138	3.5	855	3	US-08-906-769-130	Sequence 130, App	1208	133.5	3.4	5502	5	PCT-US95-02251-17	Sequence 17, Appl
1136	138	3.5	855	3	US-08-906-616-130	Sequence 130, App	1209	133.5	3.4	6811	3	US-08-651-472-67	Sequence 67, Appl
1137	138	3.5	855	3	US-08-639-075A-130	Sequence 130, App	1210	133.5	3.4	6811	3	US-08-358-928-67	Sequence 67, Appl
1138	138	3.5	855	3	US-09-012-431-130	Sequence 130, App	1211	133.5	3.4	7263	4	US-09-561-818A-31	Sequence 31, Appl
1139	138	3.5	855	3	US-09-012-692-130	Sequence 130, App	1212	133.5	3.4	7263	4	US-09-562-702A-27	Sequence 27, Appl
1140	138	3.5	855	3	US-08-906-613-130	Sequence 130, App	1213	133.5	3.4	7554	4	US-09-562-702A-29	Sequence 29, Appl
1141	137	3.5	699	1	US-08-738-413B-8	Sequence 8, Appli	1214	133.5	3.4	7554	4	US-09-561-818A-25	Sequence 25, Appl
1142	137	3.5	785	4	US-09-270-767-1349	Sequence 1349, Ap	1215	133	3.4	6049	4	US-08-793-273C-3	Sequence 3, Appli
1143	137	3.5	785	4	US-09-270-767-16631	Sequence 16631, A	1216	133	3.4	6049	5	PCT-US95-1168A-3	Sequence 3, Appli
1144	137	3.5	1213	4	US-09-270-767-12797	Sequence 12797, A	1217	132.5	3.4	865	4	US-09-270-767-1549	Sequence 1549, Ap
1145	137	3.5	2259	2	US-08-513-278-1	Sequence 1, Appli	1218	132.5	3.4	865	4	US-09-270-767-16831	Sequence 16831, A
1146	137	3.5	6153	2	US-08-347-594A-1	Sequence 1, Appli	1219	132.5	3.4	1545	4	US-09-270-767-1178	Sequence 1178, Ap
1147	137	3.5	6942	2	US-08-460-309-3	Sequence 3, Appli	1220	132.5	3.4	1545	4	US-09-270-767-16460	Sequence 16460, A
1148	137	3.5	6942	2	US-08-125-077-3	Sequence 3, Appli	1221	132	3.3	504	4	US-09-636-215-839	Sequence 839, App
1149	137	3.5	9419	4	US-09-562-702A-7	Sequence 7, Appli	1222	132	3.3	504	4	US-09-585-166A-839	Sequence 839, App
1150	137	3.5	9420	4	US-09-562-702A-3	Sequence 3, Appli	1223	132	3.3	504	4	US-09-679-426-839	Sequence 839, App
1151	137	3.5	9534	4	US-09-562-702A-5	Sequence 5, Appli	1224	132	3.3	504	4	US-09-759-143-839	Sequence 839, App
1152	137	3.5	9534	4	US-09-561-709B-8	Sequence 8, Appli	1225	132	3.3	504	4	US-09-651-236-839	Sequence 839, App
1153	137	3.5	9534	4	US-09-917-254-35	Sequence 35, Appl	1226	132	3.3	1448	3	US-09-130-491-9	Sequence 9, Appli
1154	137	3.5	9534	4	US-09-949-016-66	Sequence 66, Appli	1227	132	3.3	2481	3	US-09-188-930-64	Sequence 64, Appl
1155	137	3.5	9535	4	US-09-562-702A-1	Sequence 1, Appli	1228	132	3.3	2481	3	US-09-312-283C-64	Sequence 64, Appl
1156	137	3.5	9537	4	US-09-949-016-1646	Sequence 1646, Ap	1229	131.5	3.3	1109	3	US-09-088-651-6	Sequence 6, Appli
1157	136.5	3.5	493	3	US-09-280-116-191	Sequence 116, App	1230	131.5	3.3	1787	1	US-08-278-630A-13	Sequence 13, Appl
1158	136.5	3.5	681	1	US-07-929-198-3	Sequence 3, Appli	1231	131.5	3.3	6642	1	US-08-727-034-5	Sequence 5, Appli
1159	136.5	3.5	9391	4	US-09-562-702A-11	Sequence 11, Appli	1232	131.5	3.3	6843	1	US-08-727-034-6	Sequence 6, Appli
1160	136.5	3.5	9511	4	US-09-562-702A-9	Sequence 9, Appli	1233	131.5	3.3	6868	4	US-09-919-039-39	Sequence 39, Appl
1161	136.5	3.5	85368	4	US-09-949-016-12211	Sequence 12211, A	1234	131	3.3	3460	2	US-08-751-305-1	Sequence 1, Appli
1162	136	3.4	933	3	US-09-280-116-191	Sequence 116, App	1235	131	3.3	6639	1	US-08-727-034-1	Sequence 1, Appli
1163	136	3.4	4948	4	US-09-562-702A-23	Sequence 23, Appl	1236	131	3.3	6961	1	US-08-727-034-2	Sequence 2, Appli
1164	136	3.4	4948	4	US-09-561-818A-23	Sequence 23, Appl	1237	131	3.3	40261	4	US-09-949-016-11773	Sequence 11773, A
1165	136	3.4	4972	4	US-09-562-702A-27	Sequence 27, Appl	1238	131	3.3	40265	4	US-09-949-016-16168	Sequence 16168, A
1166	136	3.4	5306	4	US-09-562-702A-21	Sequence 21, Appl	1239	130.5	3.3	860	1	US-08-310-416A-19	Sequence 19, Appl
1167	136	3.4	5306	4	US-09-561-818A-21	Sequence 21, Appl	1240	130.5	3.3	860	2	US-08-888-171-19	Sequence 19, Appl
1168	136	3.4	5330	4	US-09-562-702A-25	Sequence 25, Appl	1241	130.5	3.3	969	2	US-08-310-416A-12	Sequence 12, Appl
1169	136	3.4	6153	3	US-08-463-682-2	Sequence 2, Appli	1242	130.5	3.3	969	2	US-08-888-171-12	Sequence 12, Appl
1170	135.5	3.4	768	3	US-09-032-215-35	Sequence 35, Appl	1243	130.5	3.3	1117	4	US-09-148-545-54	Sequence 54, Appl
1171	135.5	3.4	932	3	US-08-906-769-88	Sequence 88, Appl	1244	130.5	3.3	2017	4	US-09-844-311-1	Sequence 1, Appli
1172	135.5	3.4	932	3	US-08-906-616-88	Sequence 88, Appl	1245	130.5	3.3	2056	1	US-08-458-084-1	Sequence 1, Appli
1173	135.5	3.4	932	3	US-08-817-795-88	Sequence 88, Appl	1246	130.5	3.3	2056	1	US-08-205-508-1	Sequence 1, Appli
1174	135.5	3.4	932	3	US-08-639-075A-88	Sequence 88, Appl	1247	130.5	3.3	2096	1	US-08-278-630A-10	Sequence 10, Appl
1175	135.5	3.4	932	3	US-09-012-431-88	Sequence 88, Appl	1248	130.5	3.3	2096	5	PCT-US95-02945-1	Sequence 1, Appli
1176	135.5	3.4	932	3	US-09-032-215-33	Sequence 33, Appl	1249	130.5	3.3	2847	3	US-08-087-007-2	Sequence 2, Appli
1177	135.5	3.4	932	3	US-09-012-692-88	Sequence 88, Appl	1250	130.5	3.3	2847	3	US-08-483-433-2	Sequence 2, Appli
1178	135.5	3.4	932	3	US-08-906-613-88	Sequence 88, Appl	1251	130.5	3.3	2847	5	PCT-US92-05920-2	Sequence 2, Appli
1179	135.5	3.4	932	5	PCT-US95-1444A-88	Sequence 88, Appl	1252	130.5	3.3	5191	1	US-08-340-428B-1	Sequence 1, Appli
1180	135.5	3.4	80161	3	US-09-036-987A-1	Sequence 1, Appli	1253	130.5	3.3	5191	5	PCT-US93-07306-1	Sequence 1, Appli

1254	130	3.3	433	3	US-08-906-769-152	Sequence 152, App	1327	127	3.2	1760	4	US-09-495-050A-139	Sequence 139, App
1255	130	3.3	433	3	US-08-906-616-152	Sequence 152, App	1328	127	3.2	5683	4	US-09-845-583A-7	Sequence 7, Appli
1256	130	3.3	433	3	US-08-639-075A-152	Sequence 152, App	1329	127	3.2	5683	4	US-09-917-254-36	Sequence 36, Appl
1257	130	3.3	433	3	US-09-004-731-80	Sequence 80, Appl	1330	127	3.2	5683	4	US-09-814-915A-78	Sequence 78, Appl
1258	130	3.3	433	3	US-08-412-431-152	Sequence 152, App	1331	126.5	3.2	5184	4	US-09-845-583A-9	Sequence 9, Appli
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## RESULT 2

US-10-067-422-2  
; Sequence 2, Application US/10067422  
; Patent No. 6743613  
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## RESIST. 3

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US-09-620-312D-1006
; Sequence 1006, Application US/09620312D
; Patent No. 6569662
;
GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
;
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
;
FILE REFERENCE: Polypeptides
;
CURRENT APPLICATION NUMBER: US/09/620,312D
;
CURRENT FILING DATE: 2000-07-19
;
PRIOR APPLICATION NUMBER: 09/552,317
;
PRIOR FILING DATE: 2000-04-25
;
PRIOR APPLICATION NUMBER: 09/488,725
;
PRIOR FILING DATE: 2000-01-21
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NUMBER OF SEQ ID NOS: 1105
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SOFTWARE: Pt-FL_genes Version 1.0
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ORGANISM: Homo sapiens
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FEATURE:
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NAME/KEY: CDS
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LOCATION: (528)..(1604)
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US-09-620-312D-1006

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## RESULT 4

US-09-620-312D-969  
; Sequence 969, Application US/09620312D  
; Patent No. 659662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunging  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghaast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: Pct\_Fl\_genes Version 1.0  
; SEQ ID NO 969  
; LENGTH: 2144  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (528)..(1607)  
US-09-620-312D-969

Alignment Scores:  
Pred. No.: 8,74e-261 Length: 2144  
Score: 2678.50 Matches: 501  
Percent Similarity: 96.72% Conservative: 0  
Best Local Similarity: 96.72% Mismatches: 0  
Query Match: 67.90% Indels: 17  
DB: 4 Gaps: 1

US-10-063-692-38 (1-720) x US-09-620-312D-969 (1-2144)

Qy 220 SerAspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluIleThrAlaCys 239  
Db 51 TCGATGGCTCCAGGAATTTTGACGGTTTCATGCCATTTATGAGGAGATCAGGATGC 110  
Qy 240 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLys 259

Db 111 TCCTCATCCCTTGTGTTTCCATGACGCACGTGGTCTCTTGACAGGCTGATCTTACAAG 170  
Qy 260 CysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeu----- 274  
Db 171 TGTGCTCTGCTTGGCAGGTATCTGGGCAGCGCTGTGAAATCTTCTCGAGGCTGGGAAG 230  
Qy 275 -----LeuGluGluArgAsnCysSerAsp 282  
Db 231 TCCAAGATCAAGCGCTCAGAAAGATTCAATTGCTGTCTCTTGAAGAAAGAAATCTGCTCAG 290  
Qy 283 ProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIleAsnGly 302  
Db 291 CCTGGGGGCCCATCTCAATGGGTACCAAGAAATTAACAGGGGGGCCCTGGGCTTATCAACGGA 350  
Qy 303 ArgHisAlaLysIleGlyThrValValSerPheCysAsnAsnSerTyrValLeuSer 322  
Db 351 CGCCATGCTAAATTTGGCACCGTGGTCTTCTTTTGTAAACAACCTCTATGTTCTTAGT 410  
Qy 323 GlyAsnGluLysArgThrCysGlnGlnAsnGlyGluTyrSerGlyLysGlnProIleCys 342  
Db 411 GGCAATGAGAAAGAACTTGGCCAGCAGAAATGGAGAGTGGTCAGGAAACAGCCCATCTGC 470  
Qy 343 IleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeuProMet 362  
Db 471 ATAANAAGCCTGCCGAGAACCAAGATTTCAGACTCTGGTGAAGAGGAGATTCTCCGATG 530  
Qy 363 GlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerLysGln 382  
Db 531 CAGGTTCACTCAGGAGGAGACACCATTTACACGACTATCTCAGGGGCTTCAGCAGCAG 590  
Qy 383 LysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuProMetGly 402  
Db 591 AAATGCAGAGTGCCTCTACCAAGAACCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGA 650  
Qy 403 TyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArgArgLeu 422  
Db 651 TACCAACATCTGCATACCAGCTCCAGTATGAGTGCATCTCACCCCTTCTACCCCGGCTG 710  
Qy 423 GlySerSerArgArgThrCysLeuArgThrGlyLysTyrSerGlyArgAlaProSerCys 442  
Db 711 GGCAGCAGCAGGAGGACATGCTGAGGACTGGGAAGTGGAGTGGGGGGGACCATCTCTGC 770  
Qy 443 IleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeuArgTyr 462  
Db 771 ATCCCTATCTCGGGGAAATTTGAGAACATCACTGCTCCAAAGACCCAAAGGTTGGCGTGG 830  
Qy 463 ProTyrGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeuHisLys 482  
Db 831 CCGTGGCAGGCAGCCATCTACAGGAGGACGAGCGGGTGCATGACGCGACCTTACACAAG 890  
Qy 483 GlyAlaTyrPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValValAla 502  
Db 891 GGAGCGTGGTTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGTGTGGTGGCT 950  
Qy 503 AlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeuLysVal 522  
Db 951 GCCCACTGTGTTACTGACCTGGGGAAGGTCACTCATCAAGACAGCAGACCTGAAAGTT 1010  
Qy 523 ValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSerLeuGln 542  
Db 1011 GTTTTGGGGAATTTCTACCGGATGATGACCGGATGAGAAGACCATCCAGAGCCTACAG 1070  
Qy 543 IleSerAlaIleIleLeuHisProAsnTyrAspProIleLeuLeuAspAlaAspIleAla 562  
Db 1071 ATTTCTGCTATCAATCTGCATCCCAACTATGACCCCATCTCTGTTGATGCTGATCGCC 1130  
Qy 563 IleLeuLysLeuLeuAspLysAlaArgIleSerThrArgValGlnProIleCysLeuAla 582  
Db 1131 ATCTGAAGCTCTACAGAACGCCGTATCAGCACCCGAGTCCAGCCCATCTCGCTCGCT 1190  
Qy 583 AlaSerArgAspLeuSerThrSerPheGlnGlnSerHisIleThrValAlaGlyTyrAsn 602

Db 1191 GCCAGTCGGGATCTCAGCACTTCCTTCCAGGAGTCCACATCACTCTGGCTGGCTGGAAT 1250  
QY 603 ValLeuAlaaspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValVal 622  
Db 1251 GTCTCGCAGACGTGAGGAGCCCTGGCTTCAAGAAGCACACACTGGGCTCTGGGGTGGTC 1310  
QY 623 SerValValAspSerLeuLeuCysGluGluHisGluAspHisGlyIleProValSer 642  
Db 1311 AGTGTGTGACTTCGGCTGTGTGTGAGGACACATGAGGACCATGGCATCCAGTGAGT 1370  
QY 643 ValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThr 662  
Db 1371 GTCACTGATAAATGTTCTGTGTCAGCTGGGAACCCCACTGCCCCCTTCTGATATCTGCACT 1430  
QY 663 AlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArg 682  
Db 1431 GCAGAGACAGGAGGCATCGCGGTGTGTCTTCCCGGAGAGCATCTCTCGAGCCACGC 1490  
QY 683 TrpHisLeuMetGlyLeuValSerTrpSerTrpAspLysThrCysSerHisArgLeuSer 702  
Db 1491 TGGCATCTGATGGAGCTGTGTGCTGAGCTATGATAAACAATGACCCACAGGCTCTCC 1550  
QY 703 ThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720  
Db 1551 ACTGCCTTCCACAGGTGCTGCCTTTTAAAGACTGGATTGGAAGAAATATGAAA 1604

## RESULT 5

US-09-280-116-179  
; Sequence 179, Application US/09280116A  
; Patent No. 6331427  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
; FILE REFERENCE: 5800-24, 035800/176965  
; CURRENT APPLICATION NUMBER: US/09/280,116A  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 268  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 179  
; LENGTH: 505  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: asticin/m 12a metalloproteases  
US-09-280-116-179

Alignment Scores:  
Pred. No.: 5.5e-81 Length: 505  
Score: 893.00 Matches: 166  
Percent Similarity: 98.81% Conservative: 0  
Best Local Similarity: 98.81% Mismatches: 1  
Query Match: 22.64% Indels: 2  
DB: 3 Gaps: 0

US-10-063-692-38 (1-720) x US-09-280-116-179 (1-505)

QY 103 LeuAspAspPheTrpValLysGlyPheTrpCysAlaGluCysArgAlaGlyTrpTrpGly 122  
Db 3 TTGGATGACTTATGTGAAGGGGTTCTACTGTGCAGAGTCCGAGCAGC-TGGTAGGGA 61  
QY 123 GlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnLeuLeuGlu 142  
Db 62 GGAGACTGCGATGCGATGTGGCCAGTTCTCGAGCCCCCAAGGGTCAAGATTTTGTGGAA 121  
QY 143 SerTrpProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPheValIle 162  
Db 122 AGCTATCCCTAAATGCTCACTGTGAATGACCATTCATGCTAAACCTGGGTTTGTATC 181  
QY 163 GlnLeuArgPheValMetLeuSerLeuGluPheAspTrpMetCysGlnTrpAspTrpVal 182  
Db 182 CAACCTAAGATTTGTGTCATGTTGAGCGCTGGAGTTTGACTACATGTGCCAGTATGACTATGTT 241  
QY 183 GluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsnGlu 202

Db 242 GAGGTTCTGATGGAGACAACCGCGATGCCAGATCATCAAGCGTGTCTGTGGCAACGAG 301  
QY 203 ArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSerAspGly 222  
Db 302 CGGCCAGCTCTCTATCCAGAGCATAGGATCCTCACTCCAGCTCCTCTTCCACTCCGATGGC 361  
QY 223 SerLysAsnPheAspGlyPheHisAlaIleTrpGluGluIleThrAlaCysSerSerSer 242  
Db 362 TCCAGAGATTTTACAGGTTTCCATGTCATTTATGAGGAGATCACAGATGCTCTCATCC 421  
QY 243 ProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTrpLysCysAlaCys 262  
Db 422 CCTGTGTTCCATGAGCGCACGTGCGTCTTGTCAAGGCTGGATCTTTACAAAGTGTGCTG 481  
QY 262 sleuAlaGlyTrpThrGlyGln 269  
Db 482 CTTGGCAGGCTATACTGGGCAG 503

## RESULT 6

US-08-296-014A-3  
; Sequence 3, Application US/08296014A  
; Patent No. 5716834  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/296,014A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1781-105P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3448 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Carinoscorpius rotundicauda  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 18..3074  
US-08-296-014A-3

Alignment Scores: 1.59e-56 Length: 3448  
Pred. No.: 665.00 Matches: 222  
Score:



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QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLeuLeuLeuLeuAla 570
Db 2583 AACTAGACCCCGGCAATCTCAACTTTGACATAGCCCTAATCTCACTGAAACCTCTGTT 2642
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db 2643 ACTTGCACACAGAGTCCACCAATCTGTCTGCTACT-----GACATCAACA--- 2693
QY 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
Db 2694 -----AGAACACACTTGAAGGAGGGAACATTAGCAGTGTGTACAGGTTGGGT----- 2741
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db 2742 -----TTGAATGAAACACACACTATTTCAGAGCAGATTCAACAAGCTGTGTACTCTGTT 2795
QY 625 ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db 2796 GTTGCAGCCAGCACCTGTGNAGAGGGGTACAGAGGAGCAGACTTACCACCTGACAGTAACA 2855
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db 2856 GAGAACATGTTCTGTGAGGTTCACAG-----AAGGAGCAGTTATGATGCTGCGAGTGGGAC 2912
QY 665 ThrGlyGlyIleAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db 2913 AGTGGAGGA-----CCTTTAGTGTGTGTGATGATTCCTGATCCGTAACGAGCGGTGGTC 2966
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db 2967 TTGGAAGGATTTGACGTGGGCGAGTCCAGTGGGATGGGAGGCGAACACAGTACGGG 3026
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db 3027 GGCTTCACTAAAGTAAACGTTTCTGTCTCATGATTAAGCAG 3068

RESULT 7
US-08-596-405-3
; Sequence 3, Application US/08596405
; Patent No. 5858706
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaach & Birch
; STREET: 810 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,405
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 3:
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## SEQUENCE CHARACTERISTICS:

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; LENGTH: 3448 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Carcinoscopus rotundicauda
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 18..3074
; US-08-596-405-3
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## Alignment Scores:

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Pred. No.: 158e-56 Length: 3448
Score: 665.00 Matches: 222
Percent Similarity: 38.90% Conservative: 118
Best Local Similarity: 25.40% Mismatches: 304
Query Match: 16.86% Indels: 230
DB: 2 Gaps: 37
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US-10-063-692-38 (1-720) x US-08-596-405-3 (1-3448)

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Db 567 CCAATGGACAGTGGAGTAACCTTCCACCACCAATGTTATTCGA-----GAATGT 614
QY 54 ValCysProGlyLysArgGlu-----ValVal 62
Db 615 GCCATGGTTTCATCTCCAGAACATGGGAAAGTAATGCTCTTAGTGGTGATATGATAGAA 674
QY 63 GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
Db 675 GGGGCTACTTTA-----CGGTTCTCATGTGATAGT----- 704
QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101
Db 705 CCTACTACTTGTATGGTCAAGAACATTAACCTGTGAGGTAATGTCAGTGAATGGA 764
QY 102 ThrLeu----- 103
Db 765 CAGATACCACATGTAAGAACTTGGTCTTCTGTCTGACCTGGATCCTGTAAACCATGCT 824
QY 103 ----- 103
Db 825 GAACACAAGGTTAAATTTGGTGTGGAAACAAATAATATGGTCAGTTTCTCAAGCAGCTGAA 884
QY 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117
Db 885 GTGACCTATACGTGTTGGGTAACACTACTTCTGATGGGTTTTCACACCTTAAATATGTAAC 944
QY 118 -----AlaGlyTrpTyrGlyGly-----AspCysMetArg----- 127
Db 945 CCTGATGGGTCTTGGTCAGGATCAGCCATCCTGTGTAAAGTGGGAGCAGAGAGGTC 1004
QY 128 -----CysGlyGlnValLeuArg----- 133
Db 1005 GACTGTGACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGAGATCCAC 1064
QY 134 AlapProLysGlyGlnIleLeuLeuGluSer-----TyrPro 145
Db 1065 TGTCTGTGGCTGTTCTTTGACAGCTGGTGTGTGGGTACAGCATATACCATGAA 1124
QY 146 LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
Db 1125 CTTTCTCAGTGTGTGTGAGCAGCATCCATCTGCTGCAAGCTTCCAAACTCTGGAGGAGCG 1184
QY 162 Ile----- 162
Db 1185 GTGCATGTTGTGAACAAATGGCCCTACTCTCGGACTTCTTGGGTAGTACCTGAATGGGATA 1244
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QY 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176  
Db 1245 AAATCGGAAGAGTTGAAGTCTTTCGCCGAGATTTCGCGATTCGATTATGTCCTCCGTTCTCC 1304  
QY 177 -----CysGlnTyrAspTyrValGluValArgAsp----- 186  
Db 1305 ACAGCAGTAATCAGGATGTCCTGATGATGGTTTGGGTAGACGAGAACTGTGTGTAC 1364  
QY 187 -----GlyAspAsnArgAspGlyGlnLeuIleLeuValCysGlyAsn-----Glu 202  
Db 1365 GTTACATCAAAACAGAGAGCCTGGGAAGAGCTCAAGGTGTGTGTACCAATATGGCTGCT 1424  
QY 203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220  
Db 1425 CGTCTGTGCTGGCAAAAGATGTAATCCAAATTCGTTGACTGAGACTCTACGAGGG 1484  
QY 221 AspGly----SerLysAsnPheAspGlyPheHis----- 230  
Db 1485 AAAGGGTTACAAACCAACCGTGGATAGGATTGCACAGACTAGATGCTGAGAAGCCCTTTATT 1544  
QY 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241  
Db 1545 TGGGAGTTAATGATCGTAGTAATGCTGCTGAATGATAACCTAACATTCTGGGCTCT 1604  
QY 242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257  
Db 1605 GCGCAACCTCGAAATGAATCACTGCTGATATATGACATCCCAAGATCATGCTGCTGCT 1664  
QY 258 ---TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGlu 276  
Db 1665 GTGTGGAAACCAAGTCACTGTTTTCAGCCCTCAAGTTTGTCTGCATGATGGATCTGTCA 1724  
QY 277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysLeu 293  
Db 1725 GACAGAAATAAAGCCAAATGCGATGATCTGATCACTGGAAATGACACGCCACACTT 1784  
QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValSerPhe 313  
Db 1785 CATGGCAAAAGT-----ATTGATGGGTCTTCTGCT-----GGTCTCTTAAAGGTAC 1832  
QY 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnAsnGly 333  
Db 1833 AGCTGTGAGTTCTCCACTACCTCAGTGGAACTGAAACCGTAACCTGTACAAACAAATGGC 1892  
QY 334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351  
Db 1893 ACATGGAGTGTCTCTAAACCTCGATGATCAAAAGTCATCACTGCCAAACCCCTCGTA 1952  
QY 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371  
Db 1953 CCATCATATGTTCTGTGGAAATCAAAACCC-----CCAAAGTCGACAAACTCGATA 2003  
QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388  
Db 2004 AGTCGTGTGGTCACTTCTGAGGTGTCACCGGTATCCCTTCCCATATAGCTAGACGA 2063  
QY 389 ThrLysLysProAlaLeuProPheGlyAsp----- 398  
Db 2064 GCCAAACCTCTCCAAACCTAGATCTCACACCTCTACTGTGGACTGGCTTCTAAA 2123  
QY 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416  
Db 2124 GTTAAACTACTGAAGTCAATACCGGTAGGTGCTCGAGCCATCTACAGCTGCGAGTCG 2183  
QY 417 ProPheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436  
Db 2184 AGATACACCAACTACTTGTGATCTCAAGGCGAGAGATGCTCACTTAATGAAACTGGAGT 2243  
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGlyAsnIleThrAlaPro--- 455  
Db 2244 GGTCCGCCAGGAGTGTATTCAGTTTGTGGAGGTGCAGACTCTCTCTCTCTCTCTT 2303  
QY 456 -----LysThrGlnGlyLeuArgTrpProTrpGlnAlaIleTyrArg 470

Db 2304 ATCTGGAATGGGAATTTACAGAAATAGGTGCGCGTGGCAGGAGGAATCTCTAGA 2363  
QY 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490  
Db 2364 TGGCTTGCA-----GACCACATATGTGTGTCTTCACCTGTGGA 2402  
QY 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510  
Db 2403 GGATCTCTATTGAATGAGAAATGATGCTCACTGCTGCCACTGTGCACCTACTCTGCT 2462  
QY 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530  
Db 2463 ACTGCTGAGATTATTGACCCCAATCAGTTTAAATATGATCTGGCAAGTACTACCGTAT 2522  
QY 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550  
Db 2523 GACAGTAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2582  
QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuAspLysAla 570  
Db 2583 AACTACGACCCCGCAATCTCACTTTGACATAGCCCTTAATCACTGAAAACTCTGTT 2642  
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590  
Db 2643 ACTTTGACAAACAGAGTCCAACTAATCTGCTGCTACT-----GACATCAACA 2693  
QY 591 PheGlnLysSerHisIle-----ThrValAlaGlyTyrAsnValLeu 604  
Db 2694 -----AGAAACACTTGAAGAGGAGGACATTAGCAGTGTGACAGTTGGGT----- 2741  
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624  
Db 2742 -----TTGAATGAAACAAACACCTATTACAGACAGGATTCACAAAGCTGTGCTACTGTT 2795  
QY 625 ValAspSerLeuLysGlyGluGlnHisGluAspHisGlyIleProValSerValThr 644  
Db 2796 GTTGCAGCCAGCACCTGTGGAAGAGGGGTACAAAGAGCAGACTTACACCTGACAGTAACA 2855  
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664  
Db 2856 GAGAACATGTTCTGTGCGAGTTACAG-----AAGGAGCTTATGATGCTGCGAGTGGGAC 2912  
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684  
Db 2913 AGTGGAGGA-----CCTTTAGTGTGCTGATGATTCCTGATCCGAAAGCGGTGGTC 2966  
QY 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703  
Db 2967 TTGGAAGGGGATGCTGAGTGGGCGAGTCCAGTGGGATGTGGCAAGCGCAACAGTACGGG 3026  
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717  
Db 3027 GGCTTCACTAAAGTTAACTGTTTCTGCTCATGATTAGGCAG 3069

## RESULT 8

US-08-877-620-3  
; Sequence 3, Application US/08877620  
; Patent No. 5985590  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22042



COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/877,620  
 FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/596,405

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1781-105P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX: 248345

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3448 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Carinoscorpius rotundicauda

FEATURE:

NAME/KEY: CDS

LOCATION: 18..3074

US-08-877-620-3

#### Alignment Scores:

Pred. No.: 1.58e-56 Length: 3448  
 Score: 665.00 Matches: 222  
 Percent Similarity: 38.90% Conservative: 118  
 Best Local Similarity: 25.40% Mismatches: 304  
 Query Match: 16.86% Indels: 230  
 DB: 2 Gaps: 37

US-10-063-692-38 (1-720) x US-08-877-620-3 (1-3448)

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QY 34 ProGlyAlaGluTrpAsnIleMetCysArgGluCysCysGluTrpAspGlnIleGluCys 53
DB 657 CCAATGGACAGTGGAGTAAGTCTTCCACCCCAATGATTTCGA-----GAATGT 614

QY 54 ValCysProGlyLysArgGlu-----ValVal 62
DB 615 GCCATGGTTTCATCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTGATATGATAGAA 674

QY 63 GlyTrpThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82
DB 675 GGGGCTACTTTA-----CGGTTCATGTGATAGT----- 704

QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AenGlySerTrpGlyGly 101
DB 705 CCTTACTACTGATTGTCAGAACAAACATTAACTGTCAAGGTAATGTCAGTGAATGGA 764

QY 102 ThrLeu----- 103
DB 765 CAGATACCACAATGTAAGAACTTGGTCTTCTGCTCGACCTGGATCCTGTAAACCACTGT 824

QY 103 ----- 103
DB 825 GAACACAAGGTTAAATTTGGTGTGGAAACAAAAATATGTCAGTTTCTCAAGGCACGTGAA 884

QY 104 -----AspAspPheTrpValLysGlyPheTrpCysAlaGluCysArg 117
DB 885 GTGACCTATACGTGTTCCGGTAACTACTTCTTGATGGGTTTGTGACACCTTAAATGTAAC 944

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QY 118 -----AlaGlyTrpTrpGlyGly-----AspCysMetArg----- 127
DB 945 CCTGATGGGTCTTGGTCAGGATCACAGCCATCCTGTGTTAAAGTGGCAGACAGAGGTC 1004

QY 128 -----CysGlyGlnValLeuArg----- 133
DB 1005 GACTGTGACAGTAAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGACGATCCAC 1064

QY 134 AlaProLysGlyGlnIleLeuLeuGluSer-----TyrPro 145
DB 1065 TGTCTCTGCTGGCTGTTCTTTGACAGCTGGTACTGTGTGGGTACAGCCATATACCATGAA 1124

QY 146 LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
DB 1125 CTTTCTCAGTGTGTCGTCAGCCATCCATGCTGGCAAGCTTCCAAACTCTGGAGGAGCG 1184

QY 162 Ile----- 162
DB 1185 GTGCATGTTGTGNAACAATGGCCCTACTCGGACTTCTGGGTAGTACCTGTAATGGGATA 1244

QY 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
DB 1245 AAATCGGAAGAGTGAAGTCTCTTGGCCGAGTTCGGATTCGATTGATGTCGTCCTCCTCC 1304

QY 177 -----CysGlnTrpAspTyrValGluValArgAsp----- 186
DB 1305 ACAGCAGGTAATACAGGATGCTCTGATGGATGTTGAGGTAGACAGGAAGACTGTGTGTAC 1364

QY 187 -----GlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsn-----Glu 202
DB 1365 GTTACATCAAAACAGAGAGCCTGGGAAGAGCTCAAGGTGTGTGTTACCAATATGCTGCT 1424

QY 203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
DB 1425 CGTCTTGTCTGTGTCGACAAAGATGTAATTCAAATTCGTTGACTGAGACTTACGAGGG 1484

QY 221 AspGly---SerLysAsnPheAspGlyPheHis----- 230
DB 1485 AAAGGTTTAAACACCACGTTGATAGGATTGCACAGACTAGATCTGAGAGAGCCCTTTATT 1544

QY 231 -----AlaIleTrpGluGluIleThrAlaCysSerSer 241
DB 1545 TGGGAGTTAATGATCGTAGTAATGTGTTCTGAATGATAACCTTAACATTCTGGGCTCT 1604

QY 242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
DB 1605 GGCGAACCTGGAAATGAAACTAACTGTGTATATATGACATCCAAAGATCAGTTGCACTCT 1664

QY 258 ---TyrLysCysAlaCysLeuAlaGlyThrGlyGlnArgCysGluAsnLeuGlu 276
DB 1665 GTGTGAAAACCAAGTCATGTTTTCAGCCCTCAAGTTTCTGATGATGATGATGATGATGAT 1724

QY 277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTrpGlnLysIle 293
DB 1725 GACAGAATAAAGCCAAATGCGATGATCTCTGGATCACTGGAAATGACAGCCACACTT 1784

QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
DB 1785 CATGGACAAAGT-----ATTGATGGGTTCTATGCT-----GGTCTTCTATAAGGTAC 1832

QY 314 PheCysAsnAsnSerTrpValLeuSerGlyAsnGluLysArgThrCysGlnAsnGly 333
DB 1833 AGCTGTGAGGTTCTCCACTTACCTCAGTGGAACTGAAACCCGTAACCTTGTACACAAATGGC 1892

QY 334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
DB 1893 ACATGGAGTCTCTTAAACCTCGATGATCAAAAGTCATCACTGCCAAACCCCTCGTGA 1952

QY 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerGluThrProLeu 371
DB 1953 CCATCATATGTTCTGTGGAAATCAAAACC-----CCAAAGTCGGAACAAATCGATA 2003

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QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388  
DB 2004 AGTCGTGTTGGGTACACCTTTCTTGGAGTTGCCACGGTTACCCCTCCCATTTAGCTAGACGA 2063  
QY 389 ThrLysLysProAlaLeuProPheGlyAsp----- 398  
DB 2064 GCCAAACCTCTCCAAACCTAGATCTCTCAACCCCTACTGTGGACTTGGCTTTCTAAA 2123  
QY 399 -----LeuProMetGlyTyrGlnHisLeuHisLeuHisLeuGlnTyrGluCysIleSer 416  
DB 2124 GTTAAACTACTGAAGGTATTCACGGGTAGGGTCTCGAGCCACTTACACGTGCGAGTCG 2183  
QY 417 ProPheTyrArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTrpSer 436  
DB 2184 AGATACACAACTACTGTGATCTCAAGGCAGAGATGTCACTTAATGGAAATCGAGT 2243  
QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAenIleThrAlaPro--- 455  
DB 2244 GGTGGCCGAGCTGTATTCAGTTTGGACGGTCAGACTCTCTCTCTCTCTCTCTCT 2303  
QY 456 -----LysThrGlnGlyLeuArgTrpProTrpGlnAlaAlaIleTyrArg 470  
DB 2304 ATCTGGAATGGGAATCTCAAGAAATAGGTCACTGGCCGTGGCAGGCAGGAATCTCTAGA 2363  
QY 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490  
DB 2364 TGCGTTGCA-----GACCACAAATATGTGGTTCTCCAGTGGGA 2402  
QY 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510  
DB 2403 GGATCTCTATTGATGAGAAATGGATCGTCACTGCTGCCACCTGTGTCACTACTCTGCT 2462  
QY 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530  
DB 2463 ACTGCTGAGATTATTCACCCCAATCAGTTTAAATGTATCTGGSCAAGTACTACCGTGAT 2522  
QY 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550  
DB 2523 GACAGTAGAGACGACTATGTACAAATAGTCACTGCTGCCACCTGTGTCACTACTCTCT 2582  
QY 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLysAla 570  
DB 2583 AACTAGACCCCGGCAATCTCACTTTGATAGCCCTTAATCTCACTGAAATCTCTGTT 2642  
QY 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590  
DB 2643 ACTTTGACAAACAGAGTCCAAACCAATCTGTCTGCTACT-----GACATCAACA 2693  
QY 591 PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604  
DB 2694 -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGGTTGGGT----- 2741  
QY 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624  
DB 2742 -----TTGAATGAACAAACACTTATTCAGACGATTCACAACTGTGTCTACTCTGTT 2795  
QY 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644  
DB 2796 GTTGACCCAGCAGCTGTGAAGAGGGGTACAAGAGCAGCAGCTTACCACTGACAGTAACA 2855  
QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664  
DB 2856 GAGAACATGTTCTGTGTCAGGTTACAAG---AAGGGACGTTATGATGCTGTCAGTGGGGAC 2912  
QY 665 ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684  
DB 2913 AGTGGAGGA-----CCTTAGTGTGTGTGATGATTCGCGTACCGAAGGCGGTGGTC 2966  
QY 685 LeuMetGlyValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703  
DB 2967 TTGAAGGAGATGTGAGCTGGGCGAGTCCAGTGGGATGGCAGGCGGACCAACGATGACGG 3026  
QY 704 AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717

DB 3027 GGCTTCACTAAAGTTAAACGTTTTCCTGTCTATGATTAGGCAG 3068  
RESULT 9  
US-09-287-368-3  
; Sequence 3, Application US/09287368A  
; Patent No. 6645724  
; GENERAL INFORMATION:  
; APPLICANT: DING, Jeak Ling  
; APPLICANT: HO, Bow  
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin  
; FILE REFERENCE: 1781-0185P  
; CURRENT APPLICATION NUMBER: US/09/287,368A  
; EARLIER FILING DATE: 1999-04-07  
; EARLIER APPLICATION NUMBER: 09/201,786  
; EARLIER FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/081,767  
; EARLIER FILING DATE: 1998-05-21  
; EARLIER APPLICATION NUMBER: 60/058,816  
; EARLIER FILING DATE: 1997-09-19  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3448  
; TYPE: DNA  
; ORGANISM: Carinoscorpius rotundicauda  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (18)..(3074)  
; FEATURE:  
; OTHER INFORMATION: any n or Xaa = Unknown  
US-09-287-368-3  
Alignment Scores:  
Pred. No.: 1,58e-56 Length: 3448  
Score: 665.00 Matches: 222  
Percent Similarity: 38.90% Conservative: 118  
Best Local Similarity: 25.40% Mismatches: 304  
Query Match: 16.86% Indels: 230  
DB: 4 Gaps: 37  
US-10-063-692-38 (1-720) x US-09-287-368-3 (1-3448)  
QY 34 ProGlyValAlaGluTrpAsnIleMetCysArgGluCysCysGluTyrAspGlnIleGluCys 53  
DB 567 CCAATGGACAGTGGAGTAACTTCCACCCAAATGATTCCA-----GAATGT 614  
QY 54 ValCysProGlyLysArgGlu-----ValVal 62  
DB 615 GCCATGGTTTCATCTCCAGAACATGGGAAAGTGAATGCTCTTAGTGGTGATATGATAGAA 674  
QY 63 GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis 82  
DB 675 GGGGCTACTTTA-----CGTTCTCATGTGATAGT----- 704  
QY 83 ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly 101  
DB 705 CCTTACTACTTGTATTGGTCAAGAACATTAACTGTGAGGGTAAATGGTCAGTGGAAATGGA 764  
QY 102 ThrLeu----- 103  
DB 765 CAGATACCACAATGTAAGAACTTGGTCTTCTGTCTGACCTGGATCCTGTAAACCATGCT 824  
QY 103 ----- 103  
DB 825 GAACACAAGGTTAAATTTGGTGTGGAAACAAAATATGGTCAGTTCCTCAAGGCACCTGAA 884  
QY 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117  
DB 885 GTGACCTATACGTGTTCGGGTAACTACTTCTTGTATGGGTTTTCACACCTTAAATGTAAC 944  
QY 118 -----AlaGlyTrpTyrGlyGly-----AspCysMetArg----- 127



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Db      945  CCTGATGGGTCTTGGTCAGGATCACAGCCATCTCTGTGTTAAAGTGCAGACAGAGGTC 1004
QY      128  -----CysGlyGlnValLeuArg----- 133
Db      1005  GACTGTGACAGTAAGCTGTAGACTTCTTGGATGATGTTGGTGAACCTGTGAGGATCCAC 1064
QY      134  AlaProLysGlyGlnLeuLeuGluSer-----TyrPro 145
Db      1065  TGTCTCTGCTGGCTGTTCTTTGACAGCTGTGTACTGTGTGGGTACAGCCATATACCATGAA 1124
QY      146  LeuAsnAlaHisCysGluTrpThrIleHisAla-----LysProGlyPheVal 161
Db      1125  CTTTCTCAGTGTGTGTGTCAGCCATCCATGCTGGCAAGCTTCCAAACTCTGGAGGCG 1184
QY      162  Ile----- 162
Db      1185  GTGCATGTTGTGAACAATGGCCCTACTCGGACTTTCGGGTAGTGACCTGAATGGGATA 1244
QY      163  -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176
Db      1245  AAATCGGAAGATGTAAGTCTCTTGGCCGGAGTTTCCGATTCGATTATGTCTCCCTCTCC 1304
QY      177  -----CysGlnTyrAspTyrValGluValArgAsp----- 186
Db      1305  ACAGCAGGTAAATCAGAGATGCTCTGATGGATGTTGAGGTAGACAGAACTGTGTGTAC 1364
QY      187  -----GlyAspAsnArgAspGlyGlnIleLysArgValCysGlyAsn-----Glu 202
Db      1365  GTTACATCAAAACAGAGAGCCTGGAAAGAGCTCAAGGTGTGTGTACCAATATGGCTGCT 1424
QY      203  ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220
Db      1425  CGTCTTGCTGTGTCGCAAAAGATGTAATTCCAAATTCGTTGACTGAGACTTACGAGGG 1484
QY      221  AspGly---SerLysAsnPheAspGlyPheHis----- 230
Db      1485  AAAGGGTTAAACACCAACCGTGGATGAGTATGCACAGACTAGATCGTGAGAAGCCCTTTAT 1544
QY      231  -----AlaIleTyrGluGluIleThrAlaCysSerSer 241
Db      1545  TGGGAGTTAATGTCGTAGTAATGTGGTTCGTAATGATAACCTTAACATTCCTGGGCTCT 1604
QY      242  SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257
Db      1605  GCGCAACCTCGAAATGAACATAACTGTGTATATATGGACATCCAAGATCAGTTGCACTCT 1664
QY      258  ---TyrLysCysAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuGlu 276
Db      1665  GTGTGGAACCAAGTCATGTTTTCAGCCCTCAAGTTTCTGTCATGATGGATCTGTCA 1724
QY      277  GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293
Db      1725  GACAGAAATAAGCCAAATCGATGATCTCTGGATCACTGGAAAATGGACACGCCACACTT 1784
QY      294  ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313
Db      1785  CATGGCAAAAGT-----ATTGATGGGTTCCTATGCT-----GGTCTCTATAAGGTAC 1832
QY      314  PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333
Db      1833  AGCTGTGAGGTTCTCCACTACCTCAGTGGAACTGAAACCGCTAATCTGTACACAAATGGC 1892
QY      334  GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351
Db      1893  ACATGGAGTCTCTAAACCTCGATGTATCAAAAGTCATCACTGCCAAACCCCTCGTA 1952
QY      352  SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371
Db      1953  CCATCATATGGTCTGTGGAAATCAAAACC-----CCAAGTCGGACAAACTCGATA 2003
QY      372  HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388
Db      2004  AGTCGTGTTGGTCACTTTCTTGTAGGTTGCCACGGTTTACCCCTCCCATTAGCTAGACGA 2063
QY      389  ThrLysLysProAlaLeuProPheGlyAsp----- 398
Db      2064  GCCAAACCTCTCCAAACCTAGATCTCACAAACCTCTACTGTGGACTTGGCTTTCTTAA 2123
QY      399  -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416
Db      2124  GTTAAACTACCTGAGGTCACTTACCGGTATGGGTCTCGAGCCATCTACACGTGCGAGTCG 2183
QY      417  PropheTyrArgArgLeuGlySerSerArgThrCysLeuArgThrGlyLysIlePheSer 436
Db      2184  AGATACTACGAACCTACTTCGATCTCAAGCAGAGATGTGACTCTAATGAAACTGGAGT 2243
QY      437  GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455
Db      2244  GGTCCGCCACGAGCTGTATTCAGGTTTGTGGACGTGACACTCTCTCGTCTCTCTTTT 2303
QY      456  -----LysThrGlnGlyLeuArgTyrProTyrProTyrGlnAlaAlaIleTyrArg 470
Db      2304  ATCTGGAATGGGAATTTCTACAGAAATAGGTCACTGGCCGTGGCAGCAGGAATCTCTAGA 2363
QY      471  ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490
Db      2364  TGGCTTGCA-----GACCACAATATGTGTTTCTCCAGTGTGGA 2402
QY      491  GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510
Db      2403  GGATCTCTATTGAATGAGAAATGGATCGTCACTGTGCCACCTGTGTCACTACTCTGCT 2462
QY      511  LysValThrMetIleLysThrAlaAspLeuLeuValValLeuGlyLysPheTyrArgAsp 530
Db      2463  ACTGCTGAGATTAATGACCCCAATCAGTTTAAATGTATCTGGSCAAGTACTACCTGAT 2522
QY      531  AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro 550
Db      2523  GACAGTAGAGACGACTATGTACAAAGTAAGAGGCTCTTGAGATCCACGTGAATCCT 2582
QY      551  AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuAspLysAla 570
Db      2583  AACTAGACCCCGGCAATCTCACTTTGACATAGCCCTTAATCACTGAAACCTCTGTT 2642
QY      571  ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590
Db      2643  ACTTTGACACACAGATCCAAACCAATCTGTCTGCCTACT-----GACATCAACA 2693
QY      591  PheGlnGluSerHisIle-----ThrValAlaGlyTrpAsnValLeu 604
Db      2694  -----AGAGAACACTTGAAGGAGGGAACATTAGCAGTGTGTGACAGTTGGGGT- 2741
QY      605  AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624
Db      2742  -----TTGAATGAAACCAACACCTTATTCAGACCGAATTCACAAAGCTGTGCTACT 2795
QY      625  ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644
Db      2796  GTTGCAGCCAGCACTGTGAGAGGGGTACAGGAAGCAGACTTACCACCTGACAGTAACA 2855
QY      645  AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
Db      2856  GAGAACATGTTCTGTGCGAGGTACAAAG---AAGGGACGTTATGATGCTCGAGTGGGAC 2912
QY      665  ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTrpHis 684
Db      2913  AGTGGAGGA-----CCTTTAGTGTGTGCTGATGATTCCTCGTACCGAAGCGGTGGGTC 2966
QY      685  LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703
Db      2967  TTGGAAGGATGTCAGTGGGGCAGTCCCGAGTGGATGTGCGTACCGAAGCGGTGGGTC 3026
QY      704  AlaPheThrLysValLeuProPheLysAspTrpIleGluArg 717
Db      3027  GGCTTCACTAAAGTTAAACGTTTCTCTCATGGATTAGGCAG 3068
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Db	2184	AGATACTACGAACCTACTTGGATCTCAAGGCAGAGATGTGACTCTAATGGAACTGGAGT	2243
Qy	437	GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro---	455
Db	2244	GGTCGGCCACGCGAGCTGATTCACAGTATTGGACGGTCAGACTCTCTCGTCTCTCTTT	2303
Qy	456	-----LysThrGlnGlyLeuArgTTPProTTPGlnAlaIleIleTyrArg	470
Db	2304	ATCTGGAAATGGGAATCTACAGAAATAGTTCAGTGGCCGTGGCAGCAGGAATCTTAGA	2363
Qy	471	ArgThrSerGlyValHisAspGlySerLeuHisGlyAlaTTPheLeuValCysSer	490
Db	2364	TGGCTTGCA-----GACCACAATATGTGGTTCTCCAGTGTGGA	2402
Qy	491	GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly	510
Db	2403	GGATCTCTAATGAATGAGAAATGGTCGTCACTGCTGCCCACTGTGTCACTACTCTGCT	2462
Qy	511	LysValThrMetIleIleTyrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp	530
Db	2463	ACTGCTGAGATTATTTGACCCCAATCATGTTAAATATGATCTGGCAGAGTACTACCGTAT	2522
Qy	531	AspAspArgAspGluTyrThrIleGlnSerLeuGlnIleSerAlaIleLeuHisPro	550
Db	2523	GACGTAGACAGATGATCTATGTACAGTAAAGAGAGGCTCTTGAGATCCACGTGAATCCT	2582
Qy	551	AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLysAla	570
Db	2583	AACCTACGACCCCGCAATCTCACTTTGTGACATAGCCCTAATTCACATGAAAACCTCCTGTT	2642
Qy	571	ArgIleSerThrArgValGlnProIleCysLeuAlaIleSerArgAspLeuSerThrSer	590
Db	2643	ACTTTGACACACGAGTCCCAACCAATCTGTCTGCTACT-----GACATCAACAACA--	2693
Qy	591	PheGlnGlutSerHisIle-----ThrValAlaGlyTTPAsnValLeu	604
Db	2694	-----AGACAACACTTGAGAGGGGAACATTAGCAGTGTGACAGTGTGGGT-----	2741
Qy	605	AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal	624
Db	2742	-----TTGAATGAAAACAACACACTTATTCAGACAGGATTCACACAGCTGTGCTACCTGTT	2795
Qy	625	ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr	644
Db	2796	GTTTCAGCCAGCACCTGTGAAGAGGGGTACAAAGGAAGCAGACTTACCACATGCAGTAACA	2855
Qy	645	AspAsnMetPheCysAlaSerTTPProThrAlaProSerAspIleCysThrAlaGlu	664
Db	2856	GAGAACATGTTCTGTGCGAGTTACAG-----AAGGAGCTTATGATGCTCGATGGGGG	2912
Qy	665	ThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArgTTPHis	684
Db	2913	AGTGGAGA-----CCTTTAGTGTTTGCTGATGATTCCTCCGTACCGAAAGCGGTGGGTC	2966
Qy	685	LeuMetGlyLeuValSerTTPSerTyrAspLysThrCysSerHis---ArgLeuSerThr	703
Db	2967	TTGAAGGAGATTGTTCAGTGGGCGAGTCCCACTGGATGTGGCAGGCGAACCAGTACGGG	3026
Qy	704	AlaPheThrLysValLeuProPheLysAspTTPIleGluArg	717
b	3027	GGCTTCTCAATAAGTTAAGTTTTCTGTCTATGGATTAGGAC	3068

## RESULT 11

RESOLUT II  
US-08-296-014A-1

US-08-298-014A-1  
: Sequence 1. Application us/08296014A

Sequence I, Application  
: Parent No. 5716834

; Patent No. 3716834  
; GENERAL INFORMATION:

GENERAL INFORMATION: Ding Jeak Ling

APPLICANT: Ding, Jie

APPLICANT: HO, HOW

TITLE OF INVENTION: The Cloned Factor C cDNA of the

**TITLE OF INVENTION:** The Cloned Factor C cDNA of the Singapore Horseshoe Crab Carinoscorpius

;  
: TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinogorscorpius rotundicauda and Purification of Factor C Proenzyme

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1  NUMBER OF SEQUENCES: 4
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Birch, Stewart, Kolsach & Birch
4  STREET: 8110 Gatehouse Road, Suite 500 East
5  CITY: Falls Church
6  STATE: Virginia
7  COUNTRY: USA
8  ZIP: 22042
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: PatentIn Release #1.0, Version #1.25
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/296,014A
16 FILING DATE:
17 CLASSIFICATION: 435
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Murphy, Jr., Gerald M.
20 REGISTRATION NUMBER: 28,977
21 REFERENCE/DOCKET NUMBER: 1781-105P
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (703) 205-8000
24 TELEFAX: (703) 205-8050
25 TELEX: 248345
26 INFORMATION FOR SEQ ID NO: 1:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 4182 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: single
31 TOPOLOGY: both
32 MOLECULE TYPE: cDNA
33 HYPOTHETICAL: NO
34 ANTI-SENSE: NO
35 ORIGINAL SOURCE:
36 ORGANISM: Carinoscorpius rotundicauda
37 FEATURE:
38 NAME/KEY: CDS
39 LOCATION: 569..3817
40 US-08-296-014A-1
41
42 Alignment Scores:
43 Pred. No.: 2,17e-56 Length: 4182
44 Score: 665.00 Matches: 222
45 Percent Similarity: 38.90% Conservative: 118
46 Best Local Similarity: 25.40% Mismatches: 304
47 Query Match: 16.86% Indels: 230
48 DR: 1 Gaps: 37

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US-10-063-692-38 (1-720) x US-08-296-014A-1 (1-4182)

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Db      1310  CCAATGGCAGTGGAGTAACCTTCCACCCAATGATTGGA-----GAATGT  1357
      |||  ::|||:::  |||  ::|||  |||  |||

Qy      54  ValCysProGlyLysArgGlu-----ValVal  62
      |||  |||  |||  |||  |||  |||

Db      1358  GCCATGTTTCATCTCCAGAAACATGGAAAGTGAATGCTCTTAGTGGTGATATGATAGAA  1417
      |||  |||  |||  |||  |||  |||

Qy      63  GlyThrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis  82
      |||  |||  |||  |||  |||  |||

Db      1418  GGGGCTACTTAA-----CGGTTCTCATGTGATAGT-----  1447
      |||  |||  |||  |||  |||  |||

Qy      83  ProGlyCysThrIlePheGluAsnCysLysSerCysArg---AsnGlySerTrpGlyGly  101
      |||  |||  |||  |||  |||  |||
      CCCTACTACTTGATTGGTGCAGAAGAACATTAACTGTCAAGGTTAATGTCAGTGGAATGGA  1507
      |||  |||  |||  |||  |||  |||

Qy      102  ThrLeu-----  103
      |||  |||  |||  |||  |||  |||

Db      1508  CAGATACCACAATGTAGAACTTAGTCTTCTGCTGACCTGGATCCTGTAAACCATGCT  1567
      |||  |||  |||  |||  |||  |||

Qy      103  -----  103
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Db 1568 GAACACAAAGGTTAAATTTGGTGTGGAAACAAAATATATGTCAGTTCTCAAGGCAGCTGAA 1627  
Qy 104 -----AspAspPheTyrValLysGlyPheTyrCysAlaGluCysArg 117  
Db 1628 GTGACCTATACGTGTTCCGGGTAACTACTTCTTGATGGTTTGGACACCTTTAAATATGTAAC 1687  
Qy 118 -----AlaGlyTyrTyrGlyGly-----AspCysMetArg----- 127  
Db 1688 CCTGATGGGCTTTGGTCAGGATCACGCCATCCTCTGTGTTAAAGTGGCAGACAGAGGTC 1747  
Qy 128 -----CysGlyGlnValLeuArg----- 133  
Db 1748 GACTGTGACAGTAAGCTGTAGACTTCTTGATGATGTTGGTAACCTGTGAGATCCAC 1807  
Qy 134 AlaProLysGlyGlnLeuLeuGluSer-----TyrPro 145  
Db 1808 TGTCTGCTGGCTGTTCTTTTGACACAGCTGGTACTGTGTGGGGTACAGCCATATACCATGAA 1867  
Qy 146 LeuAsnAlaHisCysGluTyrThrIleHisAla-----LysProGlyPheVal 161  
Db 1868 CTTTCTCCTCAGTGTGTGTCAGCCATCATGCTGGCAAGCTTCCAACTCTGGAGGAGCG 1927  
Qy 162 Ile----- 162  
Db 1928 GTGCATGTTGTGAACAAATGGCCCTACTCGGACTTTCTGGGTAGTACCTGAATGGGATA 1987  
Qy 163 -----GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMet----- 176  
Db 1988 AAATCCGAAGATTGAAGTCTTGTCCCGGAGTTTCCGATTTCGATTATGTTCAGTTCTCTCC 2047  
Qy 177 -----CysGlnTyrAspTyrValGluValArgAsp----- 186  
Db 2048 ACAGCAGGTAATCAGGATGCTCTCGATGGATGTTTGAGGTAGACAGCACTGTGTGTAC 2107  
Qy 187 -----GlyAspAsnArgAspGlyGlnIleIleArgValCysGlyAsn-----Glu 202  
Db 2108 GTTACATCAAAACAGAGAGCGCTGGAAAGAGCTCAAGGTGTGTGTACCAATATGTGGTCT 2167  
Qy 203 ArgProAlaProIleGlnSer-----IleGlySerSerLeuHisValLeuPheHisSer 220  
Db 2168 CGTCTTGTGCTGGCAAAAGATGTAAATTCCAAATTCATTGACTGAGACTCTACGAGGG 2227  
Qy 221 AspGly-----SerLysAsnPheAspGlyPheHis----- 230  
Db 2228 AAAGGGTTAAACCAACAGCTGGATAGGATTGCACAGACTAGATGCTGAGAGGCCCTTTATT 2287  
Qy 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241  
Db 2288 TGGGAGTTAATGATCGTAGTAATGTGGTGTCTGAATGATAACCTAACATTTCTGGGCTCT 2347  
Qy 242 SerProCysPheHisAspGlyThrCysValLeu-----AspLysAlaGlySer 257  
Db 2348 GCGCAACCTGGAATGAACCTAACTGTATATATGACATCCCAAGATCAGTTGCAGTCT 2407  
Qy 258 -----TyrLysCysAlaCysLeuAlaGlyTyrThrGlyClnArgCysGluAsnLeuLeuGlu 276  
Db 2408 GTGTGGAACCAACCAAGTCATGTTTTCAGCCCTCAAGTTTCTTGTGCATGATGATCTGTCA 2467  
Qy 277 GluArgAsn-----CysSerAspProGlyGlyProValAsnGlyTyrGlnLysIle 293  
Db 2468 GACAGAAATAAGCCAAATCCGATGATCCTGGATCACTGGAAATATGACACGCCACACT 2527  
Qy 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIleGlyThrValValSerPhe 313  
Db 2528 CATGGACAAAGT-----ATTGATGGTTCATGCT-----GGTCTCTATAAGGTAC 2575  
Qy 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333  
Db 2576 AGCTGTGAGGTTCTCCACTACCTCAGTGGAACTGAAACCGCTAACTGTCAACAAATGGC 2635  
Qy 334 GluTyrSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351  
Db 2636 ACATGAGGTGCTCTCTAAACCTCGATGTATCAAAAGTCATCACCTGCCAAACCCCTCTGTA 2695

Qy 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371  
Db 2696 CCATCATATGTTCTGTGGAAATCAAAACCC-----CCAAGTCGACAAATCTCGATA 2746  
Qy 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388  
Db 2747 AGTCGTGTTGGGTGACCTTTCTTTGAGGTTGCCACGGTTACCTCCCATTTAGCCAGAGCA 2806  
Qy 389 ThrLysLysProAlaLeuProPheGlyAsp----- 398  
Db 2807 GCCAAACCTCTCCAAACCTAGATCCTCAACCCCTCTACTGTGGACTTGGCTTCTTAAA 2866  
Qy 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416  
Db 2867 GTTAAACTACTCAAGGTCTATTACCGGTAGGTCTCGAGCCATTTACACGTGCGAGTCG 2926  
Qy 417 ProPheTyrArgArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTyrSer 436  
Db 2927 AGATCTACGAACCTACTTGGATCTCAAGGCAGAGATGTGACTCTAATTGGAAACTGGAGT 2986  
Qy 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455  
Db 2987 GGTCCGCCAGCAGCTGTATTCCAGTTTGTGGACGTCAGACTCTCTCTCTCTCTCTTT 3046  
Qy 456 -----LysThrGlnGlyLeuArgTyrProTyrGlnAlaIleTyrArg 470  
Db 3047 ATCTGGAATGGGAATTTCTACAGAAATAGGTCTAGTGGCCGTGGCAGGCAGGAATCTCTAGA 3106  
Qy 471 ArgThrSerGlyValHisAspGlySerLeuHisGlyGlyAlaTyrPheLeuValCysSer 490  
Db 3107 TGGCTTTGCA-----GACCACAATATGTGGTTTCTCCAGTGGGA 3145  
Qy 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510  
Db 3146 GGATCTCTATTGTAATGAGAAATGGATCGTCACCTGCTGCCACCTGTCTCACTACTCTGCT 3205  
Qy 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530  
Db 3206 ACTGCTGAGATTATTGACCCCAATCATGTTTAAATGTATCTGGGCAAGTACTACCGTGTAT 3265  
Qy 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleIleLeuHisPro 550  
Db 3266 GACAGTAGAGACGATGACTATGTACAAAGTAAGAGAGGCTCTTGAGATCCACGCTGAATCCT 3325  
Qy 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLysAla 570  
Db 3326 AACTACGACCCCGGCAATCTCAACTTTGACATAGCCCTTAATTCACCTGAAAACTCCTGTT 3385  
Qy 571 ArgIleSerThrArgValGlnProIleCysLeuAlaAlaSerArgAspLeuSerThrSer 590  
Db 3386 ACTTTGACAACACGAGTCCAAACCAATCTGTCTGCCTACT-----GACATCAACA 3436  
Qy 591 PheGlnGluSerHisIle-----ThrValAlaGlyTyrAsnValLeu 604  
Db 3437 -----AGAGAACACTTGAAGGAGGGAACATTTAGCAGTGTGTGACAGTTGGGGT 3484  
Qy 605 AlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValValSerVal 624  
Db 3485 -----TTGAATGAAACAAACACCTTATTCAGAGCAGATTCACAAAGCTGTGCTACCTGTT 3538  
Qy 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644  
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Db 2408 GTGGGAACCAAGTCATGTTTCCAGCTCTCAAGTTTCTGTCATGATGGATCTGTCA 2467  
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Db 2468 GACAGAAATAAGCCAAATCGGATGATCTCTGGATCACTGGAAATGCGACACGACACTT 2527  
Qy 294 ThrGlyClyProGlyLeuIleAsnGlyArgHisAlaIleValSerPhe 313  
Db 2528 CATGGCAAAAGT-----ATTGATGGGTTCTATGCT-----GGTTCTCTAATAGATC 2575  
Qy 314 PheCysAsnAsnSerTyrValLeuSerGlyAsnGluLysArgThrCysGlnGlnAsnGly 333  
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Qy 334 GluTrpSerGlyLysGlnProIleCysIleLys-----AlaCysArgGluProLysIle 351  
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Qy 352 SerAspLeuValArgArgValLeuProMetGlnValGlnSerArgGluThrProLeu 371  
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Qy 399 -----LeuProMetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSer 416  
Db 2867 GTTAACTACTGTAAGGTCTATTACCGGTAGGCTCTCGAGCCATTTACACGTGCGAGTGC 2926  
Qy 417 ProPheTyrArgArgLeuGlySerSerArgThrCysLeuArgThrGlyLysTrpSer 436  
Db 2927 AGATCTAGAACTACTTGATCTCAAGGCAGAGATGTGACTCTTAATGGAACCTGGAT 2986  
Qy 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaPro--- 455  
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Qy 456 -----LysThrGlnGlyLeuArgTrpProTrpGlnAlaIleTyrArg 470  
Db 3047 ATCTGGAATGGGAATTTCTACAGAAATAGGTCTAGTGGCGGTGAGCAATCTCTAGA 3106  
Qy 471 ArgThrSerGlyValHisAspGlySerLeuHisLysGlyAlaTrpPheLeuValCysSer 490  
Db 3107 TGGCTTGCA-----GACCACAATATGTGGTTTCTCCAGTGTGGA 3145  
Qy 491 GlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeuGly 510  
Db 3146 GGATCTCTATTGAATGAGAAATGATCGTCACTGCTGCCCATGTGTCACTACTCTGT 3205  
Qy 511 LysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrArgAsp 530  
Db 3206 ACTGCTGAGATTTTACGCCCAATCAGTTTAAATATGATCTGGCAAGTACTACCGTGT 3265  
Qy 531 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleIleLeuHisPro 550  
Db 3266 GACAGTAGAGAGATGACTATGTACAAATGTAAGAGGCTCTTGAAGATCCACGTGAATCT 3325  
Qy 551 AsnTyrAspProIleLeuLeuAspAlaAspIleAlaIleLeuLysLeuAspLysAla 570  
Db 3326 ACTAGACCCCGCAATCTCACTTTGATAGAGCCCTTAATCACTGAAACTCTCTGT 3385  
Qy 571 ArgIleSerThrArgValGlnProIleCysLysLeuAlaAlaSerArgAspLeuSerThr 590  
Db 3386 ACTTTGACAAACAGAGTCAACCAATCTCTCTGCTACT-----GACATCAACA--- 3436  
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Qy 625 ValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSerValThr 644  
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Db 3656 AGTGGAGGA-----CCTTAGTGTTCGTGATGATCCCGTACCGAAAGCGGTGGGTC 3709  
Qy 685 LeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHis---ArgLeuSerThr 703  
Db 3710 TTGGAAGGGATTTGTCAGCTGGGGCAGTCCCGAGTGGATGTGGCAAGGCGCAACAGTACGGG 3769  
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Db 3770 GGCTTCACCTAAAGTTAAACGTTTTCCTGTCATGATTAGGCAG 3811

RESULT 13  
US-08-877-620-1  
; Sequence 1. Application US/08877620  
; Patent No. 5985590  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus  
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/877,620  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/596,405  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1781-105P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4182 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: both  
; MOLSCULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO



ORIGINAL SOURCE:				
ORGANISM: Carcinoscopus rotundicauda				
FEATURE:				
NAME/KEY: CDS				
LOCATION: 569..3817				
S:08-877-620-1				
Alignment Scores:				
red. No.:	2.17e-56	Length:	4182	
core:	665.00	Matches:	222	
Conservative:	38.90%		118	
Mismatches:	25.40%		304	
Indels:	16.86%		230	
Gaps:	2		37	
US-10-063-692-38 (1-720) x US-08-877-620-1 (1-4182)				
QY	34	ProGlyAlaGluTrpAsnIleMetCysArgGluCysGluTyraSpGlnIleGluCys	53	
Db	1310	CCAAATGGACAGTGGAGTAACCTTTCCACCCAAATGATTCGA	1357	
QY	54	ValCysProGlyLysArgGlu	62	
Db	1358	GCCATGGTTTCATCTCCAGAACATGGGAAGTGAATGCTCTTAGTGGTATATAGAA	1417	
QY	63	GlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeuIleHis	82	
Db	1418	GGGGCTACTTTA	1447	
QY	83	ProGlyCysThrIlePheGluAsnCysLysSerCysArg	101	
Db	1448	CCCTACTACTTGTGTCAGAAACATTAACTGTCAGGGTAATGTCAGTGGAAATGGA	1507	
QY	102	ThrLeu	103	
Db	1508	CAGATACCAATGTAAGAACTTAGTCTTCTGCTGACCTGGATCCTGTAAACCATGCT	1567	
QY	103		103	
Db	1568	GAACACAGGTTAAATTTGGTGTGGAAACAAAATATATGTCAGTTCTCTCAAGGCACCTGAA	1627	
QY	104	AspAspPheTyThrValLysGlyPheTyThrCysAlaGluCysArg	117	
Db	1628	GTGACCTATACGTGTTCCGGTAACCTACTTCTGATGGGTTTTCACACCTTAAATATGTAAC	1687	
QY	118	AlaGlyTrpTyThrGlyGly	127	
Db	1688	CCTGATGGGTCTTGGTCAGGATCACAGCCATCTGTGTTAAAGTGGCAGACAGAGAGGTC	1747	
QY	128		133	
Db	1748	GACTGTGACAGTAAAGCTGTAGACTTCTTGATGATGTTGGTGAACCTGTCCAGGATCCAC	1807	
QY	134	AlaProLysGlyGlnIleLeuLeuGluSer	145	
Db	1808	TGTCCTGCTGGCTCTTTTGACAGCTGGTACTGTGTGGGGTACAGCCATATACCATGAA	1867	
QY	146	LeuAsnAlaHisCysGluTrpThrIleHisAla	161	
Db	1868	CTTTCCTCAGTGTGTCGTCAGCCATCCATGCTGGCAAGCTTCCAACTCTGGAGGAGCG	1927	
QY	162	Ile	162	
Db	1928	GTGCATGTTGTGAACAATGGCCCTCTACCGGACTTTCTGGGTAGTACCTGAAATGGGATA	1987	
QY	163	GlnLeuArgPheValMetLeuSerLeuGluPheAspTyMet	176	
Db	1988	AAATCCGAAGATTGAAGTCTCTTGGCCGGAGTTTCCGATTTCGATTATGTCAGTTCCTCC	2047	
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Db 2168 CGTCTTGCTGTGTCGACAAAGATGTAATTCCAAATTCATTGACTGAGAGCTCTACGAGGG 2227  
QY 221 AspGly---SerIysAsnPheAspGlyPheHis----- 230  
Db 2228 AAAGGGTTAAACCAACACGCTGATAGATTGCACAGACTAGATGCTGAGAGCGCTTTATT 2287  
QY 231 -----AlaIleTyrGluGluIleThrAlaCysSerSer 241  
Db 2288 TGGGAGTTAATGATCGTAGTAATGTGTTCTGAATGATAACCAATTCCTGGGCTCT 2347  
QY 242 SerProCysPheHisAspGlyThrCysValLeu-----AspIysAlaGlySer 257  
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QY 372 HisGlnLeuTyrSerAlaAlaPheSerLysGlnLysLeuGln-----SerAlaPro 388  
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Db 2807 GCCAAACCTCTCCAAACCTAGATCTCAACACCTCTACTGTGGACTTGGCTTCTTAAA 2866  
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QY 456 -----LysThrGlnGlyLeuArgTrpProThrGlnAlaIleTyrArg 470  
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## RESULT 15

US-09-626-795-1  
; Sequence 1, Application US/09626795  
; Patent No. 6719973  
; GENERAL INFORMATION:  
; APPLICANT: DING, Jeak Ling  
; APPLICANT: HO, Bow  
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis  
; FILE REFERENCE: 4810-61737  
; CURRENT APPLICATION NUMBER: US/09/626,795  
; CURRENT FILING DATE: 2000-07-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4182  
; TYPE: DNA  
; ORGANISM: Carinoscorpius rotundicauda  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (569)..(3817)  
US-09-626-795-1

Alignment Scores:  
Pred. No.: 2,17e-56 Length: 4182  
Score: 665.00 Matches: 222  
Percent Similarity: 38.90% Conservative: 118  
Best Local Similarity: 25.40% Mismatches: 304  
Query Match: 16.86% Indels: 230

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c 104	102	3.6	396	4	US-09-970-966-10	Sequence 10, Appl	177	88	3.1	2434	4	US-09-489-847-67	Sequence 67, Appl
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c 106	102	3.6	1882	3	US-09-370-253-1	Sequence 1, Appl	179	87	3.1	1342	4	US-09-489-847-89	Sequence 89, Appl
c 107	101	3.5	140	1	US-08-628-417-5	Sequence 5, Appli	180	87	3.1	2852	3	US-09-027-137-2	Sequence 2, Appli
c 108	101	3.5	578	3	US-09-602-877A-95	Sequence 95, Appl	181	87	3.1	2852	3	US-09-344-441-2	Sequence 2, Appli
c 109	100	3.5	949	4	US-09-489-847-35	Sequence 35, Appl	182	87	3.1	3334	4	US-09-668-119-2	Sequence 2, Appli
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248	79	2.8	997	4	US-09-906-700-376	Sequence 376, App	321	75	2.6	1925	4	US-09-148-545-128	Sequence 128, App
249	79	2.8	997	4	US-09-903-603A-376	Sequence 376, App	322	75	2.6	2550	6	5258287-23	Patent No. 5258287
250	79	2.8	997	4	US-09-904-920A-376	Sequence 376, App	323	75	2.6	2550	6	5258287-23	Patent No. 5258287
251	79	2.8	997	4	US-09-909-064-376	Sequence 376, App	324	74	2.6	109	4	US-09-621-976-14592	Sequence 14592, A
252	79	2.8	997	4	US-09-905-381A-376	Sequence 376, App	325	74	2.6	165	4	US-09-621-976-8127	Sequence 8127, Ap
253	79	2.8	997	4	US-09-906-618-376	Sequence 376, App	326	74	2.6	166	4	US-09-621-976-18390	Sequence 18390, A
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c 255	79	2.8	1013	4	US-09-322-409-8	Sequence 8, Appli	328	74	2.6	1147	1	US-08-665-716-1	Sequence 1, Appli
256	79	2.8	1013	4	US-09-451-527-6	Sequence 6, Appli	329	74	2.6	1172	1	US-07-945-288-9	Sequence 9, Appli
c 257	79	2.8	1013	4	US-09-451-527-8	Sequence 8, Appli	330	74	2.6	1172	1	US-08-462-831-9	Sequence 9, Appli
258	79	2.8	1013	4	US-08-340-820-24	Sequence 24, Appl	331	74	2.6	1172	1	US-08-461-809-9	Sequence 9, Appli
259	79	2.8	1493	1	US-08-593-535-24	Sequence 24, Appl	332	74	2.6	1172	1	US-08-461-441-9	Sequence 9, Appli
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c 261	79	2.8	1736	3	US-09-182-816-24	Sequence 24, Appl	334	74	2.6	1927	3	US-09-336-536-66	Sequence 66, Appl
262	79	2.8	1736	3	US-09-471-528-22	Sequence 22, Appl	335	74	2.6	41736	4	US-09-949-016-17091	Sequence 17091, A
c 263	79	2.8	1736	3	US-09-471-528-24	Sequence 24, Appl	336	73	2.6	73	4	US-09-621-976-14963	Sequence 14963, A
c 264	79	2.8	1736	3	US-09-634-530-22	Sequence 22, Appl	337	73	2.6	188	4	US-09-621-976-10364	Sequence 10364, A
c 265	79	2.8	1736	3	US-09-634-530-24	Sequence 24, Appl	338	73	2.6	189	4	US-09-621-976-14761	Sequence 14761, A
266	79	2.8	2202	3	US-09-465-558-59	Sequence 59, Appl	339	73	2.6	552	4	US-09-461-325-111	Sequence 111, App
267	78	2.7	78	4	US-09-621-976-14824	Sequence 14824, A	340	73	2.6	552	4	US-10-012-542-111	Sequence 111, App
c 268	78	2.7	78	4	US-09-621-976-15092	Sequence 15092, A	341	73	2.6	552	4	US-10-115-123-111	Sequence 111, App
c 269	78	2.7	270	2	US-08-520-678A-30	Sequence 30, Appl	342	73	2.6	1129	3	US-09-227-357-40	Sequence 40, Appl
c 270	78	2.7	270	3	US-08-897-126-30	Sequence 30, Appl	343	73	2.6	1296	4	US-09-461-325-29	Sequence 29, Appl
271	78	2.7	639	4	US-09-482-273-49	Sequence 49, Appl	344	73	2.6	1296	4	US-10-012-542-29	Sequence 29, Appl
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274	78	2.7	1361	4	US-09-489-847-64	Sequence 64, Appl	347	73	2.6	1606	4	US-09-820-004-1	Sequence 1, Appli
275	78	2.7	2146	4	US-10-003-392-3	Sequence 3, Appli	348	73	2.6	1872	3	US-09-291-922-27	Sequence 27, Appl
276	78	2.7	5021	4	US-09-949-016-786	Sequence 786, App	349	73	2.6	2045	3	US-09-152-060-22	Sequence 22, Appl
c 277	77	2.7	77	4	US-08-956-171E-2883	Sequence 2883, Ap	350	73	2.6	2628	1	US-08-143-219-1	Sequence 1, Appli
c 278	77	2.7	77	4	US-08-781-986A-2883	Sequence 2883, Ap	351	72	2.5	72	4	US-09-621-976-10145	Sequence 1045, A
c 279	77	2.7	79	4	US-09-621-976-15090	Sequence 15090, A	352	72	2.5	72	4	US-09-621-976-14815	Sequence 14815, A
c 280	77	2.7	196	4	US-09-644-460-40	Sequence 40, Appl	353	72	2.5	72	4	US-09-621-976-14842	Sequence 14842, A
281	77	2.7	215	4	US-09-621-976-15321	Sequence 15321, A	354	72	2.5	101	3	US-09-404-879A-293	Sequence 293, App
282	77	2.7	215	4	US-09-248-335-57	Sequence 57, Appl	355	72	2.5	101	4	US-09-338-933-293	Sequence 293, App
283	77	2.7	1297	4	US-09-800-729-80	Sequence 80, Appl	356	72	2.5	101	4	US-09-215-681-293	Sequence 293, App
284	77	2.7	1692	4	US-09-821-803A-5	Sequence 5, Appli	357	72	2.5	101	4	US-09-216-003A-293	Sequence 293, App
285	77	2.7	2407	3	US-09-370-807-7	Sequence 7, Appli	358	72	2.5	101	4	US-09-667-857-293	Sequence 293, App
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297	76	2.7	1023	1	US-08-252-966B-16	Sequence 16, Appl	370	71	2.5	80	4	US-09-688-842-25	Sequence 25, Appl
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c 316	75	2.6	844	4	US-09-690-942-3	Sequence 3, Appli	389	70	2.5	1206	3	US-09-465-558-53	Sequence 53, Appl
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394	70	2.5	2237	1	US-08-496-631-1	Sequence 1, Appli	467	66	2.3	1138	4	US-09-800-729-44	Sequence 44, Appl
395	70	2.5	3527	1	US-08-909-965C-7	Sequence 1, Appli	468	66	2.3	1201	4	US-09-461-325-36	Sequence 36, Appl
396	70	2.5	5173	1	US-08-242-677-1	Sequence 1, Appli	469	66	2.3	1201	4	US-10-012-542-36	Sequence 36, Appl
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401	69	2.4	98	4	US-09-621-976-11744	Sequence 11744, A	474	66	2.3	3848	3	US-09-112-096-28	Sequence 28, Appl
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404	69	2.4	299	4	US-09-621-976-10211	Sequence 10211, A	477	66	2.3	3668	4	US-09-685-166A-777	Sequence 777, App
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409	69	2.4	1325	2	US-08-246-361A-1	Sequence 1, Appli	482	66	2.3	7938	3	US-09-331-581-14	Sequence 14, Appl
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413	69	2.4	1546	4	US-09-901-151-1	Sequence 1, Appli	486	65	2.3	94	4	US-09-338-933-261	Sequence 261, App
414	69	2.4	1844	4	US-10-003-392-7	Sequence 7, Appli	487	65	2.3	94	4	US-09-215-681-261	Sequence 261, App
415	69	2.4	3200	1	US-08-444-405-1	Sequence 1, Appli	488	65	2.3	94	4	US-09-216-003A-261	Sequence 261, App
416	69	2.4	3200	1	US-08-384-850-1	Sequence 1, Appli	489	65	2.3	94	4	US-09-667-857-261	Sequence 261, App
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422	68	2.4	931	4	US-09-482-273-31	Sequence 31, Appl	495	65	2.3	991	3	US-08-924-747-25	Sequence 25, Appl
423	68	2.4	1359	3	US-09-387-574-11	Sequence 11, Appl	496	65	2.3	991	3	US-09-247-373B-25	Sequence 25, Appl
424	68	2.4	1359	3	US-09-668-096-11	Sequence 11, Appl	497	65	2.3	991	3	US-09-296-715-25	Sequence 25, Appl
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429	68	2.4	6200	3	US-09-439-923-1	Sequence 1, Appli	502	65	2.3	1740	4	US-09-709-103-45	Sequence 45, Appl
430	68	2.4	6200	4	US-09-711-202A-1	Sequence 1, Appli	503	65	2.3	1740	4	US-09-439-410A-45	Sequence 45, Appl
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440	67	2.4	260	3	US-08-897-126-29	Sequence 29, Appl	513	65	2.3	2187	3	US-09-127-219B-2	Sequence 2, Appli
441	67	2.4	283	4	US-09-621-976-16989	Sequence 16989, A	514	65	2.3	2271	4	US-09-205-258-243	Sequence 243, App
442	67	2.4	316	4	US-09-513-999C-838	Sequence 838, App	515	65	2.3	2291	4	US-09-220-132-114	Sequence 114, App
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446	67	2.4	688	6	5498694-3	Patent No. 5498694	519	64	2.2	64	4	US-09-621-976-14858	Sequence 14858, A
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448	67	2.4	1412	4	US-09-614-912-197	Sequence 197, App	521	64	2.2	138	4	US-09-621-976-9595	Sequence 9595, Ap
449	67	2.4	1441	3	US-08-821-994-63	Sequence 63, Appl	522	64	2.2	227	2	US-08-520-678A-28	Sequence 28, Appl
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451	67	2.4	1559	4	US-09-489-847-42	Sequence 42, Appl	524	64	2.2	231	4	US-09-621-976-16456	Sequence 16456, A
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454	67	2.4	2158	1	US-08-261-578-1	Sequence 1, Appli	527	64	2.2	687	4	US-09-774-639-106	Sequence 106, App
455	66	2.3	66	4	US-09-621-976-12404	Sequence 12404, A	528	64	2.2	789	3	US-09-020-956-32	Sequence 32, Appl
456	66	2.3	66	4	US-09-621-976-14819	Sequence 14819, A	529	64	2.2	789	3	US-09-030-607-32	Sequence 32, Appl
457	66	2.3	68	4	US-09-621-976-11613	Sequence 11613, A	530	64	2.2	789	3	US-09-439-313-32	Sequence 32, Appl
458	66	2.3	68	4	US-09-621-976-11912	Sequence 11912, A	531	64	2.2	789	3	US-09-352-616A-32	Sequence 32, Appl
459	66	2.3	68	4	US-09-621-976-12005	Sequence 12005, A	532	64	2.2	789	3	US-09-232-149A-32	Sequence 32, Appl
460	66	2.3	105	3	US-09-284-627-23	Sequence 23, Appl	533	64	2.2	789	4	US-09-159-812-32	Sequence 32, Appl
461	66	2.3	293	4	US-09-621-976-16965	Sequence 16965, A	534	64	2.2	789	4	US-09-636-215-32	Sequence 32, Appl
462	66	2.3	443	4	US-09-936-885A-1	Sequence 1, Appli	535	64	2.2	789	4	US-08-685-166A-32	Sequence 32, Appl
463	66	2.3	572	3	US-09-342-653-5	Sequence 5, Appli	536	64	2.2	789	4	US-09-115-453-32	Sequence 32, Appl
464	66	2.3	759	4	US-09-465-559-5	Sequence 5, Appli	537	64	2.2	789	4	US-09-688-489-32	Sequence 32, Appl
465	66	2.3	796	1	US-08-104-073-2	Sequence 2, Appli	538	64	2.2	789	4	US-09-679-426-32	Sequence 32, Appl



c 539	64	2.2	789	4	US-09-759-143-32	Sequence 32, Appl	612	2.2	1864	3	US-09-149-476-130	Sequence 130, App
c 540	64	2.2	789	4	US-09-651-236-32	Sequence 32, Appl	613	2.2	2203	4	US-09-801-861-1	Sequence 1, Appl
541	64	2.2	789	4	PCT-US95-06406A-21	Sequence 21, Appl	614	2.2	2203	4	US-10-224-562-1	Sequence 1, Appl
542	64	2.2	958	2	US-08-757-046A-5	Sequence 5, Appl	615	2.2	2205	3	US-08-888-077A-41	Sequence 41, Appl
543	64	2.2	958	3	US-09-447-208-5	Sequence 5, Appl	616	2.2	2438	4	US-09-393-634-4	Sequence 4, Appl
544	64	2.2	958	3	US-09-135-988-5	Sequence 5, Appl	617	2.2	2718	4	US-09-667-135-1	Sequence 1, Appl
545	64	2.2	958	3	US-09-277-716-5	Sequence 5, Appl	618	2.2	2882	4	US-09-949-016-724	Sequence 724, App
546	64	2.2	958	3	US-08-597-274A-5	Sequence 5, Appl	619	2.2	3214	1	US-08-484-105-17	Sequence 17, Appl
547	64	2.2	958	3	US-08-908-909-5	Sequence 5, Appl	620	2.2	3214	1	US-08-484-106-17	Sequence 17, Appl
548	64	2.2	958	3	US-09-609-161B-5	Sequence 5, Appl	c 621	2.2	4055	4	US-09-620-312D-706	Sequence 706, App
549	64	2.2	958	3	US-08-990-103-5	Sequence 5, Appl	622	2.2	61	4	US-09-621-976-14680	Sequence 14680, A
550	64	2.2	958	4	US-09-746-485A-5	Sequence 5, Appl	623	2.2	61	4	US-09-621-976-14681	Sequence 14681, A
551	64	2.2	958	4	US-10-126-139-5	Sequence 5, Appl	624	2.2	61	4	US-09-621-976-14799	Sequence 14799, A
552	64	2.2	958	4	US-10-126-777-5	Sequence 5, Appl	625	2.2	61	4	US-09-621-976-14834	Sequence 14834, A
553	64	2.2	958	4	US-10-126-777-5	Sequence 5, Appl	626	2.2	61	4	US-09-621-976-14948	Sequence 14948, A
554	64	2.2	1578	3	US-09-416-050A-1	Sequence 1, Appl	627	2.2	61	4	US-09-621-976-13480	Sequence 13480, A
555	64	2.2	1578	3	US-09-664-800-1	Sequence 1, Appl	628	2.2	137	4	US-09-621-976-18434	Sequence 18434, A
556	64	2.2	1578	3	US-09-665-309-1	Sequence 1, Appl	629	2.2	145	4	US-09-621-976-16688	Sequence 16688, A
557	64	2.2	1578	3	US-09-661-569-1	Sequence 1, Appl	630	2.2	148	4	US-09-621-976-17447	Sequence 17447, A
558	64	2.2	1637	4	US-09-205-258-178	Sequence 178, App	631	2.2	148	4	US-09-621-976-17450	Sequence 17450, A
559	64	2.2	1651	4	US-09-800-729-41	Sequence 41, Appl	632	2.2	263	3	US-09-091-097-26	Sequence 26, Appl
560	64	2.2	1981	4	US-09-720-317A-3	Sequence 3, Appl	633	2.2	266	4	US-09-621-976-16813	Sequence 16813, A
561	64	2.2	3581	2	US-08-738-349-1	Sequence 1, Appl	634	2.2	350	4	US-09-621-976-15342	Sequence 15342, A
562	64	2.2	4860	4	US-09-949-016-296	Sequence 296, App	c 635	2.2	470	3	US-09-020-956-102	Sequence 102, App
563	63	2.2	63	4	US-09-621-976-13842	Sequence 13842, A	c 636	2.2	470	3	US-09-030-607-102	Sequence 102, App
564	63	2.2	63	4	US-09-621-976-14756	Sequence 14756, A	c 637	2.2	470	3	US-09-439-313-102	Sequence 102, App
565	63	2.2	142	4	US-09-621-976-10801	Sequence 10801, A	c 638	2.2	470	3	US-09-352-616A-102	Sequence 102, App
566	63	2.2	146	4	US-09-621-976-16695	Sequence 16695, A	c 639	2.2	470	3	US-09-232-149A-102	Sequence 102, App
567	63	2.2	153	4	US-09-621-976-17451	Sequence 17451, A	c 640	2.2	470	4	US-09-159-812-102	Sequence 102, App
568	63	2.2	323	4	US-09-621-976-10374	Sequence 10374, A	c 641	2.2	470	4	US-09-636-215-102	Sequence 102, App
569	63	2.2	334	4	US-09-621-976-16044	Sequence 16044, A	c 642	2.2	470	4	US-09-685-166A-102	Sequence 102, App
570	63	2.2	734	4	US-09-949-016-413	Sequence 413, App	c 643	2.2	470	4	US-09-115-453-102	Sequence 102, App
571	63	2.2	985	4	US-09-322-409-25	Sequence 25, Appl	c 644	2.2	470	4	US-09-688-489-102	Sequence 102, App
c 572	63	2.2	985	4	US-09-322-409-27	Sequence 27, Appl	c 645	2.2	470	4	US-09-679-426-102	Sequence 102, App
573	63	2.2	985	4	US-09-451-527-25	Sequence 25, Appl	c 646	2.2	470	4	US-09-759-143-102	Sequence 102, App
c 574	63	2.2	985	4	US-09-451-527-27	Sequence 27, Appl	c 647	2.2	470	4	US-09-651-236-102	Sequence 102, App
575	63	2.2	1075	3	US-08-400-006B-6	Sequence 6, Appl	648	2.2	972	1	US-07-915-934-1	Sequence 1, Appl
576	63	2.2	1522	3	US-09-413-574-1	Sequence 1, Appl	649	2.2	972	1	US-08-325-947-1	Sequence 1, Appl
577	63	2.2	1525	3	US-09-157-603-4	Sequence 4, Appl	650	2.2	1023	4	US-09-229-947-38	Sequence 38, Appl
578	63	2.2	1525	3	US-09-587-436-4	Sequence 4, Appl	651	2.2	1486	4	US-09-461-325-73	Sequence 73, Appl
579	63	2.2	1525	3	US-08-927-165A-4	Sequence 4, Appl	652	2.2	1486	4	US-10-012-542-73	Sequence 73, Appl
580	63	2.2	2010	1	US-07-864-475A-4	Sequence 4, Appl	653	2.2	1486	4	US-10-115-123-73	Sequence 73, Appl
581	63	2.2	2010	2	US-08-468-249A-4	Sequence 4, Appl	654	2.2	1780	3	US-09-202-548B-5	Sequence 5, Appl
582	63	2.2	2083	4	US-09-716-129-41	Sequence 41, Appl	655	2.2	1780	4	US-09-942-858-5	Sequence 5, Appl
583	63	2.2	2091	3	US-09-813-818-1	Sequence 1, Appl	656	2.2	1780	4	US-10-461-180-5	Sequence 5, Appl
584	63	2.2	2091	4	US-10-199-333-1	Sequence 1, Appl	657	2.2	2218	4	US-09-205-258-103	Sequence 103, App
585	63	2.2	2389	4	US-09-789-875-7	Sequence 7, Appl	658	2.2	2312	4	US-09-103-331-1	Sequence 1, Appl
586	63	2.2	2481	2	US-08-630-118A-1	Sequence 1, Appl	659	2.2	2312	4	US-09-631-594-45	Sequence 45, Appl
587	63	2.2	2481	2	US-08-838-399-1	Sequence 1, Appl	660	2.2	2378	3	US-08-802-805D-20	Sequence 20, Appl
588	63	2.2	2481	3	US-09-235-839-1	Sequence 1, Appl	661	2.2	2378	4	US-08-860-370-1	Sequence 1, Appl
589	63	2.2	2481	3	US-09-327-035-1	Sequence 1, Appl	662	2.2	2381	1	US-08-021-608D-9	Sequence 9, Appl
590	63	2.2	2604	2	US-08-630-118A-3	Sequence 3, Appl	663	2.2	2381	1	US-08-726-160-9	Sequence 9, Appl
591	63	2.2	2604	2	US-08-838-399-3	Sequence 3, Appl	664	2.2	2381	5	PCT-US94-01782-9	Sequence 1, Appl
592	63	2.2	2604	3	US-09-235-839-3	Sequence 3, Appl	665	2.2	2384	1	US-08-021-608D-1	Sequence 1, Appl
593	63	2.2	2604	3	US-09-327-035-3	Sequence 3, Appl	666	2.2	2384	5	PCT-US94-01782-1	Sequence 1, Appl
594	62	2.2	62	4	US-09-621-976-11091	Sequence 11091, A	667	2.2	2384	5	PCT-US94-01782-1	Sequence 1, Appl
595	62	2.2	62	4	US-09-621-976-14130	Sequence 14130, A	668	2.2	2483	4	US-09-205-258-68	Sequence 68, Appl
596	62	2.2	62	4	US-09-621-976-14936	Sequence 14936, A	669	2.2	2964	4	US-09-578-063-25	Sequence 25, Appl
c 597	62	2.2	91	3	US-09-404-879A-201	Sequence 201, App	670	2.2	60	3	US-09-457-959-8	Sequence 8, Appl
c 598	62	2.2	91	4	US-09-338-933-201	Sequence 201, App	671	2.2	60	4	US-09-621-976-12480	Sequence 12480, A
c 599	62	2.2	91	4	US-09-215-681-201	Sequence 201, App	672	2.2	60	4	US-09-621-976-13761	Sequence 13761, A
600	62	2.2	91	4	US-09-621-976-14925	Sequence 14925, A	673	2.2	60	4	US-09-621-976-14742	Sequence 14742, A
c 601	62	2.2	91	4	US-09-216-003A-201	Sequence 201, App	674	2.2	60	4	US-09-621-976-14884	Sequence 14884, A
c 602	62	2.2	91	4	US-09-667-857-201	Sequence 201, App	675	2.2	60	4	US-10-079-178-8	Sequence 8, Appl
603	62	2.2	145	4	US-09-621-976-16691	Sequence 16691, A	676	2.2	77	4	US-09-621-976-14176	Sequence 14176, A
604	62	2.2	146	4	US-09-621-976-16686	Sequence 16686, A	677	2.2	97	4	US-09-621-976-9086	Sequence 9086, Ap
605	62	2.2	214	4	US-09-621-976-9843	Sequence 9843, Ap	678	2.2	102	4	US-09-621-976-11436	Sequence 11436, A
606	62	2.2	332	4	US-09-621-976-16050	Sequence 16050, A	c 679	2.2	141	3	US-08-737-078A-1	Sequence 1, Appl
607	62	2.2	332	4	US-09-621-976-16053	Sequence 16053, A	c 680	2.2	141	5	PCT-US94-04706-1	Sequence 1, Appl
608	62	2.2	333	4	US-09-621-976-16032	Sequence 16032, A	681	2.2	150	4	US-09-621-976-8656	Sequence 8656, Ap
609	62	2.2	333	4	US-09-621-976-16045	Sequence 16045, A	682	2.2	204	4	US-09-621-976-1323	Sequence 1323, Ap
610	62	2.2	612	4	US-09-270-767-11643	Sequence 11643, A	683	2.2	235	4	US-09-621-976-16550	Sequence 16550, A
611	62	2.2	1579	4	US-09-403-463A-5	Sequence 5, Appl	684	2.2	255	4	US-09-621-976-9406	Sequence 9406, Ap



c	685	60	2.1	342	4	US-09-270-767-13044	Sequence 13044, A	c	758	58	2.0	509	3	US-09-439-313-202	Sequence 202, Appl	
	686	60	2.1	976	2	US-08-504-459-9	Sequence 16, Appl		c	759	58	2.0	509	3	US-09-352-616A-202	Sequence 202, Appl
	687	60	2.1	1057	4	US-09-716-129-16	Sequence 16, Appl		c	760	58	2.0	509	3	US-09-232-149A-202	Sequence 202, Appl
	688	60	2.1	1190	4	US-09-330-207-1	Sequence 1, Appl		c	761	58	2.0	509	4	US-09-159-812-202	Sequence 202, Appl
	689	60	2.1	1813	5	PCT-US94-12883-3	Sequence 3, Appl		c	762	58	2.0	509	4	US-09-636-215-202	Sequence 202, Appl
	690	60	2.1	1827	4	US-09-720-318A-9	Sequence 9, Appl		c	763	58	2.0	509	4	US-09-685-166A-202	Sequence 202, Appl
	691	60	2.1	1827	4	US-09-482-273-30	Sequence 9, Appl		c	764	58	2.0	509	4	US-09-115-453-202	Sequence 202, Appl
	692	60	2.1	1842	3	US-09-732-025-1	Sequence 1, Appl		c	765	58	2.0	509	4	US-09-688-489-202	Sequence 202, Appl
	693	60	2.1	1882	3	US-09-419-679-3	Sequence 3, Appl		c	766	58	2.0	509	4	US-09-679-426-202	Sequence 202, Appl
	694	60	2.1	1888	1	US-08-342-411A-1	Sequence 1, Appl		c	767	58	2.0	509	4	US-09-759-143-202	Sequence 202, Appl
	695	60	2.1	1965	4	US-09-482-273-27	Sequence 27, Appl		c	768	58	2.0	509	4	US-09-651-236-202	Sequence 28, Appl
	696	60	2.1	2431	1	US-07-847-743B-25	Sequence 25, Appl			769	58	2.0	530	4	US-09-461-325-28	Sequence 28, Appl
	697	60	2.1	2431	1	US-08-456-201-25	Sequence 25, Appl			770	58	2.0	530	4	US-10-012-542-28	Sequence 28, Appl
	698	60	2.1	2431	5	PCT-US92-04295A-25	Sequence 25, Appl			771	58	2.0	530	4	US-10-115-123-28	Sequence 28, Appl
	699	60	2.1	2431	5	PCT-US92-04295A-25	Sequence 25, Appl		c	772	58	2.0	703	3	US-09-313-300-6	Sequence 6, Appl
	700	60	2.1	2485	4	US-09-889-463A-9	Sequence 9, Appl		c	773	58	2.0	748	1	US-08-361-467B-3	Sequence 3, Appl
	701	60	2.1	5554	4	US-09-815-923-1	Sequence 1, Appl			774	58	2.0	748	1	US-08-484-332C-3	Sequence 3, Appl
	702	60	2.1	6065	4	US-09-800-729-35	Sequence 35, Appl			775	58	2.0	795	4	US-09-270-767-14068	Sequence 14068, A
	703	59	2.1	59	4	US-09-621-976-13084	Sequence 13084, A			776	58	2.0	1153	3	US-09-149-476-41	Sequence 41, Appl
	704	59	2.1	59	4	US-09-621-976-13752	Sequence 13752, A			777	58	2.0	1154	3	US-08-651-136C-7	Sequence 7, Appl
	705	59	2.1	146	4	US-09-621-976-16115	Sequence 16115, A			778	58	2.0	1154	3	US-09-229-911A-7	Sequence 7, Appl
	706	59	2.1	162	4	US-09-621-976-18068	Sequence 18068, A			779	58	2.0	1166	5	PCT-US96-12129B-1	Sequence 1, Appl
	707	59	2.1	232	4	US-09-621-976-17701	Sequence 17701, A			780	58	2.0	1405	4	US-09-244-111-9	Sequence 9, Appl
	708	59	2.1	233	4	US-09-621-976-16559	Sequence 16559, A			781	58	2.0	1540	3	US-08-977-001-2	Sequence 2, Appl
	709	59	2.1	234	4	US-09-621-976-16557	Sequence 16557, A			782	58	2.0	1958	3	US-08-665-034A-3	Sequence 3, Appl
	710	59	2.1	249	4	US-09-621-976-19144	Sequence 19144, A			783	58	2.0	2230	3	US-08-378-313-24	Sequence 24, Appl
	711	59	2.1	289	1	US-08-341-568-3	Sequence 3, Appl			784	58	2.0	2589	3	US-08-569-749-1	Sequence 1, Appl
	712	59	2.1	289	2	US-08-911-020-3	Sequence 3, Appl			785	58	2.0	2589	4	US-09-689-366-1	Sequence 1, Appl
	c	713	59	2.1	396	4	US-09-640-173-42	Sequence 42, Appl		786	58	2.0	2589	5	PCT-US96-12860-1	Sequence 1, Appl
	c	714	59	2.1	396	4	US-09-713-550-42	Sequence 42, Appl		787	58	2.0	2790	3	US-08-800-291B-1	Sequence 1, Appl
	c	715	59	2.1	396	4	US-09-825-294-42	Sequence 42, Appl		788	58	2.0	2908	4	US-09-904-615-35	Sequence 35, Appl
	c	716	59	2.1	396	4	US-09-970-966-42	Sequence 42, Appl		789	58	2.0	3994	4	US-09-738-946-7	Sequence 7, Appl
	717	59	2.1	491	4	US-09-311-021-191	Sequence 191, Appl			790	58	2.0	7859	1	US-07-854-596B-4	Sequence 4, Appl
	718	59	2.1	570	1	US-07-885-970A-10	Sequence 10, Appl			791	58	2.0	7859	2	US-08-450-905B-15	Sequence 15, Appl
	719	59	2.1	570	1	US-08-238-687A-10	Sequence 10, Appl			792	58	2.0	7859	3	US-07-982-759F-15	Sequence 15, Appl
	c	720	59	2.1	570	1	US-08-238-687A-10	Sequence 10, Appl	c	793	58	2.0	9472	2	US-08-150-204E-96	Sequence 96, Appl
	c	721	59	2.1	609	1	US-08-530-797-9	Sequence 9, Appl		794	58	2.0	10660	2	US-08-267-803B-8	Sequence 8, Appl
	c	722	59	2.1	609	2	US-08-787-335-9	Sequence 9, Appl		795	58	2.0	10660	3	US-09-041-886-16	Sequence 16, Appl
	c	723	59	2.1	675	4	US-09-621-976-2461	Sequence 2461, Ap		796	57	2.0	57	4	US-09-621-976-11970	Sequence 11970, A
	724	59	2.1	711	4	US-09-621-976-17854	Sequence 17854, A			797	57	2.0	57	4	US-09-621-976-13937	Sequence 13937, A
	725	59	2.1	730	4	US-09-270-767-14600	Sequence 9600, A			798	57	2.0	70	4	US-09-621-976-14750	Sequence 14750, A
	c	726	59	2.1	756	4	US-09-614-912-93	Sequence 93, Appl		799	57	2.0	134	4	US-09-621-976-18433	Sequence 18433, A
	727	59	2.1	857	1	US-08-308-683-1	Sequence 1, Appl			800	57	2.0	157	4	US-09-621-976-10871	Sequence 10871, A
	728	59	2.1	857	1	US-08-730-163-1	Sequence 1, Appl			801	57	2.0	160	4	US-09-621-976-18071	Sequence 18071, A
	729	59	2.1	966	1	US-08-514-014-7	Sequence 7, Appl			802	57	2.0	249	4	US-09-621-976-16291	Sequence 16291, A
	730	59	2.1	966	2	US-08-833-823-7	Sequence 7, Appl			803	57	2.0	249	4	US-09-621-976-16292	Sequence 16292, A
	731	59	2.1	972	3	US-09-549-831-5	Sequence 5, Appl			804	57	2.0	272	4	US-09-621-976-16932	Sequence 16932, A
	732	59	2.1	981	4	US-09-780-717-4	Sequence 4, Appl			805	57	2.0	304	4	US-09-621-976-16099	Sequence 16099, A
	733	59	2.1	1315	3	US-09-164-193-1	Sequence 1, Appl			806	57	2.0	332	3	US-09-149-476-66	Sequence 66, Appl
	734	59	2.1	1315	3	US-09-221-448A-1	Sequence 1, Appl			807	57	2.0	741	4	US-09-621-976-1894	Sequence 1894, Ap
	735	59	2.1	1319	2	US-08-504-459-7	Sequence 7, Appl			808	57	2.0	857	3	US-08-256-799-1	Sequence 1, Appl
	736	59	2.1	1358	4	US-09-949-016-463	Sequence 463, App			809	57	2.0	857	3	US-08-462-437-1	Sequence 1, Appl
	737	59	2.1	1540	4	US-09-560-761B-3	Sequence 3, Appl			810	57	2.0	1039	4	US-09-464-535-23	Sequence 23, Appl
	738	59	2.1	1639	2	US-08-737-524B-1	Sequence 1, Appl			811	57	2.0	1210	4	US-09-720-318A-3	Sequence 3, Appl
	739	59	2.1	1963	4	US-09-482-273-91	Sequence 91, Appl			812	57	2.0	1503	4	US-09-907-794A-220	Sequence 220, App
	740	59	2.1	2409	3	US-09-293-322C-8	Sequence 8, Appl			813	57	2.0	1503	4	US-09-905-125A-220	Sequence 220, App
	741	59	2.1	2409	4	US-09-839-497A-8	Sequence 8, Appl			814	57	2.0	1503	4	US-09-902-775A-220	Sequence 220, App
	742	59	2.1	2968	3	US-09-813-819-1	Sequence 1, Appl			815	57	2.0	1503	4	US-09-906-700-220	Sequence 220, App
	743	59	2.1	2968	3	US-09-920-048-1	Sequence 1, Appl			816	57	2.0	1503	4	US-09-903-603A-220	Sequence 220, App
	744	59	2.1	2968	4	US-10-014-501-1	Sequence 1, Appl			817	57	2.0	1503	4	US-09-904-920A-220	Sequence 220, App
	745	59	2.1	3145	4	US-09-949-016-1149	Sequence 1149, Ap			818	57	2.0	1503	4	US-09-909-064-220	Sequence 220, App
	746	59	2.1	4874	4	US-09-187-330-2	Sequence 2, Appl			819	57	2.0	1503	4	US-09-905-381A-220	Sequence 220, App
	747	58	2.0	4874	4	US-09-621-976-14827	Sequence 2, Appl			820	57	2.0	1503	4	US-09-906-618-220	Sequence 220, App
	748	58	2.0	72	4	US-09-621-976-15064	Sequence 15064, A			821	57	2.0	1505	2	US-08-909-965C-13	Sequence 13, Appl
	749	58	2.0	194	4	US-09-621-976-15317	Sequence 15317, A			822	57	2.0	2301	3	US-09-232-191-8	Sequence 8, Appl
	750	58	2.0	195	4	US-09-621-976-15314	Sequence 15314, A			823	57	2.0	2301	3	US-09-232-200-8	Sequence 8, Appl
	c	751	58	2.0	253	2	US-08-520-678A-25	Sequence 25, Appl		824	57	2.0	2301	3	US-09-232-201-8	Sequence 8, Appl
	c	752	58	2.0	253	2	US-08-897-126-25	Sequence 25, Appl		825	57	2.0	2301	3	US-09-232-195-8	Sequence 8, Appl
	753	58	2.0	329	4	US-09-621-976-16012	Sequence 16012, A			826	57	2.0	2540	4	US-09-949-016-431	Sequence 431, App
	754	58	2.0	332	4	US-09-621-976-16031	Sequence 16031, A			827	57	2.0	2710	3	US-09-232-200-44	Sequence 44, Appl
	c	755	58	2.0	467	2	US-08-841-349-18	Sequence 18, Appl		828	57	2.0	2710	3	US-09-232-200-70	Sequence 70, Appl
	c	756	58	2.0	467	4	US-09-431-184A-18	Sequence 18, Appl		829	57	2.0	2710	3	US-09-232-197-44	Sequence 44, Appl
	757	58	2.0	509	3	US-09-030-607-202	Sequence 202, App			830	57	2.0	2710	3	US-09-232-197-44	Sequence 44, Appl

831	57	2.0	2710	3	US-09-232-137-70	Sequence 70, Appl	904	55	1.9	940	2	US-08-471-717-1	Sequence 1, Appli
832	57	2.0	2710	3	US-09-232-201-44	Sequence 44, Appl	905	55	1.9	1181	3	US-09-149-476-310	Sequence 310, App
833	57	2.0	2710	3	US-09-232-201-70	Sequence 70, Appl	906	55	1.9	1212	3	US-09-149-476-186	Sequence 186, App
834	57	2.0	2710	4	US-09-232-195-44	Sequence 44, Appl	907	55	1.9	1291	4	US-09-524-101D-5	Sequence 5, Appli
835	57	2.0	2710	4	US-09-232-195-70	Sequence 70, Appl	908	55	1.9	1653	3	US-09-345-469-2	Sequence 2, Appli
836	57	2.0	3300	3	US-09-336-643A-82	Sequence 82, Appl	909	55	1.9	1708	4	US-09-859-053-31	Sequence 31, Appl
837	57	2.0	4895	3	US-09-053-866-1	Sequence 1, Appli	910	55	1.9	1776	3	US-08-655-352-10	Sequence 10, Appl
838	57	2.0	4895	3	US-09-479-130-1	Sequence 1, Appli	911	55	1.9	1776	3	US-09-258-016-10	Sequence 10, Appl
839	57	2.0	4895	3	US-09-472-130A-1	Sequence 1, Appli	912	55	1.9	1776	3	US-09-257-825B-10	Sequence 10, Appl
840	57	2.0	8643	4	US-10-029-907-4	Sequence 4, Appli	913	55	1.9	1886	4	US-09-594-506-31	Sequence 31, Appl
841	56	2.0	56	4	US-09-621-976-12139	Sequence 12139, A	914	55	1.9	1897	1	US-08-184-632-1	Sequence 1, Appli
842	56	2.0	56	4	US-09-621-976-14556	Sequence 14556, A	915	55	1.9	1934	3	US-08-776-844-1	Sequence 1, Appli
843	56	2.0	81	4	US-09-513-999C-17324	Sequence 17324, A	916	55	1.9	1934	3	US-09-909-325-1	Sequence 1, Appli
844	56	2.0	87	4	US-09-621-976-14849	Sequence 14849, A	917	55	1.9	1934	4	US-09-909-326-1	Sequence 1, Appli
845	56	2.0	135	4	US-09-621-976-11087	Sequence 11087, A	918	55	1.9	2331	4	US-09-866-028-54	Sequence 54, Appl
846	56	2.0	156	4	US-09-621-976-9095	Sequence 9095, Ap	919	55	1.9	2331	4	US-09-944-457-54	Sequence 54, Appl
847	56	2.0	213	4	US-09-621-976-16536	Sequence 16536, A	920	55	1.9	2349	4	US-09-805-455-1	Sequence 1, Appli
848	56	2.0	246	4	US-09-621-976-16288	Sequence 16288, A	921	55	1.9	2695	4	US-09-706-137-3	Sequence 3, Appli
849	56	2.0	269	4	US-09-621-976-16936	Sequence 16936, A	922	55	1.9	2808	4	US-09-917-254-27	Sequence 27, Appl
850	56	2.0	334	4	US-09-621-976-16434	Sequence 16434, A	923	55	1.9	2821	4	US-09-702-705-1669	Sequence 1669, Ap
851	56	2.0	1174	2	US-08-872-437-1	Sequence 186, App	924	55	1.9	2821	4	US-09-736-457-1669	Sequence 1669, Ap
852	56	2.0	1174	3	US-08-651-136C-11	Sequence 11, Appl	925	55	1.9	2821	4	US-09-671-325-1669	Sequence 1669, Ap
853	56	2.0	1174	3	US-09-229-911A-11	Sequence 11, Appl	926	55	1.9	2821	4	US-09-658-824-1669	Sequence 1669, Ap
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855	56	2.0	1534	1	US-08-300-903A-6	Sequence 6, Appli	928	55	1.9	5503	2	US-08-726-012B-1	Sequence 1, Appli
856	56	2.0	1534	4	US-08-988-197-6	Sequence 6, Appli	929	55	1.9	5503	4	US-09-023-655-989	Sequence 989, App
857	56	2.0	1534	4	US-10-385-072-6	Sequence 6, Appli	930	55	1.9	15450	4	US-09-470-661A-1	Sequence 1, Appli
858	56	2.0	1534	4	US-10-385-072-6	Sequence 6, Appli	931	55	1.9	139552	4	US-09-949-016-15300	Sequence 15300, A
859	56	2.0	1538	4	US-09-205-258-193	Sequence 193, App	932	55	1.9	192506	4	US-09-949-016-15830	Sequence 15830, A
860	56	2.0	1604	1	US-08-665-966-9	Sequence 9, Appli	933	54	1.9	54	4	US-08-621-976-14994	Sequence 14994, A
861	56	2.0	1604	3	US-09-041-780-9	Sequence 9, Appli	934	54	1.9	61	4	US-09-621-976-11967	Sequence 11967, A
862	56	2.0	1618	4	US-09-800-729-29	Sequence 29, Appli	935	54	1.9	80	3	US-09-284-627-15	Sequence 15, Appl
863	56	2.0	1804	2	US-08-504-459-5	Sequence 5, Appli	936	54	1.9	83	4	US-09-621-976-12087	Sequence 12087, A
864	56	2.0	2026	2	US-08-993-228-3	Sequence 3, Appli	937	54	1.9	83	4	US-09-621-976-12175	Sequence 12175, A
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866	56	2.0	2280	4	US-09-546-553-1	Sequence 1, Appli	939	54	1.9	83	4	US-09-621-976-12450	Sequence 12450, A
867	56	2.0	2285	2	US-08-967-101-136	Sequence 136, App	940	54	1.9	91	4	US-09-621-976-12161	Sequence 12161, A
868	56	2.0	2285	2	US-08-592-541-136	Sequence 136, App	941	54	1.9	257	2	US-08-520-678A-24	Sequence 24, Appl
869	56	2.0	2285	3	US-09-124-698-136	Sequence 136, App	942	54	1.9	257	3	US-08-897-126-24	Sequence 24, Appl
870	56	2.0	2285	3	US-09-124-480-136	Sequence 136, App	943	54	1.9	298	4	US-09-621-976-3871	Sequence 3871, Ap
871	56	2.0	2285	3	US-09-124-523-136	Sequence 136, App	944	54	1.9	365	4	US-09-621-976-14699	Sequence 14699, A
872	56	2.0	2285	4	US-09-636-736A-136	Sequence 136, App	945	54	1.9	1001	1	US-08-728-259A-10	Sequence 10, Appl
873	56	2.0	2797	4	US-09-482-273-74	Sequence 74, Appl	946	54	1.9	1001	2	US-08-473-486-10	Sequence 10, Appl
874	56	2.0	3350	2	US-08-663-566A-1	Sequence 1, Appli	947	54	1.9	1151	4	US-09-270-767-12633	Sequence 12633, A
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876	56	2.0	3350	2	US-08-288-065A-1	Sequence 1, Appli	949	54	1.9	1230	4	US-09-244-805-6	Sequence 6, Appli
877	56	2.0	3350	2	US-08-362-240A-1	Sequence 1, Appli	950	54	1.9	1271	4	US-09-905-558D-1	Sequence 1, Appli
878	56	2.0	3350	5	PCT-US95-10245-1	Sequence 1, Appli	951	54	1.9	1302	4	US-09-322-409-31	Sequence 91, Appl
879	56	2.0	3871	2	US-08-599-455B-3	Sequence 3, Appli	952	54	1.9	1302	4	US-09-322-409-33	Sequence 93, Appl
880	56	2.0	3871	3	US-09-069-781B-3	Sequence 3, Appli	953	54	1.9	1302	4	US-09-451-527-91	Sequence 91, Appl
881	56	2.0	3871	3	US-09-137-132-3	Sequence 3, Appli	954	54	1.9	1302	4	US-09-451-527-93	Sequence 93, Appl
882	56	2.0	3871	3	US-08-864-564A-3	Sequence 3, Appli	955	54	1.9	1395	2	US-08-553-367A-1	Sequence 1, Appli
883	56	2.0	3871	3	US-09-094-410-3	Sequence 3, Appli	956	54	1.9	1395	3	US-09-295-306-1	Sequence 1, Appli
884	56	2.0	3871	4	US-08-708-123D-3	Sequence 3, Appli	957	54	1.9	1395	3	US-09-734-719-1	Sequence 1, Appli
885	56	2.0	3871	4	US-08-583-153A-3	Sequence 3, Appli	958	54	1.9	1705	4	US-09-205-258-216	Sequence 216, App
886	56	2.0	3871	4	US-08-570-142D-3	Sequence 3, Appli	959	54	1.9	1707	4	US-09-311-021-51	Sequence 51, Appl
887	56	2.0	670689	4	US-08-638-524B-3	Sequence 3, Appli	960	54	1.9	2296	3	US-08-496-841C-137	Sequence 137, App
888	56	2.0	670689	4	US-09-949-016-12505	Sequence 12505, A	961	54	1.9	2311	4	US-09-614-912-91	Sequence 91, Appl
889	56	2.0	670690	4	US-09-949-016-14207	Sequence 14207, A	962	54	1.9	2369	4	US-09-057-986-13	Sequence 13, Appl
890	55	1.9	55	4	US-09-621-976-14535	Sequence 14535, A	963	54	1.9	2406	4	US-09-594-506-37	Sequence 37, Appl
891	55	1.9	55	4	US-09-621-976-14800	Sequence 14800, A	964	54	1.9	2516	4	US-09-949-016-766	Sequence 766, App
892	55	1.9	159	4	US-09-621-976-17182	Sequence 17182, A	965	54	1.9	2668	3	US-09-370-838-156	Sequence 156, App
893	55	1.9	184	4	US-09-513-999C-36135	Sequence 36135, A	966	54	1.9	2668	4	US-09-854-133-156	Sequence 156, App
894	55	1.9	204	4	US-09-621-976-16458	Sequence 16458, A	967	54	1.9	3623	4	US-09-918-909A-23	Sequence 23, Appl
895	55	1.9	270	4	US-09-621-976-17927	Sequence 17927, A	968	54	1.9	3842	3	US-09-115-954-7	Sequence 7, Appli
896	55	1.9	276	4	US-09-621-976-18329	Sequence 18329, A	969	54	1.9	3912	3	US-09-115-954-1	Sequence 1, Appli
897	55	1.9	326	4	US-09-621-976-16024	Sequence 16024, A	970	54	1.9	5878	4	US-09-949-016-939	Sequence 939, App
898	55	1.9	339	4	US-09-621-976-16015	Sequence 16015, A	971	54	1.9	118143	4	US-09-949-016-17196	Sequence 17196, A
899	55	1.9	375	3	US-08-946-026-23	Sequence 23, Appl	972	53	1.9	53	4	US-09-621-976-12332	Sequence 12332, A
900	55	1.9	474	3	US-08-516-859A-97	Sequence 97, Appl	973	53	1.9	56	4	US-09-621-976-14989	Sequence 14989, A
901	55	1.9	474	3	US-09-586-472-97	Sequence 97, Appl	974	53	1.9	56	4	US-09-621-976-13461	Sequence 13461, A
902	55	1.9	474	3	US-09-528-706-97	Sequence 97, Appl	975	53	1.9	82	4	US-09-621-976-11689	Sequence 11689, A
903	55	1.9	487	3	US-09-257-179-22	Sequence 22, Appl	976	53	1.9	82	4	US-09-621-976-11841	Sequence 11841, A

977	53	1.9	82	4	US-09-621-976-11864	Sequence 11864, A	c1050	52	1.8	685	3	US-09-227-357-66	Sequence 66, Appl
978	53	1.9	82	4	US-09-621-976-11888	Sequence 11888, A	1051	52	1.8	1050	4	US-09-482-273-58	Sequence 58, Appl
979	53	1.9	82	4	US-09-621-976-11844	Sequence 11844, A	1052	52	1.8	1184	4	US-09-489-847-76	Sequence 76, Appl
980	53	1.9	82	4	US-09-621-976-11949	Sequence 11949, A	1053	52	1.8	1525	4	US-09-461-325-110	Sequence 110, App
981	53	1.9	82	4	US-09-621-976-12015	Sequence 12015, A	1054	52	1.8	1525	4	US-10-012-542-110	Sequence 110, App
982	53	1.9	82	4	US-09-621-976-12088	Sequence 12088, A	1055	52	1.8	1525	4	US-10-115-123-110	Sequence 110, App
983	53	1.9	82	4	US-09-621-976-12103	Sequence 12103, A	1056	52	1.8	1527	4	US-09-244-111-7	Sequence 7, Appl
984	53	1.9	82	4	US-09-621-976-12127	Sequence 12127, A	1057	52	1.8	1558	1	US-08-455-550-7	Sequence 7, Appl
985	53	1.9	82	4	US-09-621-976-12131	Sequence 12131, A	1058	52	1.8	1810	4	US-09-800-729-73	Sequence 73, Appl
986	53	1.9	82	4	US-09-621-976-12137	Sequence 12137, A	1059	52	1.8	1811	4	US-09-800-729-77	Sequence 77, Appl
987	53	1.9	82	4	US-09-621-976-12132	Sequence 12132, A	1060	52	1.8	2719	3	US-08-706-216-1	Sequence 1, Appl
988	53	1.9	82	4	US-09-621-976-12434	Sequence 12434, A	1061	52	1.8	2719	3	US-09-650-284-B	Sequence 1, Appl
989	53	1.9	82	4	US-09-621-976-13499	Sequence 13499, A	1062	52	1.8	2836	3	US-08-747-221B-24	Sequence 24, Appl
990	53	1.9	82	4	US-09-621-976-13499	Sequence 13499, A	1063	52	1.8	2836	3	US-08-747-221B-26	Sequence 26, Appl
991	53	1.9	83	4	US-09-621-976-13526	Sequence 13526, A	1064	52	1.8	2836	3	US-09-005-051-24	Sequence 24, Appl
992	53	1.9	106	4	US-09-621-976-12079	Sequence 12079, A	1065	52	1.8	2836	3	US-09-005-051-26	Sequence 26, Appl
993	53	1.9	132	4	US-09-621-976-13992	Sequence 13992, A	1066	52	1.8	2836	4	US-09-403-942F-24	Sequence 24, Appl
994	53	1.9	140	4	US-09-621-976-17449	Sequence 17449, A	1067	52	1.8	2836	4	US-09-403-942F-26	Sequence 26, Appl
995	53	1.9	166	4	US-09-621-976-8651	Sequence 8651, Ap	1068	52	1.8	2837	2	US-08-993-228-11	Sequence 11, Appl
996	53	1.9	235	4	US-09-621-976-9455	Sequence 9455, Ap	1069	52	1.8	3136	4	US-09-680-728-1	Sequence 1, Appl
997	53	1.9	244	4	US-09-621-976-484	Sequence 484, App	1070	52	1.8	3136	4	US-10-017-066A-1	Sequence 1, Appl
998	53	1.9	351	4	US-09-621-976-16140	Sequence 16140, A	1071	51	1.8	57	4	US-09-621-976-12150	Sequence 12150, A
999	53	1.9	443	4	US-09-621-976-17631	Sequence 17631, A	1072	51	1.8	61	4	US-09-621-976-14754	Sequence 14754, A
1000	53	1.9	773	3	US-09-149-476-20	Sequence 20, Appl	1073	51	1.8	63	4	US-09-621-976-12231	Sequence 12231, A
1001	53	1.9	872	3	US-09-248-335-63	Sequence 63, Appl	1074	51	1.8	75	4	US-09-621-976-15073	Sequence 15073, A
1002	53	1.9	882	2	US-08-909-965C-9	Sequence 9, Appl	1075	51	1.8	327	4	US-09-621-976-16141	Sequence 16141, A
1003	53	1.9	1013	1	US-07-920-519-30	Sequence 30, Appl	1076	51	1.8	335	4	US-09-621-976-161038	Sequence 161038, A
1004	53	1.9	1013	1	US-08-086-410-23	Sequence 23, Appl	1077	51	1.8	356	2	US-08-520-678A-22	Sequence 22, Appl
1005	53	1.9	1013	1	US-08-314-586-30	Sequence 30, Appl	1078	51	1.8	356	3	US-08-897-126-22	Sequence 22, Appl
1006	53	1.9	1315	3	US-09-721-822A-10	Sequence 10, Appl	1079	51	1.8	371	4	US-09-621-976-16048	Sequence 16048, A
1007	53	1.9	1376	4	US-09-489-847-120	Sequence 120, App	1080	51	1.8	495	4	US-09-220-132-186	Sequence 186, App
1008	53	1.9	1376	4	US-09-489-847-66	Sequence 66, Appl	1081	51	1.8	508	4	US-09-621-976-17886	Sequence 17886, A
1009	53	1.9	1619	4	US-09-522-714-11	Sequence 11, Appl	1082	51	1.8	742	1	US-07-847-010-12	Sequence 12, Appl
1010	53	1.9	1722	4	US-09-482-273-102	Sequence 102, App	1083	51	1.8	769	4	US-09-513-775B-5	Sequence 5, Appl
1011	53	1.9	1810	4	US-09-369-247-11	Sequence 11, Appl	1084	51	1.8	780	2	US-08-540-804-36	Sequence 36, Appl
1012	53	1.9	1858	2	US-08-909-965C-11	Sequence 11, Appl	1085	51	1.8	780	3	US-08-590-399-36	Sequence 36, Appl
1013	53	1.9	1867	4	US-09-482-273-81	Sequence 81, Appl	1086	51	1.8	785	4	US-09-518-036-9	Sequence 9, Appl
1014	53	1.9	1949	4	US-09-461-325-26	Sequence 26, Appl	1087	51	1.8	785	4	US-10-279-130-9	Sequence 9, Appl
1015	53	1.9	1949	4	US-10-012-542-26	Sequence 26, Appl	1088	51	1.8	803	4	US-09-800-729-60	Sequence 60, Appl
1016	53	1.9	1949	4	US-10-115-123-26	Sequence 26, Appl	1089	51	1.8	974	2	US-08-504-459-13	Sequence 13, Appl
1017	53	1.9	2327	4	US-10-066-130-20	Sequence 20, Appl	1090	51	1.8	1049	4	US-09-800-729-67	Sequence 67, Appl
1018	53	1.9	2648	3	US-09-417-455-6	Sequence 6, Appl	1091	51	1.8	1100	3	US-09-248-335-53	Sequence 53, Appl
1019	53	1.9	2648	3	US-09-348-942-6	Sequence 6, Appl	1092	51	1.8	1212	3	US-09-182-145-34	Sequence 34, Appl
1020	53	1.9	2648	3	US-09-457-626-6	Sequence 6, Appl	1093	51	1.8	1212	3	US-09-182-145-35	Sequence 35, Appl
1021	53	1.9	2648	4	US-09-576-008-6	Sequence 6, Appl	1094	51	1.8	1215	4	US-09-646-693-1	Sequence 1, Appl
1022	53	1.9	2674	4	US-10-066-130-19	Sequence 19, Appl	1095	51	1.8	1332	3	US-09-333-423-1	Sequence 1, Appl
1023	53	1.9	2771	4	US-10-066-130-18	Sequence 18, Appl	1096	51	1.8	1375	3	US-09-332-422A-37	Sequence 37, Appl
1024	53	1.9	2880	3	US-09-115-954-3	Sequence 3, Appl	1097	51	1.8	1445	3	US-09-697-367-19	Sequence 19, Appl
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1027	53	1.9	3268	4	US-09-291-417D-1	Sequence 1, Appl	1100	51	1.8	1699	3	US-09-152-060-19	Sequence 19, Appl
1028	53	1.9	5860	4	US-10-066-130-17	Sequence 17, Appl	1101	51	1.8	1728	3	US-08-985-950-7	Sequence 7, Appl
c1029	53	1.9	12980	3	US-08-811-566-5	Sequence 5, Appl	1102	51	1.8	1728	3	US-09-546-049-7	Sequence 7, Appl
c1030	53	1.9	12980	3	US-09-034-756-5	Sequence 5, Appl	1103	51	1.8	1781	3	US-09-499-302A-1	Sequence 1, Appl
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1282	49	1.7	4780	3	US-08-936-135-23	Sequence 23, Appl	1355	48	1.7	2584	4	US-08-716-129-47	Sequence 47, Appl
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1286	49	1.7	5581	4	US-10-164-595-19	Sequence 19, Appl	1359	48	1.7	2643	4	US-09-949-016-365	Sequence 365, App
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1292	49	1.7	193303	4	US-09-497-855A-44	Sequence 44, Appl	1365	48	1.7	2822	4	US-08-762-500-74	Sequence 74, Appl
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c1294	49	1.7	524032	4	US-09-949-016-16929	Sequence 16929, A	1367	48	1.7	2822	4	US-09-949-016-12991	Sequence 12991, A
c1295	49	1.7	524032	4	US-09-949-016-16930	Sequence 16930, A	1368	48	1.7	2822	4	US-09-949-016-16709	Sequence 16709, A
c1296	49	1.7	524032	4	US-09-949-016-16931	Sequence 16931, A	1369	48	1.7	5894	3	US-09-949-016-13076	Sequence 13076, A
c1297	49	1.7	529885	4	US-09-949-016-14340	Sequence 14340, A	1370	48	1.7	5894	3	US-09-949-016-13076	Sequence 13076, A
c1298	49	1.7	529885	4	US-09-949-016-14341	Sequence 14341, A	1371	48	1.7	5894	3	US-09-949-016-13076	Sequence 13076, A
c1299	49	1.7	529885	4	US-09-949-016-14342	Sequence 14342, A	1372	48	1.7	5894	3	US-09-949-016-13076	Sequence 13076, A
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1307	48	1.7	138	4	US-09-621-976-8112	Sequence 8112, Ap	1380	48	1.7	5894	3	US-09-949-016-13076	Sequence 13076, A
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1335	48	1.7	1405	4	US-09-668-097A-15	Sequence 15, Appl	1408	48	1.7	5894	3	US-09-949-016-13076	Sequence 13076, A
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Qy	2586	CAGCCCAAGGGCAGCAGAGCTGGGATGTGGTGATGCTTTGTGTACATGAGCCACAGTACA	2645
Db	2111	CAGCCCAAGGGCAGCAGAGCTGGGATGTGGTGATGCTTTGTGTACATGAGCCACAGTACA	2170
Qy	2646	GTCCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAATAAATAAGGGTTGGCTTC	2705
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Qy	2706	TGAACTACAAAAAATAAAAAAAAAAAAAA	2734
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RESULT 4
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; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: astacin/m 12a metalloproteases
US-09-280-116-179

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Best Local Similarity	99.8%;	Pred. No. 5.8e-134;		
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Qy	501	GGTTTGTGATCCCACTAAGATTTGTGCATGTTGTAGTCTGGAGTTTGACTACATGTGCCAGT	560	
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Qy	561	ATGACTATGTTGAGGTTTCGTGATGGAGACAACCCCGATGGCCAGATCATCAAGCGTGTCT	620	
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Qy	621	GTGGCAACGAGCGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCAGTCTCTCTTCC	680	
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Qy	681	ACTCCGATGGCTCCAAGAAATTTTTCACGGTTTCCATGCGATTTATGAGGAGATCACAGCAT	740	
Db	351	ACTCCGATGGCTCCAAGAAATTTTTCACGGTTTCCATGCGATTTATGAGGAGATCACAGCAT	410	
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Qy      801 A 801
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Db      471 A 471

      RESULT 5
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      ; Sequence 104, Application US/09280116A
      ; Patent No. 6311427
      ; GENERAL INFORMATION:
      ; APPLICANT: Robison, Keith E.
      ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
      ; FILE REFERENCE: 5800-24, 035800/176965
      ; CURRENT APPLICATION NUMBER: US/09/280,116A
      ; CURRENT FILING DATE: 1999-03-26
      ; NUMBER OF SEQ ID NOS: 268
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      ; OTHER INFORMATION: trypsin-like serine proteases
      ; FEATURE:
      ; NAME/KEY: misc feature
      ; LOCATION: (1)..(2886)
      ; OTHER INFORMATION: n = a, t, c or g
      US-09-280-116-104

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Query Match	11.6%	Score 329,	DB 3,	Length 2885;
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DB	815	GATGGCTCCAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCC	874	
QY	746	TCATCCCTTGTGTTTCCATGACGGCA CGTGGCTCCTTGACAAGCTGGATCTTACAAGTGT	805	
DB	875	TCATCCCTTGTGTTTCCATGACGGCA CGTGGCTCCTTGACAAGCTGGATCTTACAAGTGT	934	
QY	806	GCCTGCTTGGCAGCG - TATACTGGCAGCGCTGTGAAAATCTCTTGAGAAAGAAACTG	864	
DB	935	GCCTGCTTGGCAGCGTTATACTGGCAGCGCTGTGAAAATCTCTTGAGAAAGAAACTG	994	
QY	865	CTCAGACCTTGGGGGCCAGTCAATGGGTACGAGAAAATAACAGGGGGCCCTGGGCTTAT	924	
DB	995	CTCAGACCTTGGGGGCCAGTCAATGGGTACGAGAAAATAACAGGGGGCCCTGGGCTTAT	1054	
QY	925	CAACGACGCCATGCTTAAATTCGCACCGTGGTGCTCTTCTTTTGTAAACAATCCTTATGT	984	
DB	1055	CAACGACGCCATGCTTAAATTTGGCACCGTGGTGCTCTTCTTTTGTAAACAATCCTTATGT	1114	
QY	985	TCTTAGTGGCAATGAGAAAAGAACTTGCCACGACAGAAATGGAGAGTGGTTCAGGGAACAGCC	1044	
DB	1115	TCTTAGTGGCAATGAGAAAAGAACTTGCCACGACAGAAATGGAGAGTGGTTCAGGGAACAGCC	1174	
QY	1045	CATCTGCAAAAAGCCTGCCGAGAACCAAAAGATTTTCAGACCTGGTGAAGAGGAGTCT	1104	
DB	1175	CATCTGCAAAAAGCCTGCCGAGAACCAAAAGATTTTCAGACCTGGTGAAGAGGAGTCT	1234	
QY	1105	TCCGATCGAGGTTTCAGTCAAGGGAGACAC	1134	
DB	1235	TCCGATCGAGGTTTCAGTCAAGGGAGACAC	1264	

RESULT 6  
US-09-537-654-3  
; Sequence 3, Application US/09537654  
; Patent No. 6720478  
; GENERAL INFORMATION:  
; APPLICANT: Mahajan, Pramod B.  
; APPLICANT: Shi, Jinrui

;; TITLE OF INVENTION: A No. 6720478e1 Maize Rad51-Like Gene and Uses  
;; FILE OF INVENTION: Thereof  
;; FILE REFERENCE: 1107  
;; CURRENT APPLICATION NUMBER: US/09/537,654  
;; CURRENT FILING DATE: 2000-03-29  
;; EARLIER APPLICATION NUMBER: 60/132,582  
;; EARLIER FILING DATE: 1999-05-05  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 3  
;; LENGTH: 1459  
;; TYPE: DNA  
;; ORGANISM: Zea mays  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (169)...(1011)  
US-09-537-654-3

Query Match 4.7%; Score 134; DB 4; Length 1459;  
Best Local Similarity 100.0%; Pred. No. 1.4e-42;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2713 CAAA 2772  
DB 1314 CAAA 1373  
QY 2773 AA 2832  
DB 1374 AA 1433  
QY 2833 AAAAAAAAAAAAAAAAAA 2846  
DB 1434 AAAAAAAAAAAAAAAAAA 1447

RESULT 7  
US-09-370-838-151  
;; Sequence 151, Application US/09370838  
;; Patent No. 644425  
;; GENERAL INFORMATION:  
;; APPLICANT: Reed, Steven G.  
;; APPLICANT: Lodes, Michael J.  
;; APPLICANT: Mohamath, Roadoh  
;; APPLICANT: Secrist, Heather  
;; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
;; FILE OF INVENTION: LONG CANCER AND METHODS FOR THEIR USE  
;; FILE REFERENCE: 210121.475C1  
;; CURRENT APPLICATION NUMBER: US/09/370,838  
;; CURRENT FILING DATE: 1999-08-09  
;; EARLIER APPLICATION NUMBER: US 09/285,323  
;; EARLIER FILING DATE: 1999-04-02  
;; NUMBER OF SEQ ID NOS: 289  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 151  
;; LENGTH: 3275  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-09-370-838-151

Query Match 4.7%; Score 134; DB 3; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2713 CAAA 2772  
DB 3128 CAAA 3187  
QY 2773 AA 2832  
DB 3188 AA 3247  
QY 2833 AAAAAAAAAAAAAA 2846  
|||||

Db 3248 AAAAAAAAAAAAAA 3261  
RESULT 8  
US-09-854-133-151  
;; Sequence 151, Application US/09854133  
;; Patent No. 6759508  
;; GENERAL INFORMATION:  
;; APPLICANT: Lodes, Michael J.  
;; APPLICANT: Mohamath, Roadoh  
;; APPLICANT: Henderson, Robert A.  
;; APPLICANT: Benson, Darin R.  
;; APPLICANT: Secrist, Heather  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
;; FILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.475C10  
;; CURRENT APPLICATION NUMBER: US/09/854,133  
;; CURRENT FILING DATE: 2001-05-11  
;; NUMBER OF SEQ ID NOS: 735  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 151  
;; LENGTH: 3275  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-09-854-133-151

Query Match 4.7%; Score 134; DB 4; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.3e-42;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2713 CAAA 2772  
DB 3128 CAAA 3187  
QY 2773 AA 2832  
DB 3188 AA 3247  
QY 2833 AAAAAAAAAAAAAA 2846  
DB 3248 AAAAAAAAAAAAAA 3261  
|||||

RESULT 9  
US-08-628-417-6  
;; Sequence 6, Application US/08628417  
;; Patent No. 5627054  
;; GENERAL INFORMATION:  
;; APPLICANT: GILLESPIE, DAVID  
;; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC  
;; TITLE OF INVENTION: POLYMERASE CHAIN REACTION  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL  
;; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)  
;; CITY: ABERDEEN PROVING GROUND  
;; STATE: MARYLAND  
;; COUNTRY: USA  
;; ZIP: 21010-5423  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/628,417  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BIFFONT, ULYSSES J  
;; REGISTRATION NUMBER: 39,908  
;; REFERENCE/DOCKET NUMBER: DAM 398-94

## RESULT 11



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 9, 2005, 20:53:28 ; Search time 8260 Seconds  
(without alignments)  
4223.699 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945  
Sequence: 1 MEUGCTWQLGLTFLQLLLIS.....LSTAFKTVLPFKDWIERNMK 720

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2 1/USPTO.spool/US10063692/runat\_09052005\_122254\_4863/app\_query.fasta\_1.903  
-DB=GenEmbl -QFMT=fastap -SUPPLX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -NATRIK=blotsum62 -FRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10063692 @CGN 1 1 5469 @runat\_09052005\_122254\_4863 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	2846	6	AR252533 Sequence
2	3945	100.0	2846	6	AX092306 Sequence
3	3945	100.0	2846	6	AX376102 Sequence
4	3945	100.0	2846	6	AX403343 Sequence

5	3945	100.0	2846	9	AY358346	AY358346 Homo sapi
6	3941	99.9	2768	9	HSM803699	AL832391 Homo sapi
7	3939	99.8	2306	6	AX084209	AX084209 Sequence
8	3939	99.8	2306	6	AX133839	AX133839 Sequence
9	3921.5	99.4	2289	6	BD012236	BD012236 A novel g
10	3921.5	99.4	2784	6	BD157134	BD157134 Primer fo
11	3921.5	99.4	2784	6	AX878296	AX878296 Sequence
12	3921.5	99.4	2784	6	BD012234	BD012234 A novel g
13	3921.5	99.4	2784	9	AK027841	AK027841 Homo sapi
14	3612	91.6	2244	6	BD012235	BD012235 A novel g
15	3612	91.6	2841	10	BC031841	BC031841 Mus muscu
16	3612	91.6	2841	10	BC057685	BC057685 Mus muscu
17	3500.5	88.7	2632	6	AX704692	AX704692 Sequence
18	3450.5	87.5	2886	6	AX263926	AX263926 Sequence
19	3432.5	79.4	1867	6	AX084207	AX084207 Sequence
20	2987	75.7	1669	6	CQ723377	CQ723377 Sequence
21	2977.5	75.5	2350	9	BC038457	BC038457 Homo sapi
22	2946.5	74.7	2259	6	AR541687	AR541687 Sequence
23	2823	71.6	5735	5	BC075430	BC075430 Xenopus t
24	2678.5	67.9	2142	6	AR339515	AR339515 Sequence
25	2678.5	67.9	2144	6	AR339478	AR339478 Sequence
26	1413.5	35.8	142522	9	AC090625	AC090625 Homo sapi
27	1396.5	35.4	141818	2	AL133389	AL133389 Homo sapi
28	1386.5	35.1	208659	2	AC067845	AC067845 Homo sapi
29	1298	32.9	217777	2	AC113891	AC113891 Rattus no
30	1296	32.9	188958	10	AL844605	AL844605 Mouse DNA
31	1295	32.8	222330	2	AC096255	AC096255 Rattus no
32	1191	30.2	705	6	BD150061	BD150061 Primer fo
33	1191	30.2	705	6	AX869999	AX869999 Sequence
34	1124.5	28.5	246369	2	AC125707	AC125707 Rattus no
35	949	24.1	1088	9	HSM800511	AR264001 Sequence
36	893	22.6	505	6	AR264001	AR264001 Sequence
37	824	20.9	421	6	CQ723379	CQ723379 Sequence
38	755	19.1	106657	9	AL354921	AL354921 Human DNA
39	681.5	17.3	657	5	CR387267	CR387267 Gallus ga
40	672	17.2	3060	3	AP467804	AP467804 Tachypieu
41	672	17.0	3467	3	TATLFC1	D90271 Tachypieu
42	665	16.9	3438	6	S77063	S77063 factor C-en
43	665	16.9	3448	6	AR028519	AR028519 Sequence
44	665	16.9	3448	6	AR086513	AR086513 Sequence
45	665	16.9	3448	6	I88008	I88008 Sequence 3
46	665	16.9	3448	6	AR429665	AR429665 Sequence
47	665	16.9	3448	6	AX12199	AX12199 Sequence
48	665	16.9	3448	6	AX112199	AX112199 Sequence
49	665	16.9	4182	3	S77064	S77064 factor C-en
50	665	16.9	4182	6	AR028518	AR028518 Sequence
51	665	16.9	4182	6	AR086512	AR086512 Sequence
52	665	16.9	4182	6	I88007	I88007 Sequence 1
53	665	16.9	4182	6	AR429664	AR429664 Sequence
54	665	16.9	4182	6	AR42794	AR42794 Sequence
55	665	16.9	4182	6	AX112197	AX112197 Sequence
56	608.5	15.4	2695	3	AB089267	AB089267 Branchios
57	597	15.1	2782	3	AB089268	AB089268 Branchios
58	580	14.7	340	6	BD076812	BD076812 5' EST of
59	512.5	13.0	3305	5	BC073178	BC073178 Xenopus l
60	490.5	12.4	3636	5	AY567829	AY567829 Gallus ga
61	489.5	12.4	2550	5	D83276	D83276 Xenopus lae
62	483	12.2	2108	10	RNO277423	AJ277423 Rattus no
63	482.5	12.2	5112	10	RNO457084	AJ457084 Rattus no
64	482	12.2	2787	9	HUMWASP	D28593 Human mRNA
65	482	12.2	4457	5	AB078636	AB078636 Xenopus l
66	476	12.1	4489	9	D17525	D17525 Human mRNA
67	475	12.0	2752	6	CQ714371	CQ714371 Sequence
68	475	12.0	5135	10	MUSCRARF	D16492 Mouse mRNA
69	471	11.9	3895	6	AX156466	AX156466 Sequence
70	469.5	11.9	4696	5	AB078637	AB078637 Xenopus l
71	468	11.9	3895	9	AF284421	AF284421 Homo sapi
72	461	11.7	3863	6	AX254423	AX254423 Sequence
73	459.5	11.6	369	6	AX395272	AX395272 Sequence
74	457	11.6	2407	5	AB009074	AB009074 Triakla s
75	455	11.5	3713	9	HSM807381	EX647237 Homo sapi
76	452	11.5	3736	10	AB049755	AB049755 Mus muscu
77	450.5	11.4	2217	5	BC084139	BC084139 Xenopus t



78	448	11.4	3229	5	AB009073	AB009073 Cyprinus	151	335.5	8.5	3147	6	AX207945	AX207945 Sequence
79	447	11.3	2449	5	AY567828	AY567828 Gallus ga	152	335.5	8.5	3147	9	AF057145	AF057145 Homo sapi
80	436.5	11.1	3255	5	AB089265	AB089265 Lethenter	153	335	8.5	4989	3	AY380790	AY380790 Manduca s
81	435	11.0	162877	2	CR318591	CR318591 Danio rer	154	334	8.5	1662	5	AF515270	AF515270 Danio rer
82	429	10.9	2416	10	AF148216	AF148216 Mus muscu	155	333	8.4	3073	9	AK055183	AK055183 Homo sapi
83	428	10.8	2409	10	BC004637	BC004637 Mus muscu	156	331.5	8.4	3696	6	AX207959	AX207959 Sequence
84	425.5	10.8	3950	10	BC004637	BC004637 Mus muscu	157	331.5	8.4	3696	6	AX677073	AX677073 Sequence
85	425	10.8	2282	5	AB009072	AB009072 Rattus no	158	331.5	8.4	3696	6	HSU09860	HSU09860 Human enter
86	424	10.7	2037	10	RNO277747	Y18572 Rattus no	159	331	8.4	1182	9	AB036334	AB036334 Homo sapi
87	420	10.6	1937	10	RNO18572	Y18572 Rattus norv	160	331	8.4	2616	9	HSC1S	X06596 Human mRNA
88	417	10.6	3070	10	BC013893	BC013893 Mus muscu	161	330.5	8.4	3586	4	PIGENPR	D30799 Sus scrofa
89	416.5	10.6	2166	10	AF459018	AF459018 Mus muscu	162	329.5	8.4	10944	9	AY017307	AY017307 Homo sapi
90	412	10.4	2090	10	AB009459	AB009459 Mus muscu	163	329.5	8.4	11580	9	AF333704	AF333704 Homo sapi
91	406.5	10.3	3202	5	BC079773	BC079773 Xenopus l	164	329	8.3	11221	10	AY017475	AY017475 Mus muscu
92	404	10.2	2450	9	HSMA5P2PR	Y98400 H.sapiens m	165	328.5	8.3	5598	6	AX306886	AX306886 Sequence
93	404	10.2	2455	9	HSMA5P2PR	Y09926 Homo sapien	166	328.5	8.3	5667	6	AX306889	AX306889 Sequence
94	403.5	10.2	2386	6	AX250080	AX250080 Sequence	167	328.5	8.3	6145	6	AX306887	AX306887 Sequence
95	403.5	10.2	2386	6	HSC1R	X04701 Human mRNA	168	328.5	8.3	6409	6	AX306888	AX306888 Sequence
96	403.5	10.2	2492	6	AR130745	AR130745 Sequence	169	328.5	8.3	7323	6	AX306890	AX306890 Sequence
97	403.5	10.2	2492	6	AR448569	AR448569 Sequence	170	328.5	8.3	8034	6	AX306891	AX306891 Sequence
98	403.5	10.2	2492	6	BD080942	BD080942 Detection	171	324	8.2	2900	6	AR081725	AR081725 Sequence
99	403.5	10.2	2493	6	AX302547	AX302547 Sequence	172	324	8.2	2900	6	AR229705	AR229705 Sequence
100	403.5	10.2	2493	6	AX409609	AX409609 Sequence	173	324	8.2	2900	6	AR430931	AR430931 Sequence
101	403.5	10.2	2493	9	HUMC1R	M14058 Human compl	174	324	8.2	2900	6	HSU20428	U20428 Human SNC19
102	403.5	10.2	2526	9	BC035220	BC035220 Homo sapi	175	324	8.2	3490	9	AK126857	AK126857 Homo sapi
103	403.5	10.2	1490	10	GPI457086	AJ457086 Cavia por	176	324	8.2	12525	6	AX374893	AX374893 Sequence
104	401.5	10.2	2061	6	Q8827400	Q8827400 Sequence	177	323	8.2	8010	6	AX685959	AX685959 Sequence
105	400.5	10.2	2555	3	DB8204	DB8204 Halocynthia	178	323	8.2	10136	6	AX685957	AX685957 Sequence
106	399.5	10.1	2449	6	Q0720832	Q0720832 Sequence	179	323	8.2	13113	9	AY210418	AY210418 Homo sapi
107	398.5	10.1	2550	5	AB042609	AB042609 Cyprinus	180	322.5	8.2	1499	10	MUSCP	D10445 Mouse mRNA
108	395	10.0	3170	5	AB089266	AB089266 Lethenter	181	322.5	8.2	2249	5	BC081673	BC081673 Danio rer
109	386	9.8	2135	5	AY349426	AY349426 Sus scrofa	182	322	8.2	2589	6	Q0729246	Q0729246 Sequence
110	385.5	9.8	3708	5	AB009075	AB009075 Lampetra	183	321.5	8.1	2568	10	AB037898	AB037898 Rattus no
111	384	9.7	2662	10	AF459020	AF459020 Mus muscu	184	321.5	8.1	3174	10	AB049189	AB049189 Rattus no
112	382.5	9.7	2507	3	D88205	D88205 Halocynthia	185	321	8.1	1386	6	AX149646	AX149646 Sequence
113	380	9.6	2534	3	AK112393	AK112393 Ciona int	186	320.5	8.1	2212	9	AK025309	AK025309 Homo sapi
114	378.5	9.6	2711	10	MACASP	X16160 Mesocricetu	187	320.5	8.1	10433	6	AX374896	AX374896 Sequence
115	376	9.5	1898	10	RNO18564	Y18564 Rattus norv	188	320.5	8.1	10673	6	AX374891	AX374891 Sequence
116	371.5	9.4	1657	10	RNO18566	Y18566 Rattus norv	189	319.5	8.1	1580	10	BC013896	BC013896 Mus muscu
117	368	9.3	2249	5	AB042610	AB042610 Cyprinus	190	319.5	8.1	1603	10	AF042822	AF042822 Mus muscu
118	365	9.3	208659	2	AC067845	AC067845 Homo sapi	191	318.5	8.1	3106	6	AX395268	AX395268 Sequence
119	364	9.2	2830	10	AF459019	AF459019 Mus muscu	192	318.5	8.1	3106	10	BC005496	BC005496 Mus muscu
120	364	9.2	2855	10	BC018319	BC018319 Mus muscu	193	318.5	8.1	3248	2	AC111821	AC111821 Rattus no
121	364	9.2	2915	10	BC022123	BC022123 Homo sapi	194	318	8.1	32808	2	AC111821	AC111821 Rattus no
122	361.5	9.2	3519	9	AK024951	AK024951 Homo sapi	195	317.5	8.0	164576	6	I64576	I64576 Sequence 1
123	361	9.2	4628	5	XLU81290	XLU81290 Xenopus lae	196	317.5	8.0	2581	6	ARS44611	ARS44611 Sequence
124	357	9.0	2225	5	AY643493	AY643493 Cyprinus	197	317.5	8.0	3860	4	BTU09859	BTU09859 Bos taurus
125	351	8.9	2647	6	Q0776438	Q0776438 Sequence	198	315.5	8.0	1386	6	AX149643	AX149643 Sequence
126	351	8.9	2647	6	Q0776438	Q0776438 Sequence	199	315.5	8.0	1680	5	BC053182	BC053182 Danio rer
127	351	8.9	2647	9	HUMC1RS	JO4080 Human compl	200	315	8.0	1386	6	AX149645	AX149645 Sequence
128	351	8.9	9378	3	AB089507	AB089507 Branchios	201	315	8.0	1619	4	OCU77477	OCU77477 Oryctolagus
129	349	8.8	2582	9	HUMC1SAB	M18767 Human compl	202	314.5	8.0	2246	5	CHRVAP	CHRVAP Gallus gall
130	345	8.7	2915	5	OMY519930	OMY519930 Oncorhync	203	314	8.0	1386	6	AX149644	AX149644 Sequence
131	342	8.7	2915	10	BC027183	BC027183 Mus muscu	204	314	8.0	3173	5	AB042611	AB042611 Cyprinus
132	340.5	8.6	561	11	G91095	G91095 S210P6215RE	205	312.5	7.9	1843	6	AR390799	AR390799 Sequence
133	340.5	8.6	2908	6	AX401672	AX401672 Sequence	206	312.5	7.9	1843	6	AX411026	AX411026 Sequence
134	340.5	8.6	2908	10	D88250	D88250 Rattus norv	207	312.5	7.9	1843	9	HSPOTC	HSPOTC Human liver
135	340.5	8.6	2910	10	BC062042	BC062042 Rattus no	208	312	7.9	1386	6	AX207787	AX207787 Sequence
136	340.5	8.6	3128	9	AB030036	AB030036 Homo sapi	209	312	7.9	1386	6	AX212334	AX212334 Sequence
137	340.5	8.6	3273	9	BC030532	BC030532 Homo sapi	210	311.5	7.9	2580	6	AX748409	AX748409 Sequence
138	337.5	8.5	2790	9	BC056903	BC056903 Homo sapi	211	311.5	7.9	2580	6	AK094009	AK094009 Homo sapi
139	336.5	8.5	2139	9	BC056903	BC056903 Homo sapi	212	311	7.9	1341	10	AF532184	AF532184 Rattus no
140	336.5	8.5	2955	6	BD274670	BD274670 Matriptas	213	311	7.9	1386	6	AX207788	AX207788 Sequence
141	336.5	8.5	3120	9	AF133086	AF133086 Homo sapi	214	311	7.9	1386	6	AX207788	AX207788 Sequence
142	336.5	8.5	3149	6	BD274671	BD274671 Matriptas	215	310.5	7.9	1245	6	BD232213	BD232213 Human pro
143	336.5	8.5	3149	6	AF118224	AF118224 Homo sapi	216	310.5	7.9	1257	6	Q0821347	Q0821347 Sequence
144	335.5	8.5	2838	6	AX921703	AX921703 Sequence	217	310.5	7.9	1257	6	AX427736	AX427736 Sequence
145	335.5	8.5	3147	6	AR081724	AR081724 Sequence	218	310.5	7.9	1260	6	BD246882	BD246882 Protein C
146	335.5	8.5	3147	6	AR229704	AR229704 Sequence	219	310.5	7.9	1260	6	I00579	I00579 Sequence 1
147	335.5	8.5	3147	6	AR229712	AR229712 Sequence	220	310.5	7.9	1260	6	AR404691	AR404691 Sequence
148	335.5	8.5	3147	6	AR430930	AR430930 Sequence	221	310.5	7.9	1260	6	AX044041	AX044041 Sequence
149	335.5	8.5	3147	6	AR430938	AR430938 Sequence	222	310.5	7.9	1260	6	AX149639	AX149639 Sequence
150	335.5	8.5	3147	6	AX207897	AX207897 Sequence	223	310.5	7.9	1260	6	AX207783	AX207783 Sequence



224	310.5	7.9	1260	6	AX212330	Sequence	297	290.5	7.4	1260	6	E00961	E00961 cDNA encodi
225	310.5	7.9	1383	6	CQ821348	Sequence	298	290.5	7.4	1557	6	I00300	Sequence 5
226	310.5	7.9	1383	6	CQ821348	Sequence	299	290.5	7.4	1557	6	I00300	Sequence 2
227	310.5	7.9	1383	6	AX427734	Sequence	300	290.5	7.4	2544	9	BC007231	Homo sapi
228	310.5	7.9	1386	6	AR070468	Sequence	301	289.5	7.3	1774	6	I00296	Sequence 1
229	310.5	7.9	1386	6	BD246883	Protein C	302	289.5	7.3	1834	6	I01047	Sequence 1
230	310.5	7.9	1386	6	BD246884	Protein C	303	289.5	7.3	1834	6	I02179	Sequence 1
231	310.5	7.9	1386	6	E01708	Sequence	304	289.5	7.3	2151	6	A04842	H.sapiens T
232	310.5	7.9	1386	6	I06643	Sequence 1	305	289.5	7.3	2151	6	E00654	cDNA encodi
233	310.5	7.9	1386	6	I08112	Sequence 1	306	289.5	7.3	2153	6	A11976	Synthetic n
234	310.5	7.9	1386	6	AR044692	Sequence	307	289.5	7.3	2162	6	AR017909	Sequence
235	310.5	7.9	1386	6	AX044042	Sequence	308	289.5	7.3	2162	6	AR017931	Sequence
236	310.5	7.9	1386	6	AX044043	Sequence	309	289.5	7.3	2162	6	I18796	Sequence 3
237	310.5	7.9	1386	6	AX149640	Sequence	310	289.5	7.3	2170	6	E08757	cDNA of tis
238	310.5	7.9	1386	6	AX149641	Sequence	311	289.5	7.3	2509	6	E02027	Sequence
239	310.5	7.9	1386	6	AX149642	Sequence	312	289.5	7.3	2509	6	AX787057	Sequence
240	310.5	7.9	1386	6	AX207784	Sequence	313	289.5	7.3	2509	6	HSTPAR	Human fetal
241	310.5	7.9	1386	6	AX212331	Sequence	314	289.5	7.3	2519	6	A07251	Artificial
242	310.5	7.9	1755	6	AR363767	Sequence	315	289.5	7.3	2519	6	AX427760	Sequence
243	310.5	7.9	1756	6	CQ730237	Sequence	316	289.5	7.3	2519	9	HUMPLAT	Human tissu
244	310.5	7.9	1756	6	I05477	Sequence 12	317	289.5	7.3	2544	6	I09136	Sequence 4
245	310.5	7.9	1759	6	E01189	cDNA encodi	318	289.5	7.3	2544	6	AR353675	Sequence
246	310.5	7.9	1792	9	BC034377	Homo sapi	319	289.5	7.3	2546	9	BC013968	Homo sapi
247	310.5	7.9	1386	6	AR404695	Sequence	320	289.5	7.3	2546	9	BC018636	Homo sapi
248	310.5	7.9	1386	6	AR404696	Sequence	321	289.5	7.3	2560	6	A01465	H.sapiens c
249	310.5	7.8	1386	6	AX207786	Sequence	322	289.5	7.3	2672	6	AX207905	Sequence
250	309.5	7.8	1386	6	BD246885	Protein C	323	289.5	7.3	2859	6	CQ412921	Sequence
251	309.5	7.8	1386	6	BD246886	Protein C	324	289.5	7.3	3104	6	AX207903	Sequence
252	309.5	7.8	1386	6	AX044044	Sequence	325	289	7.3	7360	6	I26927	Sequence 1
253	309.5	7.8	1386	6	AX044045	Sequence	326	288.5	7.3	2409	6	AX360098	Sequence
254	309.5	7.8	3142	10	BC057674	Mus muscu	327	288.5	7.3	2475	6	CQ716095	Sequence
255	309.5	7.8	3183	10	AY240929	Mus muscu	328	288.5	7.3	3143	6	CQ767701	Sequence
256	309.5	7.8	3183	10	BC029645	Mus muscu	329	288.5	7.3	3143	6	AX538206	Sequence
257	309	7.8	1386	6	AR404693	Sequence	330	288.5	7.3	3143	9	AY358398	Homo sapi
258	309	7.8	1386	6	AX212332	Sequence	331	288.5	7.3	3547	6	BD217672	Choline a
259	308.5	7.8	1389	6	E02492	DNA encodin	332	288	7.3	1689	6	I06609	Sequence 44
260	308	7.8	1386	6	AR404694	Sequence	333	288	7.3	2547	6	E01092	cDNA encodi
261	308	7.8	1386	6	AX212333	Sequence	334	288	7.3	2547	6	E01163	cDNA encodi
262	306	7.8	1383	6	E02246	DNA Sequence	335	288	7.3	2547	6	I07841	Sequence 1
263	305.5	7.7	1671	5	AY040345	Danio rer	336	288	7.3	2547	6	I07989	Sequence 1
264	305.5	7.7	5994	6	CQ723917	Sequence	337	288	7.3	2547	6	I09622	Sequence 1
265	304	7.7	4215	10	MMU73378	Mus musculu	338	288	7.3	2549	6	E01055	DNA encodin
266	303.5	7.7	2409	9	BC002795	Homo sapi	339	287.5	7.3	1366	6	AR474607	Sequence
267	302.5	7.7	1869	10	BC061149	Mus muscu	340	287.5	7.3	1366	9	HUNPRC	Human prote
268	301.5	7.6	1383	6	E01914	DNA encodin	341	287.5	7.3	2449	9	HSX319876	Homo sapi
269	301.5	7.6	2078	12	AF272773	Synthetic	342	287.5	7.3	3194	9	AY055384	Homo sapi
270	300.5	7.6	1850	10	MMU44795	Mus musculu	343	287	7.3	1686	6	E01273	DNA encodin
271	300.5	7.6	2219	5	AY631238	Pseudonaj	344	287	7.3	2294	5	BC056804	Danio rer
272	300.5	7.6	2459	6	E01466	DNA encodin	345	287	7.3	2359	9	HUMTPARN	Homo sapien
273	300.5	7.6	2459	9	HSTPA1	Human mRNA	346	287	7.3	2582	3	AK116731	Ciona int
274	299.5	7.6	2231	5	AY631239	Pseudonaj	347	287	7.3	7533	6	E01324	Recombinant
275	299	7.6	3645	10	AY251285	Rattus no	348	286	7.2	1689	6	A14927	tPA-DNA fro
276	298.5	7.6	2466	5	BC061654	Xenopus l	349	286	7.2	1689	6	A14930	tPA-DNA fro
277	297.5	7.5	1428	5	AF465276	Takifugu	350	286	7.2	1689	6	A34204	Human t-PA
278	297	7.5	1514	4	AF191307	Sus scrof	351	286	7.2	1689	6	A34205	Human t-PA
279	297	7.5	2459	6	E00880	DNA encodin	352	286	7.2	1689	6	E01665	cDNA encodi
280	296.5	7.5	1387	6	AR364387	Sequence	353	286	7.2	1689	6	E02663	DNA encodin
281	296	7.5	1558	4	OCU49933	Oryctolagus	354	286	7.2	1689	6	I08637	Sequence 1
282	296	7.5	65326	2	AC124815	Mus muscu	355	286	7.2	1689	6	I08789	Sequence 3
283	295.5	7.5	1326	5	AF465273	Takifugu	356	286	7.2	1689	6	AX427761	Sequence
284	295.5	7.5	1537	4	BTCFX1	Bovine mRNA	357	286	7.2	1689	9	BT007060	Homo sapi
285	295.5	7.5	1554	6	AR3583	Sequence 1	358	286	7.2	1689	12	BT007513	Synthetic
286	295.5	7.5	1554	6	AR001423	Sequence	359	286	7.2	1738	6	AR363266	Sequence
287	295	7.5	1278	5	AF465268	Gallus ga	360	286	7.2	1955	6	AR086682	Sequence
288	294.5	7.5	1543	6	AX401899	Sequence	361	286	7.2	1974	6	A07195	Artificial
289	294.5	7.5	1543	10	RMPROC	Rattus norv	362	286	7.2	1974	6	A27425	DNA sequen
290	294	7.5	1535	10	BC078879	Rattus no	363	286	7.2	1974	6	AR059984	Sequence
291	293	7.4	1293	5	AF465275	Takifugu	364	286	7.2	1989	6	I01256	Sequence 2
292	293	7.4	1689	6	E02664	DNA encodin	365	286	7.2	2100	6	A07197	H.sapiens m
293	293	7.4	1738	6	I08077	Sequence 1	366	286	7.2	2100	6	A27429	cDNA sequen
294	292	7.4	2550	6	I08531	Sequence 2	367	286	7.2	2100	6	E01934	DNA encodin
295	291.5	7.4	1193	4	AY349421	Sus scrof	368	286	7.2	2101	6	AR059986	Sequence
296	291	7.4	1738	6	I06376	Sequence 37	369	286	7.2	2310	6	A03776	H.sapiens m

370	286	7.2	2434	6	E02025	E02025 DNA sequenc	443	279	7.1	1689	6	E01666	E01666 cDNA encodi
371	286	7.2	2457	6	E00896	E00896 cDNA encodi	444	279	7.1	2460	4	AF364605	AF364605 Sus scrofa
372	286	7.2	2457	6	E01221	E01221 cDNA human	445	279	7.1	2913	6	AX360086	AX360086 Sequence
373	286	7.2	2457	6	AR364602	AR364602 Sequence	446	279	7.1	3522	6	CQ819022	CQ819022 Sequence
374	286	7.2	2460	6	I09411	I09411 Sequence 1	447	278.5	7.1	877	6	AX704801	AX704801 Sequence
375	286	7.2	2461	9	HUMUPAA	M18182 Human plasm	448	278.5	7.1	1221	6	E62998	E62998 Hemocoagula
376	286	7.2	2482	6	E00629	E00629 DNA encodin	449	278.5	7.1	1440	6	AR112953	AR112953 Sequence
377	286	7.2	2544	6	I08530	I08530 Sequence 1	450	278.5	7.1	1440	6	AR112969	AR112969 Sequence
378	286	7.2	2544	6	I08638	I08638 Sequence 2	451	278.5	7.1	1440	6	BD194674	BD194674 Tissue fa
379	285.5	7.2	1874	6	I01184	I01184 Sequence 1	452	278.5	7.1	1440	6	I19358	I19358 Sequence 3
380	285.5	7.2	2869	4	DOGPIX	M21757 Canis famil	453	278.5	7.1	1440	6	I19360	I19360 Sequence 3
381	285.5	7.2	3080	4	DOGFIXA	M33826 Canine bloo	454	278.5	7.1	1491	10	MMCOAGULX	AJ222677 Mus muscu
382	285	7.2	1689	6	E02448	E02448 DNA encodin	455	278.5	7.1	2236	4	VMPBAA2A	M63988 Desmodus ro
383	285	7.2	1689	9	AY221101	AY221101 Homo sapi	456	278.5	7.1	2257	6	A07244	A07244 Artificial
384	284.5	7.2	1800	6	E04506	E04506 DNA encodin	457	278.5	7.1	2459	6	CQ723338	CQ723338 Sequence
385	284.5	7.2	1800	6	E05896	E05896 DNA sequenc	458	278.5	7.1	2462	6	AR095304	AR095304 Sequence
386	284.5	7.2	2512	6	A19618	A19618 Mammalian c	459	278.5	7.1	2462	6	AR103988	AR103988 Sequence
387	284.5	7.2	2520	10	BC061508	BC061508 Mus muscu	460	278.5	7.1	2462	6	AX335083	AX335083 Sequence
388	284.5	7.2	2542	10	BC057967	BC057967 Mus muscu	461	278.5	7.1	2462	6	AX409604	AX409604 Sequence
389	284.5	7.2	2585	10	BC061565	BC061565 Rattus no	462	278.5	7.1	2462	9	HUMFVII	M13232 Human facto
390	284.5	7.2	4864	10	AB013874	AB013874 Mus muscu	463	278.5	7.1	2483	6	E01076	E01076 cDNA sequen
391	284	7.2	1598	6	I08550	I08550 Sequence 1	464	278.5	7.1	2483	6	I07990	I07990 Sequence 3
392	284	7.2	2537	5	BC073613	BC073613 Xenopus l	465	278.5	7.1	2691	9	CR456446	CR456446 Homo sapi
393	284	7.2	3028	5	AB070367	AB070367 Bufo japo	466	278	7.0	1302	5	AF465270	AF465270 Gallus ga
394	283.5	7.2	1486	10	AF087644	AF087644 Mus muscu	467	278	7.0	1467	6	CQ723339	CQ723339 Sequence
395	283.5	7.2	1497	10	RNFXRAT	X79807 R.norvegicu	468	278	7.0	1507	6	AX774765	AX774765 Sequence
396	283.5	7.2	1500	4	AF003200	AF003200 Oryctolag	469	278	7.0	1517	9	AY318867	AY318867 Human coagu
397	283.5	7.2	1925	10	BC003877	BC003877 Mus muscu	470	278	7.0	1507	9	AX318867	AX318867 Homo sapi
398	283.5	7.2	2519	6	AX305289	AX305289 Sequence	471	278	7.0	1541	9	BC046125	BC046125 Homo sapi
399	283.5	7.2	2519	10	MUSTPA	J03520 Mouse tisseu	472	278	7.0	1569	6	CQ614289	CQ614289 Sequence
400	283	7.2	1630	6	E00994	E00994 cDNA encodi	473	278	7.0	1573	9	BC040125	BC040125 Homo sapi
401	283	7.2	1689	6	I06614	I06614 Sequence 46	474	278	7.0	1707	3	AY071128	AY071128 Drosophil
402	283	7.2	1780	6	A06611	A06611 Synthetic n	475	278	7.0	1836	6	E01176	E01176 DNA encodin
403	283	7.2	1780	6	A10226	A10226 Synthetic D	476	278	7.0	1836	6	I01581	I01581 Sequence 1
404	282	7.1	1373	4	BOVPBC	K02435 Bovine prot	477	278	7.0	1981	6	I01583	I01583 Sequence 3
405	282	7.1	1599	4	AF275654	AF275654 Ornithorh	478	278	7.0	2009	6	E01177	E01177 DNA encodin
406	281.5	7.1	901	6	BD209910	BD209910 Human nuc	479	277	7.0	1327	6	CQ767703	CQ767703 Sequence
407	281.5	7.1	901	6	AX014224	AX014224 Sequence	480	277	7.0	1327	6	AX538208	AX538208 Sequence
408	281.5	7.1	1221	6	E63000	E63000 Hemocoagula	481	277	7.0	1338	6	CQ798455	CQ798455 Sequence
409	281.5	7.1	1838	5	BC074475	BC074475 Xenopus l	482	277	7.0	1338	6	CQ880376	CQ880376 Sequence
410	281.5	7.1	2172	10	AB177406	AB177406 Rattus no	483	277	7.0	1338	6	AX211659	AX211659 Sequence
411	281.5	7.1	2190	10	AK128915	AK128915 Mus muscu	484	277	7.0	1338	6	AX951866	AX951866 Sequence
412	281.5	7.1	2455	10	RATPATISS	M23697 Rat tissue-	485	277	7.0	1357	6	CQ880378	CQ880378 Sequence
413	281	7.1	1443	9	HUMFXM	K03194 Human facto	486	277	7.0	1357	6	AX211661	AX211661 Sequence
414	281	7.1	1467	6	A86859	A86859 Sequence 43	487	276.5	7.0	1620	6	I08184	I08184 Sequence 4
415	281	7.1	1467	6	A86886	A86886 Sequence 26	488	276.5	7.0	1725	4	VMPPTA	J05082 Vampire bat
416	281	7.1	1467	6	AR316969	AR316969 Sequence	489	276.5	7.0	1727	6	AR363981	AR363981 Sequence
417	281	7.1	1467	6	AR340866	AR340866 Sequence	490	276.5	7.0	2033	6	E07591	E07591 DNA encodin
418	281	7.1	1467	6	AX082959	AX082959 Sequence	491	276.5	7.0	2033	6	I15469	I15469 Sequence 14
419	281	7.1	1467	6	BD070392	BD070392 Factor X-	492	276.5	7.0	2033	6	I69315	I69315 Sequence 14
420	281	7.1	1467	6	BD070435	BD070435 Factor X	493	276.5	7.0	2036	6	AX333070	AX333070 Sequence
421	281	7.1	1605	6	AR363979	AR363979 Sequence	494	276.5	7.0	2036	6	AX408965	AX408965 Sequence
422	281	7.1	2130	4	VMPBAP	M63989 Desmodus ro	495	276.5	7.0	2036	9	HUMGFAP	D14012 Homo sapien
423	281	7.1	2137	6	A07246	A07246 Artificial	496	276.5	7.0	2040	6	CQ768744	CQ768744 Sequence
424	280.5	7.1	922	9	BC063475	BC063475 Homo sapi	497	276.5	7.0	2040	9	AF272774	AF272774 Homo sapi
425	280.5	7.1	928	9	BC039716	BC039716 Homo sapi	498	276.5	7.0	7427	6	CQ768745	CQ768745 Sequence
426	280.5	7.1	1169	6	CQ723499	CQ723499 Sequence	499	276.5	7.0	1505	6	AX523898	AX523898 Sequence
427	280.5	7.1	1184	6	AX337830	AX337830 Sequence	500	276	7.0	2119	10	BC031775	BC031775 Mus muscu
428	280.5	7.1	1184	6	AX774731	AX774731 Sequence	501	275.5	7.0	889	5	BX935351	BX935351 Gallus ga
429	280.5	7.1	1184	9	HSCHVPRO	X71877 H.sapiens m	502	275.5	7.0	899	5	BX935315	BX935315 Gallus ga
430	280.5	7.1	2438	6	I07991	I07991 Sequence 6	503	275.5	7.0	899	5	BX936273	BX936273 Gallus ga
431	280.5	7.1	2747	10	BC057186	BC057186 Mus muscu	504	275.5	7.0	911	5	BX933638	BX933638 Gallus ga
432	280.5	7.1	2771	10	BC014773	BC014773 Mus muscu	505	275.5	7.0	937	5	CR352633	CR352633 Gallus ga
433	280.5	7.1	5956	9	HSMB06659	BS641029 Homo sapi	506	275.5	7.0	1221	6	E62997	E62997 Hemocoagula
434	280.5	7.1	10774	9	AB067481	AB067481 Homo sapi	507	275.5	7.0	1646	5	AF515271	AF515271 Danio rer
435	280	7.1	1605	12	SYNHUMTPAA	M26666 Synthetic h	508	275.5	7.0	2177	6	E01075	E01075 cDNA sequen
436	280	7.1	1689	6	E01667	E01667 cDNA encodi	509	275.5	7.0	2230	4	AB022425	AB022425 Sus scrof
437	279.5	7.1	2106	6	CQ768741	CQ768741 Sequence	510	275.5	7.0	2402	4	BTTPA	X85800 B.taurus mr
438	279.5	7.1	2540	10	BC011256	BC011256 Mus muscu	511	275.5	7.0	2422	6	AR030786	AR030786 Sequence
439	279.5	7.1	2604	6	I05002	I05002 Sequence 4	512	275.5	7.0	2422	6	AR045090	AR045090 Sequence
440	279.5	7.1	7493	6	CQ768742	CQ768742 Sequence	513	275.5	7.0	2422	6	AR052946	AR052946 Sequence
441	279	7.1	889	5	BX933670	BX933670 Gallus ga	514	275.5	7.0	2422	6	AR122899	AR122899 Sequence
442	279	7.1	1206	6	E63002	E63002 Hemocoagula	515	275.5	7.0	2422	6	AR127821	AR127821 Sequence

516	275.5	7.0	2720	10	MUSPLGN	J04766 Mouse plasma	589	267.5	6.8	1404	6	A93124	A93124 Sequence 15
517	275.5	7.0	4436	6	AX249945	AX249945 Sequence	590	267.5	6.8	1414	9	HUMCFX	M22613 Human blood
518	275.5	7.0	6098	6	AX565990	AX565990 Sequence	591	267	6.8	835	5	AX931595	AX931595 Gallus ga
519	275	7.0	1683	6	BD177602	BD177602 Detection	592	267	6.8	841	5	AX931604	AX931604 Gallus ga
520	275	7.0	1683	6	BD177603	BD177603 Detection	593	267	6.8	841	5	AX931627	AX931627 Gallus ga
521	275	7.0	1683	6	AX383954	AX383954 Sequence	594	267	6.8	841	5	AX935230	AX935230 Gallus ga
522	275	7.0	1683	6	AX383955	AX383955 Sequence	595	267	6.8	842	5	AX931598	AX931598 Gallus ga
523	275	7.0	2005	4	BOVTHBNM	J00041 Bovine prot	596	267	6.8	844	5	AX933624	AX933624 Gallus ga
524	275	7.0	2251	9	BC031412	BC031412 Homo sapi	597	267	6.8	1027	10	RNO18565	Y18565 Rattus Norv
525	275	7.0	2408	9	S83182	S83182 hyaluronan-	598	267	6.8	1389	6	AX431491	AX431491 Sequence
526	275	7.0	3008	6	AX409021	AX409021 Sequence	599	267	6.8	1437	6	AR095305	AR095305 Sequence
527	275	7.0	3008	6	HUMGEFAL	D49742 Human mRNA	600	267	6.8	1437	6	AR103989	AR103989 Sequence
528	274.5	7.0	1911	6	A08501	A08501 Artificial	601	267	6.8	1437	9	HUMFIX	J00136 Human facto
529	274.5	7.0	2060	4	AY532633	AY532633 Canis fam	602	267	6.8	1749	5	BC054968	BC054968 Xenopus l
530	274.5	7.0	2200	3	AK112434	AK112434 Clona int	603	266.5	6.8	2626	5	LARCFB	D13568 Lampetra ja
531	274.5	7.0	3943	3	ABJ831414	ABJ831414 Clona int	604	266	6.7	1473	6	E02114	E02114 cDNA sequen
532	274.5	7.0	12486	9	AY210419	AY210419 Homo sapi	605	266	6.7	1473	6	E08289	E08289 Synthetic D
533	274.5	7.0	13040	9	AB114605	AB114605 Homo sapi	606	266	6.7	2561	4	AY029518	AY029518 Oryctolag
534	274.5	7.0	13148	9	AB114604	AB114604 Homo sapi	607	266	6.7	4993	5	BC082854	BC082854 Xenopus l
535	274	6.9	1500	9	BC015525	BC015525 Homo sapi	608	265.5	6.7	753	6	CQ596802	CQ596802 Sequence
536	274	6.9	1503	9	AY318869	AY318869 Homo sapi	609	265.5	6.7	1359	6	AX451990	AX451990 Sequence
537	274	6.9	1839	5	AF465278	AF465278 Takifugu	610	265.5	6.7	3094	6	BD242873	BD242873 Secreted
538	274	6.9	4276	6	AX249946	AX249946 Sequence	611	265.5	6.7	3118	6	AX250079	AX250079 Sequence
539	273.5	6.9	1722	5	AF515269	AF515269 Danio rer	612	265.5	6.7	3345	9	AF178985	AF178985 Homo sapi
540	273	6.9	929	9	AY318870	AY318870 Homo sapi	613	285	6.7	2078	5	U75331	U75331 Gallus gall
541	273	6.9	1112	10	RNO18571	Y18571 Rattus Norv	614	285	6.7	3689	5	XL081291	XL081291 Xenopus lae
542	273	6.9	1206	6	E63001	E63001 Hemococogula	615	265	6.7	5532	6	AR105803	AR105803 Sequence
543	273	6.9	9120	10	AK122567	AK122567 Mus muscu	616	264.5	6.7	1236	6	E02710	E02710 Human prour
544	272.5	6.9	1533	9	MFFIX	X65473 M.fascicula	617	264.5	6.7	1236	6	E02710	E02710 DNA sequenc
545	271.5	6.9	732	6	I95869	I95869 Sequence 2	618	264.5	6.7	1393	6	CQ722424	CQ722424 Sequence 6
546	271.5	6.9	735	9	BT006852	BT006852 Homo sapi	619	264.5	6.7	1981	6	I01586	I01586 Sequence 6
547	271.5	6.9	735	12	BT008102	BT008102 Synthetic	620	264.5	6.7	1998	10	BC013662	BC013662 Mus muscu
548	271.5	6.9	1221	6	E62999	E62999 Hemococogula	621	264.5	6.7	2010	6	E01178	E01178 DNA encodin
549	271.5	6.9	1419	9	D78203	D78203 Homo sapien	622	264.5	6.7	2031	10	WMPTHROM	X52308 Mouse mRNA
550	271.5	6.9	1438	6	E13202	E13202 Human gene	623	264.5	6.7	256455	2	AC129138	AC129138 Rattus no
551	271.5	6.9	1451	6	CQ874887	CQ874887 Sequence	624	264	6.7	2035	10	AF099017	AF099017 Mus muscu
552	271.5	6.9	1451	6	CQ874963	CQ874963 Sequence	625	264	6.7	2063	10	AF224724	AF224724 Mus muscu
553	271.5	6.9	1451	9	AF013988	AF013988 Homo sapi	626	264	6.7	2300	5	BC055574	BC055574 Synthetic H
554	271.5	6.9	1506	6	CQ720601	CQ720601 Sequence	627	263.5	6.7	875	5	BC055574	BC055574 Danio rer
555	271.5	6.9	1506	6	CQ874889	CQ874889 Sequence	628	263.5	6.7	1398	10	AF456428	AF456428 Mus muscu
556	271.5	6.9	1506	6	CQ874965	CQ874965 Sequence	629	263.5	6.7	1667	6	AX250017	AX250017 Sequence
557	271.5	6.9	1506	6	AX329982	AX329982 Sequence	630	263.5	6.7	1891	6	AX250019	AX250019 Sequence
558	271.5	6.9	1506	6	AX926503	AX926503 Sequence	631	263.5	6.7	1726	10	BC070472	BC070472 Mus muscu
559	271.5	6.9	1506	6	AX951756	AX951756 Sequence	632	263	6.7	1296	6	BD183647	BD183647 Anti-HIV
560	271.5	6.9	1506	6	AX960034	AX960034 Sequence	633	263	6.7	1296	6	E02577	E02577 DNA encodin
561	271.5	6.9	1506	9	HSU62801	U62801 Human prote	634	263	6.7	1296	6	E02647	E02647 DNA sequenc
562	271	6.9	1443	6	E02473	E02473 DNA encodin	635	263	6.7	1296	6	E02649	E02649 DNA sequenc
563	271	6.9	1443	6	E08290	E08290 Synthetic D	636	263	6.7	1296	6	E02711	E02711 DNA sequenc
564	271	6.9	1549	4	AY222285	AY222285 Oryctolag	637	263	6.7	1296	6	E06064	E06064 DNA encodin
565	271	6.9	1689	6	E02360	E02360 DNA sequenc	638	263	6.7	1296	6	AX512750	AX512750 Sequence
566	271	6.9	2350	4	AY029517	AY029517 Oryctolag	639	263	6.7	1296	9	BT007391	BT007391 Homo sapi
567	271	6.9	2358	4	AB087224	AB087224 Oryctolag	640	263	6.7	1296	12	AX335599	AX335599 Synthetic
568	271	6.9	3016	3	AK116923	AK116923 Clona int	641	263	6.7	1394	6	E00421	E00421 cDNA coding
569	270.5	6.9	2803	3	AB030007	AB030007 Polyandro	642	263	6.7	1474	6	E00924	E00924 cDNA encodi
570	270	6.8	2005	6	AX395273	AX395273 Sequence	643	263	6.7	1474	6	E01238	E01238 cDNA encodi
571	270	6.8	1605	6	I06014	I06014 Sequence 6	644	263	6.7	1474	6	E01559	E01559 cDNA sequen
572	270	6.8	2245	4	VMPPA1A	M63987 Desmodus ro	645	263	6.7	1474	6	E01580	E01580 cDNA encodi
573	270	6.8	2252	6	A07242	A07242 Artificial	646	263	6.7	1474	6	E02095	E02095 DNA sequenc
574	270	6.8	2252	6	A07250	A07250 Artificial	647	263	6.7	1475	6	BD226054	BD226054 Compound
575	270	6.8	2266	4	VMPPA1S	M63986 Desmodus ro	648	263	6.7	1475	6	BD275725	BD275725 COMPOUNDS
576	269.5	6.8	3610	5	BC071077	BC071077 Xenopus l	649	263	6.7	1475	6	E01560	E01560 cDNA sequen
577	269	6.8	795	5	BX931589	BX931589 Gallus ga	650	263	6.7	1475	6	AR220510	AR220510 Sequence
578	269	6.8	1032	6	CQ578484	CQ578484 Sequence	651	263	6.7	1475	6	AR255504	AR255504 Sequence
579	269	6.8	1186	3	AB020543	AB020543 Haemaphys	652	263	6.7	1475	6	AR281074	AR281074 Sequence
580	269	6.8	1209	6	BD001742	BD001742 Tick vacc	653	263	6.7	1475	6	AR437865	AR437865 Sequence
581	269	6.8	1589	5	BC076035	BC076035 Danio rer	654	263	6.7	1475	6	AR476401	AR476401 Sequence
582	269	6.8	2310	6	A03777	A03777 H.sapiens m	655	263	6.7	1475	6	AR486592	AR486592 Sequence
583	269	6.8	2737	10	RNO242649	AJ72649 Rattus no	656	263	6.7	1475	6	AR541095	AR541095 Sequence
584	269	6.8	3136	3	AF059284	AF059284 Strongylo	657	263	6.7	1475	6	AX365729	AX365729 Sequence
585	268	6.8	1689	6	A04051	A04051 H.sapiens t	658	263	6.7	1475	9	HUMUKM1	K03226 Human prepr
586	268	6.8	4464	9	HOSN18286	Y18286 Homo sapien	659	263	6.7	1500	6	AI0915	AI0915 Artificial
587	268	6.8	4465	9	HOSAI8287	Y18287 Homo sapien	660	263	6.7	1500	6	AI0916	AI0916 Artificial
588	267.5	6.8	974	5	BC072795	BC072795 Xenopus l	661	263	6.7	1964	6	AI8397	AI8397 Human uPA c

662	6.7	1964	6	AX402384	Sequence	735	259.5	6.6	2375	4	SSUPAR	X02724 Porcine mrn
663	6.7	1964	6	AX451989	Sequence	736	259.5	6.6	16984	3	AGTRY1C	222930 A.gambiae A
664	6.7	2067	10	BC019376	Sequence	737	259	6.6	1575	6	BC01670	E01670 CDNA encodi
665	6.7	2293	6	A11978	Synthetic n	738	259	6.6	1746	3	AF149789	AF149789 Strongylo
666	6.7	2294	6	A09202	Artificial	739	259	6.6	2304	5	BC084671	BC084671 Xenopus l
667	6.7	2294	6	BD226055	Compound	740	258.5	6.6	1236	6	E02493	E02493 CDNA encodi
668	6.7	2294	6	BD275726	COMPOUNDS	741	258.5	6.6	1236	6	E02832	E02832 DNA encodin
669	6.7	2294	6	AR220511	Sequence	742	258.5	6.6	1236	6	E02833	E02833 DNA encodin
670	6.7	2294	6	AR255505	Sequence	743	258.5	6.6	1236	6	E03359	E03359 CDNA encodi
671	6.7	2294	6	AR281075	Sequence	744	258.5	6.6	1236	6	AR380382	AR380382 Sequence
672	6.7	2294	6	AR380672	Sequence	745	258.5	6.6	1236	9	HUMUPAB	D11143 Human RNA f
673	6.7	2294	6	AR437866	Sequence	746	258.5	6.6	1455	6	E03404	E03404 DNA encodin
674	6.7	2294	6	AR476402	Sequence	747	258.5	6.6	1455	6	E03405	E03405 DNA encodin
675	6.7	2294	6	AR486593	Sequence	748	258.5	6.6	1548	6	AR008972	AR008972 Sequence
676	6.7	2294	6	AR541096	Sequence	749	258.5	6.6	1548	6	E04008	E04008 Sequence 15
677	6.7	2294	6	AR541096	Sequence	750	258.5	6.6	2594	3	AY119618	AY119618 Drosophil
678	6.7	2294	6	AX365730	Sequence	751	258.5	6.6	3736	6	CO612939	CO612939 Sequence
679	6.7	2294	11	G27040	Homo sapien	752	258.5	6.6	3749	3	DROSTUBBLE	L11451 Drosophila
680	6.7	2296	6	A35395	H.sapiens u	753	258	6.5	869	5	GMO242521	AJ242521 Gadus mor
681	6.7	2299	6	Q0718477	Sequence	754	258	6.5	1597	9	PCUOKIN	X51935 Papio cynoc
682	6.7	2300	6	A21571	pro-Urokina	755	257.5	6.5	1236	6	E04897	E04897 gDNA encodi
683	6.7	2301	6	E01467	DNA encodin	756	257.5	6.5	1236	6	E05128	E05128 DNA sequenc
684	6.7	2303	6	I07013	Sequence 4	757	257.5	6.5	139312	5	BX571739	BX571739 Zebrafish
685	6.7	2303	6	I08092	Sequence 1	758	257	6.5	2413	3	AY118964	AY118964 Drosophil
686	6.7	2304	6	E00178	CDNA encodi	759	256.5	6.5	898	10	AB016228	AB016228 Mus muscu
687	6.7	2304	6	I03932	Sequence 6	760	256.5	6.5	156011	6	I56011	I56011 Sequence 2
688	6.7	2304	6	I04632	Sequence 1	761	256.5	6.5	1335	12	ASHPAAB	X54317 Synthetic g
689	6.7	2304	9	HUMUKPM	Human pro-u	762	256.5	6.5	2717	9	BC009305	BC009305 Homo sapi
690	6.7	2333	3	BC013575	Homo sapi	763	256.5	6.5	2738	9	BC002593	BC002593 Homo sapi
691	6.7	969	3	AF486486	Aurelia a	764	256.5	6.5	2740	9	BC032105	BC032105 Homo sapi
692	6.7	1389	6	A07407	H.sapiens D	765	255.5	6.5	915	5	BC005385	BC005385 Homo sapi
693	6.7	1389	6	A93125	Sequence 16	766	255.5	6.5	967	5	BC080976	BC080976 Xenopus t
694	6.7	1389	6	AR365693	Sequence	767	255.5	6.5	1236	6	E02708	E02708 DNA sequenc
695	6.7	1413	9	PTFIX	Sequence	768	255	6.5	1244	3	AB002407	AB002407 Sarcophag
696	6.7	1533	9	X65472	P.troglyodyt	769	255	6.5	1296	6	I08788	I08788 Sequence 1
697	6.7	1548	6	AR430579	Sequence	770	255	6.5	1340	5	HSPAUKR	X02760 Human mRNA
698	6.7	1610	6	AR009140	Sequence	771	255	6.5	2610	5	BC077104	BC077104 Danio rer
699	6.7	1610	6	AR202300	Sequence	772	255	6.5	3546	9	U50330	U50330 Human proco
700	6.7	1639	6	A01819	H.sapiens m	773	255	6.5	3552	6	AX577979	AX577979 Sequence
701	6.7	1639	6	A13997	H.sapiens m	774	255	6.5	3557	6	AX393311	AX393311 Sequence
702	6.7	1639	6	A14017	H.sapiens m	775	254.5	6.5	1416	5	AF465269	AF465269 Gallus ga
703	6.7	1639	9	HUMFIXA	Human facto	776	254.5	6.5	1467	6	E03403	E03403 DNA encodin
704	6.7	1823	5	BC060330	Xenopus l	777	254.5	6.5	3311	5	BC059801	BC059801 Danio rer
705	6.7	2038	6	Q0718548	Sequence	778	254	6.4	714	6	AX763031	AX763031 Sequence
706	6.7	2775	6	AR178034	Sequence	779	254	6.4	1372	6	AR363528	AR363528 Sequence
707	6.7	2775	6	Q0714145	Sequence	780	254	6.4	2045	10	RNPOTRH	X52835 Rattus norv
708	6.7	2775	11	G28615	human STS S	781	254	6.4	2249	6	A07209	A07209 Artificial
709	6.7	2775	6	HSFACIXM	H.sapiens f	782	254	6.4	3405	6	CO859271	CO859271 Sequence
710	6.7	2802	6	A47227	Sequence 1	783	254	6.4	3405	6	CO873358	CO873358 Sequence
711	6.7	2802	6	CO882048	Sequence	784	254	6.4	167208	2	AC034190	AC034190 Homo sapi
712	6.7	2804	6	AR452580	Sequence	785	253.5	6.4	946	5	BX935330	BX935330 Gallus ga
713	6.7	2804	6	BD217671	Choline a	786	253.5	6.4	947	5	BX935324	BX935324 Gallus ga
714	6.7	4933	6	AX207957	Sequence	787	253.5	6.4	947	5	BX933641	BX933641 Gallus ga
715	6.7	4933	6	AF133845	Homo sapi	788	253.5	6.4	948	5	BX935312	BX935312 Gallus ga
716	6.7	4933	9	AF133845	Homo sapi	789	253.5	6.4	948	5	BX933680	BX933680 Gallus ga
717	6.7	5753	6	BD270196	Complex o	790	253.5	6.4	948	5	BX935221	BX935221 Gallus ga
718	6.7	5753	6	CO871378	Sequence	791	253.5	6.4	950	5	BX933671	BX933671 Gallus ga
719	6.7	5753	6	AX033474	Sequence	792	253.5	6.4	951	5	BX933648	BX933648 Gallus ga
720	6.7	5753	6	AX253513	Sequence	793	253.5	6.4	957	5	BX933649	BX933649 Gallus ga
721	6.7	5905	6	BD270207	Complex o	794	253.5	6.4	962	5	CR338996	CR338996 Gallus ga
722	6.7	5905	6	AX033486	Sequence	795	253.5	6.4	969	5	BX933689	BX933689 Gallus ga
723	6.7	6052	6	BD270208	Complex o	796	253.5	6.4	975	5	BX933686	BX933686 Gallus ga
724	6.7	6052	6	AX033487	Sequence	797	253.5	6.4	976	5	BX933641	BX933641 Gallus ga
725	6.7	6052	6	A20747	Artificial	798	253.5	6.4	983	5	BX936261	BX936261 Gallus ga
726	6.6	1316	6	E02578	DNA encodin	799	253.5	6.4	2006	5	BC073504	BC073504 Gallus ga
727	6.6	1236	6	E02578	DNA encodin	800	253.5	6.4	2487	6	I78454	I78454 Sequence 1
728	6.6	2228	4	BTUPA	Bos taurus	801	253.5	6.4	2487	9	HUMBMP1A	M22488 Human bone
729	6.6	2355	4	BOVUKPA	Bos taurus	802	253.5	6.4	2500	6	I08629	I08629 Sequence 30
730	6.6	798	10	AB020757	Rattus no	803	253.5	6.4	3289	9	AB067477	AB067477 Homo sapi
731	6.6	1680	6	I06432	Sequence 42	804	253.5	6.4	3715	9	AY358174	AY358174 Homo sapi
732	6.6	2387	6	AX743686	Sequence	805	253.5	6.4	4161	3	ACUS7369	ACUS7369 Aplysia cal
733	6.6	1607	6	CO729780	Sequence	806	253.5	6.4	173534	2	AC007920	AC007920 Homo sapi
734	6.6	1236	6	E02709	DNA sequenc	807	253.5	6.4	207841	2	AC072019	AC072019 Homo sapi

808	253	6.4	1680	6	I06422	106422	Sequence 40	881	248	6.3	2902	10	BC063079	BC063079 Mus muscu
809	253	6.4	2055	4	AB022426	AB022426 Sus scrofa		882	248	6.3	3705	10	BC066062	BC066062 Mus muscu
810	253	6.4	2697	10	MUSFIX	M23109 Mouse coagu		883	247.5	6.3			Q0592056	Q0592056 Sequence
811	253	6.4	4140	6	Q275613	Q275613 Sequence		884	247.5	6.3	937	5	BX933662	BX933662 Gallus ga
812	252.5	6.4	1419	6	A27725	A27725 DNA sequenc		885	247.5	6.3	954	5	BX935323	BX935323 Gallus ga
813	252.5	6.4	1419	6	E01944	E01944 Synthetic D		886	247.5	6.3	957	5	CR338993	CR338993 Gallus ga
814	252.5	6.4	1440	6	E01668	E01668 cDNA encodi.		887	247.5	6.3	969	5	BX933653	BX933653 Gallus ga
815	252	6.4	881	5	BC081638	BC081638 Danio rer		888	247.5	6.3	1323	10	BC055854	BC055854 Mus muscu
816	252	6.4	947	5	BC064277	BC064277 Xenopus t		889	247.5	6.3	1494	6	AX814647	AX814647 Sequence
817	252	6.4	1506	6	E02247	E02247 cDNA sequen		890	247.5	6.3	1787	6	BD139221	BD139221 Soluble i
818	252	6.4	2099	6	A07207	A07207 Artificial		891	247.5	6.3	1810	9	AF280546	AF280546 Homo sapi
819	252	6.4	2901	5	BC076742	BC076742 Xenopus l		892	247.5	6.3	2976	10	MUSEBPIA	L24755 Mus musculu
820	251.5	6.4	959	5	EX931608	EX931608 Gallus ga		893	247	6.3	826	4	RABTHRO	M81396 Oryctolagus
821	251.5	6.4	3180	9	HS488946	AJ488946 Homo sapi		894	247	6.3	995	4	DOGMCTRPA	M24664 Dog mast ce
822	251.5	6.4	3387	6	AX360082	AX360082 Sequence		895	247	6.3	1095	6	Q0600633	Q0600633 Sequence
823	251.5	6.4	3711	6	AX786888	AX786888 Sequence		896	247	6.3	2804	6	Q0592055	Q0592055 Sequence
824	251	6.4	888	10	AY149996	AY149996 Rattus no		897	247	6.3	3095	6	Q0600632	Q0600632 Sequence
825	251	6.4	1614	5	AF465277	AF465277 Takifugu		898	247	6.3	3146	6	AX685997	AX685997 Sequence
826	251	6.4	2152	6	AR379612	AR379612 Sequence		899	247	6.3	4674	6	Q0590238	Q0590238 Sequence
827	250.5	6.3	1243	4	AF372520	AF372520 Oryctolag		900	247	6.3	6119	3	AY075422	AY075422 Drosophil
828	250	6.3	1321	10	AB010778	AB010778 Mus muscu		901	247	6.3	11095	2	AC017524	AC017524 Drosophil
829	250	6.3	1341	6	A30593	A30593 DNA for tis		902	247	6.3	56080	2	AC018086	AC018086 Drosophil
830	250	6.3	2017	5	AB028871	AB028871 Struthio		903	247	6.3	86884	3	AC004366	AC004366 Drosophil
831	250	6.3	2267	6	AX335042	AX335042 Sequence		904	247	6.3	155553	3	AC007802	AC007802 Drosophil
832	250	6.3	2267	6	AX409602	AX409602 Sequence		905	247	6.3	155553	3	AC007802	AC007802 Drosophil
833	250	6.3	2267	3	HUMPPKPA	M13143 Nucleotide		906	247	6.3	198244	3	AC007803	AC007803 Drosophil
834	249.5	6.3	1887	9	TATCFBP	D14701 Tachyples		907	247	6.3	291250	3	AE003455	AE003455 Drosophil
835	249.5	6.3	2695	9	HSBMP15	Y08724 H.sapiens m		908	246.5	6.2	291250	3	AE003455	AE003455 Drosophil
836	249.5	6.3	2770	4	BTPLASMIN	X79402 B.taurus mR		909	246.5	6.2	813	5	NEWTHRO	M81395 Cynops pyrr
837	249.5	6.3	3344	9	HSNEUROTR	AJ001531 Homo sapi		910	246.5	6.2	885	6	AR108139	AR108139 Sequence
838	249.5	6.3	3350	6	AX83630	AX83630 Sequence 1		911	246.5	6.2	1072	6	BD189695	BD189695 A method
839	249	6.3	708	6	A0207901	AX207901 Sequence		912	246.5	6.2	1139	6	AR076901	AR076901 Sequence
840	249	6.3	792	6	AX360081	AX360081 Sequence		913	246.5	6.2	1139	6	AR167292	AR167292 Sequence
841	249	6.3	792	6	BT007356	BT007356 Homo sapi		914	246.5	6.2	1259	10	RAA5642	AJ005642 Rattus ra
842	249	6.3	792	12	BT007599	BT007599 Synthetic		915	246.5	6.2	1409	6	Q0613929	Q0613929 Sequence
843	249	6.3	865	9	HUMCTRP	M24400 Human chymo		916	246.5	6.2	1869	6	AS8753	AS8753 Sequence 7
844	249	6.3	873	9	AK131056	AK131056 Homo sapi		917	246.5	6.2	1869	6	AR102461	AR102461 Sequence
845	249	6.3	909	10	BC061083	BC061083 Mus muscu		918	246.5	6.2	1947	6	AR095303	AR095303 Sequence
846	249	6.3	960	9	BC073145	BC073145 Homo sapi		919	246.5	6.2	1947	6	AR103987	AR103987 Sequence
847	249	6.3	1823	9	BC018146	BC018146 Homo sapi		920	246.5	6.2	1947	6	I16618	I16618 Sequence 2
848	249	6.3	2038	6	AX511622	AX511622 Sequence		921	246.5	6.2	1947	6	I19057	I19057 Sequence 2
849	249	6.3	2447	9	S67310	S67310 Homo sapien		922	246.5	6.2	1947	6	I22331	I22331 Sequence 2
850	249	6.3	2483	6	AR034619	AR034619 Sequence		923	246.5	6.2	1947	6	AX774839	AX774839 Sequence
851	249	6.3	2555	9	AK130533	AK130533 Homo sapi		924	246.5	6.2	1947	9	HSTHR1	V00595 Homo sapien
852	249	6.3	2733	6	AR447886	AR447886 Sequence		925	246.5	6.2	1988	6	AR105746	AR105746 Sequence
853	248.5	6.3	1314	6	A27435	A27435 DNA sequenc		926	246.5	6.2	1988	6	I14101	I14101 Sequence 15
854	248.5	6.3	1314	6	A27437	A27437 DNA sequenc		927	246.5	6.2	1997	6	Q0717780	Q0717780 Sequence
855	248.5	6.3	1314	6	A27441	A27441 DNA sequenc		928	246.5	6.2	1998	9	BC051332	BC051332 Homo sapi
856	248.5	6.3	1314	6	AR059989	AR059989 Sequence		929	246	6.2	2470	11	BV178314	BV178314 sqm99805
857	248.5	6.3	1314	6	AR059990	AR059990 Sequence		930	246	6.2	3430	5	XELXTLDP	D83476 Xenopus lae
858	248.5	6.3	1314	6	AR059992	AR059992 Sequence		931	245.5	6.2	1494	6	AX814649	AX814649 Sequence
859	248.5	6.3	1314	6	AR059993	AR059993 Sequence		932	245.5	6.2	1801	3	AP357226	AP357226 Panulirus
860	248.5	6.3	1314	6	E01937	E01937 Synthetic D		933	245.5	6.2	4380	6	Q0850562	Q0850562 Sequence
861	248.5	6.3	1314	6	E01938	E01938 Synthetic D		934	245.5	6.2	4380	9	AK127722	AK127722 Homo sapi
862	248.5	6.3	1314	6	E01940	E01940 Synthetic D		935	245	6.2	854	5	BC073555	BC073555 Xenopus 1
863	248.5	6.3	1314	6	E01941	E01941 Synthetic D		936	245	6.2	1440	6	E01669	E01669 cDNA encodi
864	248.5	6.3	2096	3	AY061936	AY061936 Bombyx mo		937	245	6.2	2198	3	SUSSUBMX	L23383 Strongyloce
865	248.5	6.3	2345	9	HSBF	Y72875 H.sapiens m		938	245	6.2	2398	10	BC026555	BC026555 Mus muscu
866	248.5	6.3	2388	6	Q0730887	Q0730887 Sequence		939	245	6.2	3487	5	AB038498	AB038498 Xenopus 1
867	248.5	6.3	2388	6	AX330489	AX330489 Sequence		940	245	6.2	6717	9	AB023149	AB023149 Homo sapi
868	248.5	6.3	2388	6	AX409518	AX409518 Sequence		941	245	6.2	6753	6	Q0873941	Q0873941 Sequence
869	248.5	6.3	2388	9	HUMCOMPACB	Li5702 Human compl		942	244.5	6.2	807	6	AR220086	AR220086 Sequence
870	248.5	6.3	2503	9	BC004143	BC004143 Homo sapi		943	244.5	6.2	807	6	AX150967	AX150967 Sequence
871	248.5	6.3	2503	9	BC007990	BC007990 Homo sapi		944	244.5	6.2	842	6	AX375290	AX375290 Sequence
872	248	6.3	860	5	BC078367	BC078367 Danio rer		945	244.5	6.2	989	6	I08551	I08551 Sequence 3
873	248	6.3	861	6	AX800024	AX800024 Sequence		946	244.5	6.2	1317	12	SYNUTUPA	M69037 Synthetic h
874	248	6.3	869	5	AY179345	AY179345 Danio rer		947	244.5	6.2	1488	6	AX814651	AX814651 Sequence
875	248	6.3	885	6	BD209905	BD209905 Human nuc		948	244.5	6.2	1739	6	AR034820	AR034820 Sequence
876	248	6.3	885	6	AX014219	AX014219 Sequence		949	244.5	6.2	3024	9	AK055872	AK055872 Homo sapi
877	248	6.3	907	5	AB029753	AB029753 Paralicht		950	244.5	6.2	65326	2	AC124815	AC124815 Mus muscu
878	248	6.3	1419	6	AR059996	AR059996 Sequence		951	244.5	6.2	216636	2	AC117672	AC117672 Mus muscu
879	248	6.3	1575	6	E01671	E01671 cDNA encodi		952	244	6.2	1128	10	AB049453	AB049453 Mus muscu
880	248	6.3	1621	5	AY216598	AY216598 Meleagris		953	244	6.2	1329	5	AF465274	AF465274 Takifugu

954	244	6.2	1521	6	AX014631	Sequence	1027	239.5	6.1	1468	6	CO414741	Sequence
955	244	6.2	1587	3	AGA675	Anopheles	1028	239.5	6.1	3989	6	CO49871	Sequence
956	244	6.2	2174	6	CO720386	Sequence	1029	239.5	6.1	3989	6	AK126936	Homo sapi
957	244	6.2	2728	10	RNO487623	Sequence	1030	239.5	6.1	11230	6	AR435510	Sequence
958	244	6.2	2753	10	MUSPKA	M58588 Mouse plas	1031	239.5	6.1	11230	6	AX375163	Sequence
959	244	6.2	276258	2	AC136872	Rattus no	1032	239.5	6.1	11289	10	AF206329	Mus muscu
960	243.5	6.2	991	12	AB053399	Synthetic	ci033	239.5	6.1	152909	10	AL929406	Mouse DNA
961	243.5	6.2	2362	9	HSBMP14	H. sapiens m	1034	239	6.1	987	6	AX360076	Sequence
962	243	6.2	869	4	OAR18224	Ovis aries	1035	239	6.1	1170	6	AR059998	Sequence
963	243	6.2	1979	6	CO845801	Sequence	ci1036	239	6.1	3215	11	BV176814	Sequence
964	243	6.2	1979	9	AK131261	Homo sapi	ci1037	239	6.1	3658	6	CO596606	Sequence
965	243	6.2	2810	10	AX13552852	Rattus no	1038	238.5	6.0	875	5	AB029754	Paralicht
966	243	6.2	2991	6	AX577904	Sequence	1039	238.5	6.0	900	3	PLAJ658	Pacifasta
967	243	6.2	3584	6	CO613928	Sequence	1040	238.5	6.0	1188	6	E06063	ECOD63 DNA encodi
968	243	6.2	5021	6	BD225401	Mammalian	1041	238.5	6.0	1207	9	BC058031	Homo sapi
969	243	6.2	5021	6	AR343520	Sequence	1042	238.5	6.0	1501	3	TATPROCL0T	Tachyples
970	243	6.2	5021	9	AF059516	Homo sapi	1043	238.5	6.0	1739	10	RNHEPA	X70900 R.norvegicu
971	243	6.2	28628	2	AC020159	Drosophil	1044	238.5	6.0	1776	4	AY569316	Bos tauru
972	243	6.2	184272	3	AC009211	Sequence	1045	238.5	6.0	2444	3	AK115605	Ciona int
973	243	6.2	247955	3	AB003698	Drosophil	1046	238.5	6.0	5463	9	AB067471	Homo sapi
974	242.5	6.1	929	3	AGTRYLA	Z18889 A.gambiae t	1047	238	6.0	820	10	RATTHRO	M81397 Rattus norv
975	242.5	6.1	1068	6	E02336	Sequence 7	1048	238	6.0	828	6	E40571	Novel prote
976	242.5	6.1	1176	6	E01673	Human fact	1049	238	6.0	882	4	DOGCTRP	K01173 Dog (canine
977	242.5	6.1	1571	9	HUMCFX11B	Sequence	1050	238	6.0	1047	4	AB038652	Sus scrof
978	242.5	6.1	1605	6	AR085656	Sequence	1051	238	6.0	1230	9	HSHPALIS	X00637 Human mRNa
979	242.5	6.1	1724	3	AF499913	Ilyanassa	1052	238	6.0	1234	9	HUMHPALB	K01763 Human hapto
980	242.5	6.1	2457	6	AR162262	Sequence	1053	238	6.0	1485	6	AX814628	Sequence
981	242.5	6.1	2457	6	AR317164	Sequence	1054	238	6.0	1487	3	AGA250916	Sequence
982	242.5	6.1	4796	5	XLXOLL	Y09661 X.laavis mR	1055	238	6.0	1497	6	AX814642	Sequence
983	242	6.1	1176	6	E01672	cdNA encodi	1056	238	6.0	1663	3	AY061564	Drosophil
984	242	6.1	1497	6	AX814639	Sequence	1057	238	6.0	1831	6	CO613029	Sequence
985	242	6.1	1848	6	CO730299	Sequence	1058	238	6.0	2419	5	XEUBMPIA	L12249 Xenopus lae
986	242	6.1	1959	6	AX774785	Sequence	1059	238	6.0	2625	6	AR164818	Sequence
987	242	6.1	1959	9	HUMCFX11A	Human blood	1060	238	6.0	2625	6	AR490618	Sequence
988	242	6.1	1980	9	HUMF12A	M13115 Human coagu	1061	238	6.0	2625	5	AB038497	Xenopus 1
989	241.5	6.1	1840	10	AF305425	Mus muscu	1062	238	6.0	3507	5	AB038497	Xenopus 1
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991	241.5	6.1	1248	6	AX262412	Sequence	1064	238	6.0	4072	6	AR164817	Sequence
992	241.5	6.1	1618	3	AY075233	Drosophil	1065	238	6.0	4072	6	AR490617	Sequence
993	241.5	6.1	1639	6	CO414399	Sequence	1066	238	6.0	4072	6	AR532391	Sequence
994	241.5	6.1	1641	6	AX262410	Sequence	1067	238	6.0	4510	9	MACAPOA	J04635 Rhesus monk
995	241.5	6.1	1872	6	AX254430	Sequence	1068	238	6.0	8589	6	AR164816	Sequence
996	241.5	6.1	2320	9	HSBMP16	Y08725 H.sapiens m	1069	238	6.0	8589	6	AR490616	Sequence
997	241.5	6.1	2658	9	HSM806478	Alu833167 Homo sapi	1070	238	6.0	8589	6	AR532390	Sequence
998	241.5	6.1	2663	9	HSM806070	BX537945 Homo sapi	1071	238	6.0	8589	6	AR532390	Sequence
999	241.5	6.1	3210	3	AK112764	AK112764 Ciona int	ci072	238	6.0	154160	2	AC017357	Drosophil
1000	241.5	6.1	3440	10	AY135525S2	AY135526 Mus muscu	ci073	238	6.0	169863	3	AC064154	Homo sapi
1001	241.5	6.1	3915	6	CO734404	Sequence	ci074	238	6.0	183948	3	AC009376	Drosophil
1002	241	6.1	1065	6	AR27447	DNA sequence	1075	238	6.0	289990	3	AE003516	Drosophil
1003	241	6.1	1065	6	AR059995	Sequence	1076	237.5	6.0	960	6	CO735672	Sequence
1004	241	6.1	1065	6	E01943	Synthetic D	1077	237.5	6.0	1068	6	E05898	Sequence
1005	241	6.1	1076	10	AB006130	AB006130 Mesocric	1078	237.5	6.0	1798	3	AY119095	X.laavis mR
1006	241	6.1	1497	6	AX814644	Sequence	1079	237.5	6.0	2531	5	XLEMP1	Y09660 X.laavis mR
1007	241	6.1	3546	6	AR162263	Sequence	1080	237.5	6.0	2585	5	BC080382	BC080382 Xenopus 1
1008	241	6.1	3546	6	AR317165	Sequence	1081	237.5	6.0	2585	5	BC080382	BC080382 Xenopus 1
1009	241	6.1	4493	4	AF531101	Rattus no	1082	237.5	6.0	3819	9	AF106861	Homo sapi
1010	240.5	6.1	833	5	AB029751	Paralicht	1083	237.5	6.0	11152	6	AX686198	Sequence
1011	240.5	6.1	1068	6	AX254967	Sequence	1084	237.5	6.0	11158	6	AX686196	Sequence
1012	240.5	6.1	1068	6	AR363691	Sequence	1085	237	6.0	818	5	TRU25747	Takifugu ru
1013	240.5	6.1	1233	6	I48917	Sequence 1	1086	237	6.0	819	10	MUSTHRO	M81394 Mus musculu
1014	240.5	6.1	2388	5	AF089860	Oncorhync	1087	237	6.0	923	9	AF113248	Homo sapi
1015	240.5	6.1	3350	6	AX685995	Sequence	1088	237	6.0	1700	5	BC056849	Xenopus 1
1016	240.5	6.1	10878	6	AR435509	Sequence	1089	237	6.0	2320	5	EPPTHROM	M81393 Eptatretus
1017	240.5	6.1	10878	6	AX375161	Sequence	1090	237	6.0	4771	6	AR170997	Sequence
1018	240	6.1	877	5	PWTRVPS1N	X82223 P.magellani	1091	237	6.0	4883	6	CO720933	Sequence
1019	240	6.1	1521	6	AX814634	Sequence	1092	237	6.0	4754	10	MMU34042	Mus musculu
1020	240	6.1	1801	6	CO727939	Sequence	1093	236.5	6.0	1065	6	I62335	Sequence 1
1021	240	6.1	2949	6	CO737049	Sequence	1094	236.5	6.0	1065	6	I62335	Sequence 1
1022	239.5	6.1	832	5	AB041929	Engraulis	1095	236.5	6.0	1065	6	AX431270	Sequence
1023	239.5	6.1	832	6	BD056354	Novel DNA	1096	236.5	6.0	1065	6	AX431270	Sequence
1024	239.5	6.1	1397	9	HUMHPAB	K00422 Human hapto	1097	236.5	6.0	1068	6	A00762	Synthetic t
1025	239.5	6.1	1411	9	L29394	L29394 Homo sapien	1098	236.5	6.0	1068	6	A27431	DNA sequenc
1026	239.5	6.1	1441	6	BD276276	Serine pr	1099	236.5	6.0	1068	6	A27433	DNA sequenc



1100	236.5	6.0	1068	6	A27445	A27445 DNA sequenc	1173	235	6.0	9177	10	AJ584850	AJ584850 Mus muscu
1101	236.5	6.0	1068	6	AR059987	AR059987 Sequence	1174	234.5	5.9	1185	9	AF260825	AF260825 Homo sapi
1102	236.5	6.0	1068	6	AR059988	AR059988 Sequence	1175	234.5	5.9	1566	3	BT011129	BT011129 Drosophi
1103	236.5	6.0	1068	6	AR059994	AR059994 Sequence	1176	234.5	5.9	2231	10	BC019485	BC019485 Mus muscu
1104	236.5	6.0	1068	6	E01935	E01935 Synthetic D	1177	234	5.9	785	6	AX921749	AX921749 Sequence
1105	236.5	6.0	1068	6	E01936	E01936 Synthetic D	1178	234	5.9	1701	6	AX814625	AX814625 Sequence
1106	236.5	6.0	1068	6	E01942	E01942 Synthetic D	1179	234	5.9	2394	10	BC005451	BC005451 Mus muscu
1107	236.5	6.0	1068	6	E18744	E18744 Sequence 2	1180	233.5	5.9	867	5	CMRECT	X78490 G.morhua mR
1108	236.5	6.0	1068	6	E162334	E162334 Sequence 3	1181	233.5	5.9	870	6	AX226513	AX226513 Sequence
1109	236.5	6.0	1067	6	AR080456	AR080456 Sequence	1182	233.5	5.9	1163	6	AR076898	AR076898 Sequence
1110	236.5	6.0	1097	10	RATRMCT	D38455 Rat mRNA fo	1183	233.5	5.9	1163	6	AR167289	AR167289 Sequence
1111	236.5	6.0	1128	6	AX431268	AX431268 Sequence	1184	233.5	5.9	1803	6	AX814646	AX814646 Sequence
1112	236.5	6.0	1128	6	AX431271	AX431271 Sequence	1185	233.5	5.9	2363	6	AR220138	AR220138 Sequence
1113	236.5	6.0	1137	6	AR175771	AR175771 Sequence	1186	233.5	5.9	2363	6	AX336397	AX336397 Sequence
1114	236.5	6.0	1137	6	AR232006	AR232006 Sequence	1187	233.5	5.9	2363	6	AX411046	AX411046 Sequence
1115	236.5	6.0	1137	6	AX136012	AX136012 Sequence	1188	233.5	5.9	2363	6	AX511632	AX511632 Sequence
1116	236.5	6.0	1137	6	AX136781	AX136781 Sequence	1189	233.5	5.9	2363	9	HSRPSH	X07732 Human hepat
1117	236.5	6.0	1137	6	AX137832	AX137832 Sequence	1190	233.5	5.9	6567	10	AK172967	AK172967 Mus muscu
1118	236.5	6.0	1137	6	BD000154	BD000154 Process f	1191	233.5	5.9	6609	10	AY688677	AY688677 Mus muscu
1119	236.5	6.0	1137	6	BD010886	BD010886 Process f	1192	233	5.9	1002	4	OAR18223	Y18223 Ovis aries
1120	236.5	6.0	1170	6	A27727	A27727 DNA sequenc	1193	233	5.9	1077	6	AX780068	AX780068 Sequence
1121	236.5	6.0	1170	6	E01945	E01945 Synthetic D	1194	233	5.9	2385	10	AF537098	AF537098 Rattus no
1122	236.5	6.0	1173	6	E01674	E01674 cDNA -encodi	1195	232.5	5.9	1283	6	CO979781	CO979781 Sequence
1123	236.5	6.0	1179	6	A00137	A00137 Synthetic g	1196	232.5	5.9	1283	9	AF283670	AF283670 Homo sapi
1124	236.5	6.0	1179	6	A00140	A00140 Synthetic g	1197	232.5	5.9	1500	6	AR024194	AR024194 Sequence
1125	236.5	6.0	1179	6	A14893	A14893 Plasmidogen	1198	232.5	5.9	3125	5	BC068636	BC068636 Xenopus l
1126	236.5	6.0	1179	6	E02397	E02397 DNA encodin	1199	232.5	5.9	3517	3	CG1431705	AJ431705 Crassostr
1127	236.5	6.0	1616	6	I06017	I06017 Sequence 9	1200	232.5	5.9	3919	6	AR085400	AR085400 Sequence
1128	236.5	6.0	1724	6	AR363268	AR363268 Sequence	1201	232.5	5.9	3919	6	AR170998	AR170998 Sequence
1129	236.5	6.0	1781	10	AF030065	AF030065 Mus muscu	1202	232.5	5.9	3919	9	HSU91963	U91963 Human toll
1130	236.5	6.0	1950	4	S70164	S70164 Hageman fac	1203	232.5	5.9	4284	10	AB062913	AB062913 Mesocrice
1131	236.5	6.0	2331	4	AF395821	AF395821 Oryctolag	1204	232.5	5.9	5139	9	AF282732	AF282732 Homo sapi
1132	236.5	6.0	2499	10	RNU0311671	AJ311671 Rattus no	1205	232.5	5.9	5145	6	AR096487	AR096487 Sequence
1133	236.5	6.0	2752	10	MMU300738	AJ300738 Mus muscu	1206	232.5	5.9	5145	6	BD165892	BD165892 Human hea
1134	236.5	6.0	266868	2	AC096906	AC096906 Rattus no	1207	232.5	5.9	5145	6	E30055	E30055 Human heart
1135	236	6.0	881	6	BC054136	BC054136 Danio rer	1208	232.5	5.9	5145	6	AR204076	AR204076 Sequence
1136	236	6.0	1068	6	A27439	A27439 DNA sequenc	1209	232.5	5.9	6690	9	HSM804919	AL833606 Homo sapi
1137	236	6.0	1068	6	AR059991	AR059991 Sequence	1210	232	5.9	1068	6	A07690	A07690 Synthetic D
1138	236	6.0	1068	6	E01939	E01939 Synthetic D	1211	232	5.9	1677	6	AX814626	AX814626 Sequence
1139	236	6.0	1164	6	E01118	E01118 cDNA encodi	1212	232	5.9	2246	6	CO715376	CO715376 Sequence
1140	236	6.0	1170	6	A27729	A27729 DNA sequenc	1213	232	5.9	2464	10	RATKALP	M30282 Rat plasma
1141	236	6.0	1170	6	E01946	E01946 Synthetic D	1214	232	5.9	2464	10	RATRPK	M55590 Rat plasma
1142	236	6.0	2402	10	AK098094	AK098094 Mus muscu	1215	232	5.9	2563	6	AX401888	AX401888 Sequence
1143	236	6.0	2443	10	MUSCCBFA	M57890 Mouse facto	1216	232	5.9	2609	6	AX477377	AX477377 Sequence
1144	235.5	6.0	978	6	E0365498	AX365498 Sequence	1217	232	5.9	3366	6	CO587289	CO587289 Sequence
1145	235.5	6.0	1068	6	E05897	E05897 DNA sequenc	1218	232	5.9	3374	3	DRDVP	M76976 D.melanogas
1146	235.5	6.0	1103	10	RNU67909	U67909 Rattus norv	1219	232	5.9	3427	3	BT010008	BT010008 Drosophi
1147	235.5	6.0	1445	6	I01255	I01255 Sequence 1	1220	232	5.9	12811	6	CO576228	CO576228 Sequence
1148	235.5	6.0	1595	10	BC079254	BC079254 Rattus no	1221	231.5	5.9	848	5	GMU57055	U57055 Gadus morhu
1149	235.5	6.0	2730	6	AR400897	AR400897 Sequence	1222	231.5	5.9	917	4	BTPELAS	X97635 B.taurus mR
1150	235.5	6.0	2730	6	BD073481	BD073481 Semaphori	1223	231.5	5.9	955	6	CO729939	CO729939 Sequence
1151	235.5	6.0	2730	9	AF022859	AF022859 Homo sapi	1224	231.5	5.9	1170	6	AR059997	AR059997 Sequence
1152	235.5	6.0	2745	4	EU033171	U33171 Erinaceus e	1225	231.5	5.9	1701	12	SYNCHPL	M69273 Cloning vec
1153	235.5	6.0	2781	6	CO714485	CO714485 Sequence	1226	231.5	5.9	2163	10	AF537099	AF537099 Rattus no
1154	235.5	6.0	2781	6	AR400898	AR400898 Sequence	1227	231.5	5.9	2175	6	AX833435	AX833435 Sequence
1155	235.5	6.0	2781	6	AX743086	AX743086 Sequence	1228	231.5	5.9	2175	9	AK095160	AK095160 Homo sapi
1156	235.5	6.0	2781	6	BD073482	BD073482 Semaphori	1229	231.5	5.9	2265	9	AB028140	AB028140 Homo sapi
1157	235.5	6.0	2781	9	AF022860	AF022860 Homo sapi	1230	231	5.9	723	5	E13204	E13204 Human cDNA
1158	235.5	6.0	2796	9	AF016098	AF016098 Homo sapi	1231	231	5.9	907	5	AF012463	AF012463 Pleuronec
1159	235.5	6.0	3357	9	AF280544	AF280544 Homo sapi	1232	231	5.9	1098	6	A42131	A42131 Sequence 21
1160	235.5	6.0	3372	9	AF280545	AF280545 Homo sapi	1233	231	5.9	1167	6	A42127	A42127 Sequence 17
1161	235.5	6.0	3404	6	BD139219	BD139219 Soluble i	1234	231	5.9	1176	6	A42135	A42135 Sequence 25
1162	235.5	6.0	3404	6	AR409883	AR409883 Sequence	1235	231	5.9	1176	6	A42139	A42139 Sequence 29
1163	235	6.0	1193	10	BC011328	BC011328 Mus muscu	1236	231	5.9	1182	6	A42111	A42111 Sequence 1
1164	235	6.0	1219	6	AR080457	AR080457 Sequence	1237	231	5.9	1182	6	A42113	A42113 Sequence 3
1165	235	6.0	1219	10	MUIMCT	D31789 Mongolian g	1238	231	5.9	1182	6	A42115	A42115 Sequence 5
1166	235	6.0	1521	6	AX814636	AX814636 Sequence	1239	231	5.9	1182	6	A42117	A42117 Sequence 7
1167	235	6.0	1709	5	BC055596	BC055596 Danio rer	1240	231	5.9	1182	6	A42119	A42119 Sequence 9
1168	235	6.0	1992	6	BD130508	BD130508 Secretary	1241	231	5.9	1182	6	A42123	A42123 Sequence 13
1169	235	6.0	6004	6	AX537467	AX537467 Sequence	1242	231	5.9	1182	6	A42125	A42125 Sequence 15
1170	235	6.0	6402	11	BV177788	BV177788 sqm96732	1243	231	5.9	1182	6	A42153	A42153 Sequence 43
1171	235	6.0	6402	11	BV177912	BV177912 sqm97463	1244	231	5.9	1182	6	A42155	A42155 Sequence 45
1172	235	6.0	6670	9	HSM805725	BS537423 Homo sapi	1245	231	5.9	1182	6	A42157	A42157 Sequence 47



1246	231	5.9	1185	6	A42133	A42133 Sequence 23	1319	229	5.8	804	3	AF312826	AF312826 Luidia fo
1247	231	5.9	1185	6	A42143	A42143 Sequence 33	1320	229	5.8	825	10	AF184895	AF184895 Mus muscu
1248	231	5.9	1185	6	A42145	A42145 Sequence 35	1321	229	5.8	1187	6	AX338503	AX338503 Sequence
1249	231	5.9	1185	6	A42147	A42147 Sequence 37	1322	229	5.8	1200	6	AR125379	AR125379 Sequence
1250	231	5.9	1185	6	A42149	A42149 Sequence 39	cl323	229	5.8	1200	6	AR125380	AR125380 Sequence
1251	231	5.9	1185	6	A42151	A42151 Sequence 41	1324	229	5.8	1200	6	AR144651	AR144651 Sequence
1252	231	5.9	1191	6	A42151	A42151 Sequence 11	cl325	229	5.8	1200	6	AR144652	AR144652 Sequence
1253	231	5.9	1191	6	A42121	A42121 Sequence 19	1326	229	5.8	1200	6	AR214385	AR214385 Sequence
1254	231	5.9	1191	6	A42129	A42129 Sequence 27	1327	229	5.8	1200	6	AR214385	AR214385 Sequence
1255	231	5.9	1194	6	A42137	A42137 Sequence 31	1328	229	5.8	1200	6	BD022582	BD022582 Flea prot
1256	231	5.9	1197	6	A42141	A42141 Sequence 31	1329	229	5.8	1200	6	BD022582	BD022582 Flea prot
1257	231	5.9	1479	6	E00853	E00853 Hybrid gene	cl329	229	5.8	1736	3	PLR7668	AJ007668 Pacifasta
1258	231	5.9	2590	6	Q086992	Q086992 Sequence	1330	229	5.8	1887	10	AY234104	AY234104 Mus muscu
1259	231	5.9	2627	6	Q086994	Q086994 Sequence	1331	229	5.8	1892	10	BC061800	BC061800 Rattus no
1260	231	5.9	3027	5	GGA012462	AJ012462 Gallus ga	1332	229	5.8	1894	6	AR125377	AR125377 Sequence
1261	231	5.9	4661	6	BD225402	BD225402 Mammalian	1333	229	5.8	1894	6	AR125378	AR125378 Sequence
1262	231	5.9	4661	6	AR343521	AR343521 Sequence	cl334	229	5.8	1894	6	AR142763	AR142763 Sequence
1263	230.5	5.8	780	6	AF073526	AF073526 Mus muscu	1335	229	5.8	1894	6	AR144649	AR144649 Sequence
1264	230.5	5.8	780	9	AR487614	AR487614 Sequence	1336	229	5.8	1894	6	AR144650	AR144650 Sequence
1265	230.5	5.8	873	6	AX577741	AX577741 Homo sapi	cl337	229	5.8	1894	6	AR214284	AR214284 Sequence
1266	230.5	5.8	888	6	AR487613	AR487613 Sequence	1338	229	5.8	1894	6	BD022580	BD022580 Flea prot
1267	230.5	5.8	888	9	AY344793	AY344793 Homo sapi	cl339	229	5.8	1894	6	BD022581	BD022581 Flea prot
1268	230.5	5.8	967	6	BD243371	BD243371 Treatment	1340	229	5.8	1894	6	BD022581	BD022581 Flea prot
1269	230.5	5.8	967	6	BD003281	BD003281 Enzyme an	cl341	229	5.8	2202	6	CQ615018	CQ615018 Sequence
1270	230.5	5.8	1509	3	AK115721	AK115721 Ciona inc	1342	229	5.8	4234	12	AB007632	AB007632 Signal se
1271	230.5	5.8	1916	9	AF045649	AF045649 Homo sapi	1343	229	5.8	678	6	CQ716937	CQ716937 Sequence
1272	230.5	5.8	2158	6	AX147449	AX147449 Sequence	1344	228.5	5.8	891	4	BOVEKCS	LI9663 Bos taurus
1273	230.5	5.8	2568	9	AX147449	AX147449 Sequence	1345	228.5	5.8	1099	9	AY358867	AY358867 Homo sapi
1274	230.5	5.8	3180	10	BC061712	BC061712 Rattus no	1346	228.5	5.8	1133	6	AX392231	AX392231 Sequence
1275	230.5	5.8	5381	3	DMU34777	U12634 Drosophila	1347	228.5	5.8	1234	10	S67972	S67972 Mus sp. hap
1276	230.5	5.8	5392	3	DMU12634	AF229448 Danio rer	1348	228.5	5.8	1842	6	BD203763	BD203763 Human nuc
1277	230.5	5.8	6669	5	AF229448	CQ587274 Sequence	1349	228.5	5.8	1842	6	AX014918	AX014918 Sequence
1278	230	5.8	798	6	CQ587274	CQ587274 Sequence	1350	228.5	5.8	1842	6	AX014918	AX014918 Sequence
1279	230	5.8	891	6	CQ714155	AB070720 Anguilla	1351	228.5	5.8	3429	3	AF224491	AF224491 Halocynth
1280	230	5.8	906	5	AB070720	AB070720 Anguilla	1352	228.5	5.8	7596	6	AX695382	AX695382 Sequence
cl281	230	5.8	1078	6	AX190545	AX190545 Sequence	1353	228.5	5.8	8064	6	AX695381	AX695381 Sequence
1282	230	5.8	1161	6	AR142768	AR142768 Sequence	1354	228.5	5.8	8913	10	MN0TCH	Z11886 M.musculus
cl283	230	5.8	1161	6	AR142769	AR142769 Sequence	1355	228.5	5.8	9193	10	AF508809	AF508809 Mus muscu
1284	230	5.8	1161	6	AR142773	AR142773 Sequence	1356	228	5.8	1806	6	AX814638	AX814638 Sequence
cl285	230	5.8	1161	6	AR142774	AR142774 Sequence	1357	228	5.8	3690	6	AR096488	AR096488 Sequence
1286	230	5.8	1175	6	AR142771	AR142771 Sequence	1358	228	5.8	3690	6	BD165893	BD165893 Human hea
cl287	230	5.8	1175	6	AR142772	AR142772 Sequence	1359	228	5.8	3690	6	E30056	E30056 Human heart
1288	230	5.8	1314	6	AX190543	AX190543 Sequence	1360	228	5.8	3690	6	AR204077	AR204077 Sequence
cl289	230	5.8	1314	6	AX190546	AX190546 Sequence	1361	227.5	5.8	827	6	CQ714827	CQ714827 Sequence
1290	230	5.8	1373	6	AR142766	AR142766 Sequence	1362	227.5	5.8	838	9	BC074904	BC074904 Homo sapi
cl291	230	5.8	1373	6	AR142767	AR142767 Sequence	1363	227.5	5.8	838	9	BC074905	BC074905 Homo sapi
1292	230	5.8	1375	6	CQ729940	CQ729940 Sequence	1364	227.5	5.8	862	5	SSTRYP1	X70075 Salmo salar
1293	230	5.8	1376	3	AF117749	AF117749 Anopheles	1365	227.5	5.8	888	6	AX360070	AX360070 Sequence
1294	230	5.8	1614	6	AX360089	AX360089 Sequence	1366	227.5	5.8	929	5	GECTHRO	M81392 Gecko gecko
1295	230	5.8	1689	6	AX149579	AX149579 Sequence	1367	227.5	5.8	1018	6	AX370454	AX370454 Sequence
1296	230	5.8	1748	6	AR534544	AR534544 Sequence	1368	227.5	5.8	1460	9	HSHPRGNE	X89214 H. sapiens m
1297	230	5.8	1748	6	AX369323	AX369323 Sequence	1369	227.5	5.8	1494	6	AX814655	AX814655 Sequence
1298	230	5.8	1830	6	AX814630	AX814630 Sequence	1370	227.5	5.8	2255	6	AX786894	AX786894 Sequence
1299	230	5.8	2048	9	AB095845	AB095845 Homo sapi	1371	227	5.8	726	6	AX473052	AX473052 Sequence
1300	230	5.8	2067	6	AX149581	AX149581 Sequence	1372	227	5.8	777	5	SSTRYP1B	X70072 Salmo salar
1301	230	5.8	2237	9	AY190317	AY190317 Homo sapi	1373	227	5.8	868	5	SSTRYP1A	X70071 Salmo salar
1302	230	5.8	2393	9	AB048796	AB048796 Homo sapi	1374	227	5.8	869	5	AX496969	AX496969 Tautogola
1303	230	5.8	3005	5	CHKTHROM	MB1391 Gallus gall	1375	227	5.8	927	6	AX375719	AX375719 Sequence
1304	230	5.8	3222	9	BC018715	BC018715 Homo sapi	1376	227	5.8	959	6	AR253969	AR253969 Sequence
1305	230	5.8	3324	6	AB048797	AB048797 Homo sapi	1377	227	5.8	968	6	BD003277	BD003277 Enzyme an
1306	229.5	5.8	1043	6	CQ725563	CQ725563 Sequence	1378	227	5.8	1030	5	BC054286	BC054286 Xenopus l
1307	229.5	5.8	1059	6	AX360080	AX360080 Sequence	1379	227	5.8	1055	10	AY005145	AY005145 Mus muscu
1308	229.5	5.8	1494	6	AX814653	AX814653 Sequence	1380	227	5.8	1055	10	AB059415	AB059415 Mus muscu
1309	229.5	5.8	2025	10	AF356627	AF356627 Mus muscu	1381	227	5.8	1084	10	AB033822	AB033822 Mus muscu
1310	229.5	5.8	2559	6	AB078887	AB078887 Sequence	1382	227	5.8	1084	10	AF176209	AF176209 Mus muscu
1311	229.5	5.8	3469	6	CQ573579	CQ573579 Sequence	1383	227	5.8	1098	4	ECAS15902	AJ515902 Equus cab
1312	229.5	5.8	4711	3	BF003214	BF003214 Drosophil	1384	227	5.8	1123	10	BC049588	BC049588 Mus muscu
1313	229.5	5.8	5366	6	CQ612366	CQ612366 Sequence	1385	227	5.8	1467	3	SMJL11561	AJ011561 Schistoso
1314	229.5	5.8	5376	3	AY051585	AY051585 Drosophil	1386	227	5.8	1647	6	AX375310	AX375310 Sequence
1315	229	5.8	726	6	AR125381	AR125381 Sequence	1387	227	5.8	1647	6	AX375718	AX375718 Sequence
1316	229	5.8	726	6	AR144653	AR144653 Sequence	1388	227	5.8	1849	9	AK126396	AK126396 Homo sapi
1317	229	5.8	726	6	AR214287	AR214287 Sequence	1389	227	5.8	1895	3	AF053915	AF053915 Ctenoceph
1318	229	5.8	726	6	BD022584	BD022584 Flea prot	1390	227	5.8	3896	6	AX149475	AX149475 Sequence
							1391	226.5	5.7	810	5	SSTRYP1II	X70074 Salmo salar



Db 26 ATGGAGCTGGTGTGGAGCGAGTTGGGCTCACTTTTCTTCAGCTCCTCTTCATCTCG 85  
Qy  
21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40  
Db TCCTTGCCAAAGAGTACACAGTCATTAAAGAGCCCTGCCCTGGAGCAGAGTGGAAATATC 145  
Qy 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60  
Db 146 ATGTGTGGGAGTGTGTGAATATGATCAGATTGAGTGGCTGTGCCCGGAAAGAGGGAA 205  
Qy 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80  
Db 206 GTCTGGGTATACCAATCCCTTCTGCTGCAGAGAAATGAGGAGATCAGTGTGACTCTCGCTG 265  
Qy 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100  
Db 266 ATCCACCAGGTTGTACCATCTTTGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG 325  
Qy 101 GlyThrLeuAspPheTyrValIleGlyPheTyrCysAlaGluCysArgAlaGlyTyr 120  
Db 326 GSTACCTTGGATGACTTCTATGTAAGGGGTCTTACTGTGCAGAGTCCGAGCAGGCTGG 385  
Qy 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140  
Db 386 TACGAGGAGACTGCATGCGATGTGGCAGGTTCTGGGAGCCCCAAAGGGTCAGATTGG 445  
Qy 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe 160  
Db 446 TTGGAAAGCTATCCCTTAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTT 505  
Qy 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180  
Db 506 GTCATCCAATAAGATTGTGATGTTGAGTCTGGAGTTGACTACATGTCGCCAGTAGAC 565  
Qy 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200  
Db 566 TAIGTTGAGTTTGTGATGAGACCAACCGCGATGGCCAGATCATCAAGGTGTCTGTGGC 625  
Qy 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220  
Db 626 AACGAGCGGCAGCTCTATCCAGAGCATAGGATCCTCACTCCACGTCTCTTCCACTCC 685  
Qy 221 AspGlySerLysAsnAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240  
Db 686 GATGGCTCCAAAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCAGCATGTCTC 745  
Qy 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260  
Db 746 TCATCCCTTGTTCATGACGGCACGTGGTCTCTTGACAAGGCTGGATCTTACAAGTGT 805  
Qy 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluAlaArgAsnCys 280  
Db 806 GCCTGCTTGGCAGGCTATCTGGGACGGCTGTGAAAATCTCTTGAAGAAAGAAACTGC 865  
Qy 281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIle 300  
Db 866 TCAGACCTCGGGGCCCCAGTCATATGGGTACAGAAAATAACAGGGGCCCTTGGGCTTATC 925  
Qy 301 AsnGlyArgHisAlaLysIleGlyThrValValSerPhePheCysAsnAsnSerTyrVal 320  
Db 926 AACGGACCCATGCTAAATAATGGACCGTGGTGTCTTTCTTTGTAACTACTCTATGTT 985  
Qy 321 LeuSerGlyAsnGluLysArgThrCysGlnAsnGlyGluTyrSerGlyLysGlnPro 340  
Db 986 CTTAGTGGCAATGAGAAAGAACTTGCAGCAGAAATGGAGAGTGGTTCAGGGAAACAGCCC 1045  
Qy 341 IleCysIleLysAlaCysArgGluProLysIleSerAspLeuValArgArgValLeu 360  
Db 1046 ATCTGCATAAAGCCCTCCGAGAACCAAGATTTTCAGACCTGGTGGAGAGAGATGTTCT 1105  
Qy 361 ProMetGlnValGlnSerArgGluThrProLeuHisGlnLeuTyrSerAlaAlaPheSer 380  
Db 1106 CCGATGCAGGTTTCAGTCAAGGGAGACACCATTTACACGAGCTATACTCAGCGGCTTCAGC 1165

## RESULT 2

AX092306

LOCUS

DEFINITION

Sequence 37 from Patent WO0116318.  
2846 bp DNA linear PAT 21-MAR-2001

Qy 381 LysGlnLysLeuGlnSerAlaProThrLysLysProAlaLeuProPheGlyAspLeuPro 400  
Db 1166 AAGCAGAAATCTGAGAGTGCCTTACCAAGAGCCAGCCCTTCCCTTTTGAGATCTGCC 1225  
Qy 401 MetGlyTyrGlnHisLeuHisThrGlnLeuGlnTyrGluCysIleSerProPheTyrArg 420  
Db 1226 ATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGC 1285  
Qy 421 ArgLeuGlySerSerArgArgThrCysLeuArgThrGlyLysTyrTrpSerGlyArgAlaPro 440  
Db 1286 CGCTCGGAGCAGCAGCAGGAGGACATCTCTCAGGACTTGGGAAGTGGAGTGGCGGGACCA 1345  
Qy 441 SerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLysThrGlnGlyLeu 460  
Db 1346 TCTTGCATCCCTATCTGCGGGAATTTGAGAACATCCTCTCCAAAGACCCCAAGGGTTG 1405  
Qy 461 ArgTrpProTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHisAspGlySerLeu 480  
Db 1406 CGCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCCAGCGGGTGCATGACGCGCCTA 1465  
Qy 481 HisLysGlyAlaTrpPheLeuValCysSerGlyAlaLeuValAsnGluArgThrValVal 500  
Db 1466 CACAGGAGCGGTGTCTTAGTCTCAGCGGTGCCCTGGTGAATGAGCGCATCTGGTG 1525  
Qy 501 ValAlaAlaHisCysValThrAspLeuGlyLysValThrMetIleLysThrAlaAspLeu 520  
Db 1526 GTGGCTGGCCACCTGTGTACTGACCTGGGGAAGGTCAACATGATCAAGACAGCAGACTG 1585  
Qy 521 LysValValLeuGlyLysPheTyrArgAspAspArgAspGluLysThrIleGlnSer 540  
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Baton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,  
 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and  
 Wood,W.I.  
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 JOURNAL Patent: WO 0116318-A 37.08-MAR-2001;  
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VERSION AX403343.1 GI:21436887  
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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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## REFERENCE

## AUTHORS

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Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,  
Pavoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.

Secreted and transmembrane polypeptides and nucleic acids encoding  
the same

Patent: WO 0073454-A 230 07-DEC-2000;

## JOURNAL

## Genentech Inc. (US)

## FEATURES

## source

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Qy	461	ArgTrpProTrpGlnAlaAlaIleTyrArgTrpSerGlyValHisAspGlySerLeu	480		TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment	
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## ORIGIN

## Alignment Scores:

Pred. No.: 3.03e-280 Length: 2846  
 Score: 3945.00 Matches: 720  
 Percent Similarity: 100.00% Conservativeness: 0  
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 DB: 9 Gaps: 0

US-10-063-692-38 (1-720) x AY358346 (1-2846)

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AX084209

LOCUS AX084209 2306 bp DNA linear PAT 28-FEB-2001  
DEFINITION Sequence 3 from Patent WO0110902.  
ACCESSION AX084209  
VERSION AX084209.1 GI:13185712  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Fernandes, E.  
TITLE Nucleic acids and secreted polypeptides encoded thereby  
JOURNAL Patent: WO 0110902-A 3 15-FEB-2001;  
Curagen Corporation (US)  
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Best Local Similarity: 99.72% Mismatches: 0  
Query Match: 99.85% Indels: 0  
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DEFINITION Sequence 25 from Patent WO0119856.
ACCESSION AX133839
VERSION AX133839.1 GI:14139791
KEYWORDS
SOURCE
ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Shimkets,R.A., Fernandes,E., Herrmann,J.L., Liu,X., Yang,M. and
Boldog,F.L.
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Curagen Corporation (US)
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 ACCESSION BD012236  
 VERSION BD012236.1 GI:22092425  
 KEYWORDS WO 0109349-A/3.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 1 (bases 1 to 2289)  
 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,  
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T., Yano, K.,  
 Murakami, K., Kanazaki, K., Inoue, Y., Hashimoto, E. and Kashima, A.  
 A novel gene encoding a serine protease-like protein  
 Patent: WO 0109349-A 3 08-FEB-2001;  
 HBLIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,  
 KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU  
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 PF 28-JUL-2000 WO 2000JP005062  
 PR 29-JUL-1999 JP 99P 248036, 27-AUG-1999 JP 99P 300253 PR  
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 18-OCT-1999 US 60/159590, 17-FEB-2000 US 60/183322 PI TOSHIO  
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Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,			
AUTHORS			
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 1 (bases 1 to 2784)  
 Ota.T., Isogai.T., Nishikawa.T., Hayaashi.K., Saiko.K., Yamamoto.J.,  
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 A novel gene encoding a serine protease-like protein  
 Patent: WO 0109349-A 1 08-FEB-2001;  
 HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,  
 KOJI HAYASHI,KAZUO SAITO,JUNICHI YAMAMOTO,SHIZUKO ISHII, OMOYASU  
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 Best Local Similarity: 97.56% Mismatches: 1  
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AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oyayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Hara, K., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiro, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.  
Complete sequencing and characterization of 21,243 full-length human cDNAs  
Nat. Genet. 36 (1), 40-45 (2004)  
JOURNAL PUBMED 14702039  
TITLE

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2
REFERENCE
AUTHORS
  Isogai,T., Ota,T., Hayaashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
  Nishikawa,T., Nagai,K., Sakano,S., Shiratori,A., Sudo,H.,
  Watanabe,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H.,
  Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
  Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
  Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
  Nakamura,Y., Nagahara,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  NEDO human cDNA sequencing project
  Unpublished
  3 (bases 1 to 2784)
REFERENCE
AUTHORS
  Isogai,T. and Otsuki,T.
  Direct Submission
  Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
  Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
  (E-mail:genomics@ri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
  NEDO human cDNA sequencing project supported by Ministry of
  Economy, Trade and Industry of Japan; cDNA full insert sequencing:
  Research Association for Biotechnology; cDNA library construction,
  5'- & 3'-end pass sequencing and clone selection: Helix
  Research Institute (supported by Japan Key Technology Center etc.)
  and Department of Virology, Institute of Medical Science,
  University of Tokyo.
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 A novel gene encoding a serine protease-like protein  
 Patent: WO 0109349-A 2 08-FEB-2001;  
 HELIX RESEARCH INSTITUTE, TOSHIO OTO, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAOJI SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, OJI MURAKAMI, KOJI KANZAKI, YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO KASHIMA  
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 11-JAN-2000 JP OOP 118776, 02-MAY-2000 JP OOP 183767 PR TOSHIO  
 18-OCT-1999 US 60/159590, 17-FEB-2000 US 60/183322 PI  
 OTO, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAOJI SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, PI KOJI KANZAKI  
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 2841)  
 Strausberg, R.  
 Direct Submission  
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [csaabs-r@mail.nih.gov](mailto:csaabs-r@mail.nih.gov)  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H.,  
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 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
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gene

CDS

## ORIGIN

## Alignment Scores:

Pred. No.: 9,18e-256 Length: 2841  
 Score: 3612.00 Matches: 649  
 Percent Similarity: 94.72% Conservative: 33  
 Best Local Similarity: 90.14% Mismatches: 38  
 Query Match: 91.56% Indels: 0  
 DB: 10 Gaps: 0

US-10-063-692-38 (1-720) x BC031841 (1-2841)

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Search completed: May 10, 2005, 03:40:30  
Job time : 8462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 8101 Seconds  
(without alignment)  
17023.027 Million cell updates/sec

Title: US-10-063-692-37  
Perfect score: 2846  
Sequence: 1 cgtctggccaccgcccgcgg.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sta.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	2846	100.0	2846	6	AX092306 Sequence
3	2846	100.0	2846	6	AX376102 Sequence
4	2846	100.0	2846	6	AX403343 Sequence
5	2846	100.0	2846	9	AX358346 Homo sapi
6	2564	90.1	2768	9	AX832391 Homo sapi
7	2043	71.8	2306	6	AX084209 Sequence
8	1906	67.0	2350	9	AX133839 Sequence
9	1880	66.1	2144	6	AX339478 Sequence
10	1827	64.2	2142	6	AX339515 Sequence
11	1787	62.8	2259	6	AX541687 Sequence
12	1747	61.4	2784	6	BD157134 Primer fo
13	1747	61.4	2784	6	AX878296 Sequence
14	1747	61.4	2784	6	BD012234 A novel g
15	1747	61.4	2784	9	AX027841 Homo sapi
16	1747	61.4	2784	9	AX027841 Homo sapi
17	1672	58.7	2632	6	AX704692 Sequence
18	1653	58.1	1669	6	CQ723377 Sequence
19	1633	57.4	1867	6	AX084207 Sequence

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22	1028	36.1	1088	9	BSM00511
23	1017	35.7	208659	2	AC067845
24	948	33.3	142522	9	AC090625
25	522	18.3	705	6	BD150061
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27	421	14.8	421	6	CQ723379
28	370	13.0	505	6	AR264001
29	337	11.8	337	6	AX331347
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31	329	11.6	2886	6	AX263926
32	293	10.3	106657	9	AL354921
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92	134	4.7	396	6	CQ525748

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BD150061	Primer fo
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AR264001	Sequence
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BC060558	Rattus no
BC067590	Danio rer
BSM07752	Homo sapi
BC049720	Mus muscu
BC059191	Mus muscu
BC027800	Mus muscu
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BC022180	Mus muscu
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BC084269	Xenopus l
BC051760	Homo sapi
BSM806272	Homo sapi
BC079972	Xenopus l
BC083550	Rattus no
BSM805935	Homo sapi
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BSM807488	Homo sapi
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AL321260	Homo sapi
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94	134	4.7	589	10	BC049706	Mus muscu	167	134	4.7	1974	10	BC083571
95	134	4.7	596	9	BC008387	Homo sapi	168	134	4.7	1995	10	BC050759
96	134	4.7	601	5	BC082926	Xenopus l	169	134	4.7	1999	9	BC020684
97	134	4.7	682	10	BC049545	Mus muscu	170	134	4.7	2005	9	HSM803426
98	134	4.7	704	10	BC049749	Mus muscu	171	134	4.7	2030	10	BC0588229
99	134	4.7	705	10	BC059084	Mus muscu	172	134	4.7	2039	9	HSM806781
100	134	4.7	749	10	BC060563	Rattus no	173	134	4.7	2046	9	HSM808718
101	134	4.7	794	9	BC058920	Homo sapi	174	134	4.7	2074	9	BC014433
102	134	4.7	800	10	BC034163	Mus muscu	175	134	4.7	2167	10	BC028325
103	134	4.7	812	10	BC061144	Mus muscu	176	134	4.7	2172	9	AB096991
104	134	4.7	844	9	BC009571	Homo sapi	177	134	4.7	2173	9	HSM806315
105	134	4.7	859	9	BC043551	Homo sapi	178	134	4.7	2194	10	BC031202
106	134	4.7	883	10	BC049726	Mus muscu	179	134	4.7	2201	5	BC068355
107	134	4.7	900	10	BC049654	Mus muscu	180	134	4.7	2202	10	BC052362
108	134	4.7	901	10	BC055108	Mus muscu	181	134	4.7	2214	9	HSM807772
109	134	4.7	910	10	BC049687	Mus muscu	182	134	4.7	2217	9	BC073932
110	134	4.7	920	10	BC027780	Mus muscu	183	134	4.7	2235	9	BC022267
111	134	4.7	935	10	BC049693	Mus muscu	184	134	4.7	2244	9	HSM807352
112	134	4.7	940	10	BC060548	Rattus no	185	134	4.7	2250	5	BC061708
113	134	4.7	950	9	BC063550	Homo sapi	186	134	4.7	2319	9	HSM805518
114	134	4.7	953	10	BC049732	Mus muscu	187	134	4.7	2329	9	HSM805883
115	134	4.7	973	9	BC043578	Homo sapi	188	134	4.7	2329	10	BC050816
116	134	4.7	1017	10	BC034217	Mus muscu	189	134	4.7	2439	10	BC061540
117	134	4.7	1017	10	BC049561	Mus muscu	190	134	4.7	2453	9	HSM807676
118	134	4.7	1030	5	BC054286	Xenopus l	191	134	4.7	2499	9	HSM801350
119	134	4.7	1037	10	BC061131	Mus muscu	192	134	4.7	2553	10	BC061558
120	134	4.7	1057	3	AY588476	Ciona int	193	134	4.7	2688	10	BC021912
121	134	4.7	1080	9	BC063605	Homo sapi	194	134	4.7	2724	9	HSM806666
122	134	4.7	1080	10	BC049655	Mus muscu	195	134	4.7	2730	9	BC053349
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124	134	4.7	1100	9	BC063599	Homo sapi	197	134	4.7	2789	3	AK114441
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129	134	4.7	1265	10	BC061243	Mus muscu	202	134	4.7	2832	10	BC052176
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133	134	4.7	1377	5	BC063336	Xenopus t	206	134	4.7	3001	6	CQ787448
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137	134	4.7	1409	5	BC064261	Xenopus t	210	134	4.7	3230	9	BC063118
138	134	4.7	1424	5	BC063367	Xenopus t	211	134	4.7	3275	6	BD237099
139	134	4.7	1433	5	BC068286	Xenopus l	212	134	4.7	3275	6	AR225499
140	134	4.7	1459	6	BD270519	Novel mai	213	134	4.7	3275	6	AR562922
141	134	4.7	1459	6	AR494847	Sequence	214	134	4.7	3275	6	AX321620
142	134	4.7	1459	6	AX046603	Sequence	215	134	4.7	3305	10	BC040407
143	134	4.7	1464	9	IR2005397	AL389978 Homo sapi	216	134	4.7	3329	10	BC054371
144	134	4.7	1493	9	BC032462	Homo sapi	217	134	4.7	3422	9	HSM805920
145	134	4.7	1493	9	HSM805897	AX538346 Homo sapi	218	134	4.7	3564	10	BC065123
146	134	4.7	1500	3	AK174058	Ciona int	219	134	4.7	3645	10	BC062916
147	134	4.7	1500	5	XLNAXATP	Y11587 X.laevir mR	220	134	4.7	3724	5	BC068927
148	134	4.7	1500	9	BC056861	Homo sapi	221	134	4.7	3836	9	BC063854
149	134	4.7	1500	10	BC049755	Mus muscu	222	134	4.7	3870	9	HSM806049
150	134	4.7	1591	9	HSM807298	BC647154 Homo sapi	223	134	4.7	4154	9	HSM803629
151	134	4.7	1603	6	CQ490224	Sequence	224	134	4.7	4259	9	HSM805206
152	134	4.7	1603	6	CQ491236	Sequence	225	134	4.7	4345	9	HSM808518
153	134	4.7	1603	6	CQ496086	Sequence	226	134	4.7	4385	9	HSM806219
154	134	4.7	1603	6	CQ497104	Sequence	227	134	4.7	4518	9	HSM802971
155	134	4.7	1620	10	BC046622	Mus muscu	228	134	4.7	4659	9	HSM806121
156	134	4.7	1652	9	BC028121	Homo sapi	229	134	4.7	4863	9	HSM808808
157	134	4.7	1657	10	BC057688	Mus muscu	230	134	4.7	4930	9	HSM803373
158	134	4.7	1701	9	BC071665	Homo sapi	231	134	4.7	5280	10	BC052198
159	134	4.7	1742	9	HSM806670	BC640624 Homo sapi	232	134	4.7	5338	9	HSM808825
160	134	4.7	1802	9	BC025776	Homo sapi	233	134	4.7	5344	9	HSM807425
161	134	4.7	1860	9	BC058897	Mus muscu	234	134	4.7	5359	10	BC054082
162	134	4.7	1885	9	HSM807866	BC058897 Homo sapi	235	134	4.7	5395	9	BC078662
163	134	4.7	1891	9	HSM807589	AX647720 Homo sapi	236	134	4.7	5517	9	HSM807238
164	134	4.7	1959	10	BC060504	Mus muscu	237	134	4.7	6171	6	AX345690
165	134	4.7	1963	10	BC083817	Rattus no	238	134	4.7	6458	9	HSM806837

BCX647923	Homo sapi
BC083571	Rattus no
BC050759	Mus muscu
BC020684	Homo sapi
AL832119	Homo sapi
BC058229	Mus muscu
BCX640711	Homo sapi
BCX648570	Homo sapi
BC014433	Homo sapi
BC028325	Mus muscu
AB096991	Macaca fa
BCX538120	Homo sapi
BC031202	Mus muscu
BC068355	Danio rer
BC052362	Mus muscu
BCX647626	Homo sapi
BC073932	Homo sapi
BC022267	Homo sapi
BCX647208	Homo sapi
BC061708	Danio rer
AL834428	Homo sapi
BCX537499	Homo sapi
BC050816	Mus muscu
BC061540	Rattus no
BCX647530	Homo sapi
AL133016	Homo sapi
BC061558	Rattus no
BC021912	Mus muscu
BCX641033	Homo sapi
BC034120	Mus muscu
AK114441	Ciona int
BCX647345	Homo sapi
AL157431	Homo sapi
BC038597	Homo sapi
BC068211	Homo sapi
BC052176	Mus muscu
BC025599	Mus muscu
BC030556	Homo sapi
CQ787448	Sequence
CQ787464	Sequence
BC032271	Mus muscu
BC068331	Danio rer
BC063118	Homo sapi
BD237099	Compounds
AR225499	Sequence
AX562922	Sequence
BC040407	Mus muscu
BC054371	Mus muscu
BCX537826	Homo sapi
BC065123	Mus muscu
BC062916	Mus muscu
BC068927	Xenopus l
BC063854	Homo sapi
BCX537527	Homo sapi
AL832322	Homo sapi
AL833300	Homo sapi
BCX648370	Homo sapi
BCX538049	Homo sapi
AL713745	Homo sapi
BCX537988	Homo sapi
BCX648657	Homo sapi
AL832066	Homo sapi
BC052198	Mus muscu
BCX648674	Homo sapi
BCX647281	Homo sapi
BC054082	Homo sapi
BC078662	Homo sapi
BCX647094	Homo sapi
AX345690	Sequence
BCX641067	Homo sapi

C 239	134	4.7	6486	6	AX458534	AX458534 Sequence	312	133	4.7	760	9	BC032326	BC032326 Homo sapi
C 240	134	4.7	6644	6	E23356	E23356 Virus vecto	313	133	4.7	760	9	BC040885	BC040885 Homo sapi
C 241	134	4.7	7369	6	AX598937	AX598937 Sequence	314	133	4.7	781	10	BC049734	BC049734 Mus muscu
C 242	134	4.7	7369	6	AX705387	AX705387 Sequence	315	133	4.7	788	5	BC072244	BC072244 Xenopus l
C 243	134	4.7	7372	6	E23357	E23357 Virus vecto	316	133	4.7	789	9	BC061900	BC061900 Homo sapi
C 244	134	4.7	7609	9	BSM807874	BSM807874 Homo sapi	317	133	4.7	805	10	BC063183	BC063183 Rattus no
C 245	134	4.7	7797	6	E23355	E23355 Virus vecto	318	133	4.7	818	9	BC026261	BC026261 Homo sapi
C 246	134	4.7	7796	6	E23359	E23359 Virus vecto	319	133	4.7	819	9	BSM807474	BSM807474 Homo sapi
C 247	134	4.7	8899	6	AX345739	AX345739 Sequence	320	133	4.7	819	10	BC064002	BC064002 Mus muscu
C 248	134	4.7	8899	6	AX348461	AX348461 Sequence	321	133	4.7	824	9	BC070291	BC070291 Homo sapi
C 249	134	4.7	8946	6	AX345813	AX345813 Sequence	322	133	4.7	828	10	BC049756	BC049756 Mus muscu
C 250	134	4.7	12178	10	AP456694	AP456694 Rattus no	323	133	4.7	837	9	S78214	S78214 APC-tumor g
C 251	134	4.7	15528	6	AP3016	AP3016 Sequence 4	324	133	4.7	845	9	S78214	S78214 APC-tumor g
C 252	134	4.7	15528	12	PEAVGEN	PEAVGEN Cloning vec	325	133	4.7	845	9	BC044653	BC044653 Homo sapi
C 253	134	4.7	15832	6	AX277943	AX277943 Sequence	326	133	4.7	848	5	BC062495	BC062495 Xenopus t
C 254	134	4.7	15832	6	AX323630	AX323630 Sequence	327	133	4.7	854	5	BC084189	BC084189 Xenopus t
C 255	134	4.7	15832	6	AX346245	AX346245 Sequence	328	133	4.7	860	9	BC039722	BC039722 Homo sapi
C 256	134	4.7	40324	6	AX458633	AX458633 Sequence	329	133	4.7	863	10	BC061014	BC061014 Mus muscu
C 257	134	4.7	349980	6	AX344563	AX344563 Sequence	330	133	4.7	885	10	BC060948	BC060948 Mus muscu
C 258	134	4.7	349980	6	AX344565	AX344565 Sequence	331	133	4.7	873	6	AX780227	AX780227 Sequence
C 259	133	4.7	202	6	BD190570	BD190570 Secretary	332	133	4.7	879	9	BC007021	BC007021 Homo sapi
C 260	133	4.7	202	6	AX099441	AX099441 Sequence	333	133	4.7	881	10	BC049733	BC049733 Mus muscu
C 261	133	4.7	212	6	CQ677317	CQ677317 Sequence	334	133	4.7	887	6	BD260630	BD260630 49 human
C 262	133	4.7	231	6	CQ685486	CQ685486 Sequence	335	133	4.7	889	10	BC049685	BC049685 Mus muscu
C 263	133	4.7	240	6	I48979	I48979 Sequence 6	336	133	4.7	897	10	BC049625	BC049625 Mus muscu
C 264	133	4.7	260	6	CQ695445	CQ695445 Sequence	337	133	4.7	909	10	BC035323	BC035323 Mus muscu
C 265	133	4.7	309	6	CQ513146	CQ513146 Sequence	338	133	4.7	911	10	BC061108	BC061108 Mus muscu
C 266	133	4.7	351	6	CQ410508	CQ410508 Sequence	339	133	4.7	935	3	AK174210	AK174210 Ciona int
C 267	133	4.7	368	10	BC049735	BC049735 Mus muscu	340	133	4.7	936	6	BD107846	BD107846 36 human
C 268	133	4.7	375	6	CQ513063	CQ513063 Sequence	341	133	4.7	942	9	BC043511	BC043511 Homo sapi
C 269	133	4.7	384	3	AF155365	AF155365 Buthus ma	342	133	4.7	970	10	BC049752	BC049752 Mus muscu
C 270	133	4.7	394	6	CQ481688	CQ481688 Sequence	343	133	4.7	970	10	BC061464	BC061464 Mus muscu
C 271	133	4.7	396	6	AR391230	AR391230 Sequence	344	133	4.7	970	10	BC064826	BC064826 Mus muscu
C 272	133	4.7	396	6	AR392935	AR392935 Sequence	345	133	4.7	971	10	BC030946	BC030946 Mus muscu
C 273	133	4.7	396	6	AR489665	AR489665 Sequence	346	133	4.7	1000	10	BC038055	BC038055 Mus muscu
C 274	133	4.7	396	6	AR493906	AR493906 Sequence	347	133	4.7	1001	10	BC049605	BC049605 Mus muscu
C 275	133	4.7	396	6	AX093235	AX093235 Sequence	348	133	4.7	1004	10	BC025458	BC025458 Mus muscu
C 276	133	4.7	397	3	AF135818	AF135818 Mesobuthu	349	133	4.7	1018	9	BC022044	BC022044 Homo sapi
C 277	133	4.7	406	6	CQ397829	CQ397829 Sequence	350	133	4.7	1024	9	BC012602	BC012602 Homo sapi
C 278	133	4.7	406	6	CQ404124	CQ404124 Sequence	351	133	4.7	1030	10	BC049544	BC049544 Mus muscu
C 279	133	4.7	408	6	CQ511687	CQ511687 Sequence	352	133	4.7	1035	10	BC055104	BC055104 Mus muscu
C 280	133	4.7	431	9	BC070144	BC070144 Homo sapi	353	133	4.7	1038	9	BC038366	BC038366 Homo sapi
C 281	133	4.7	431	9	AF155369	AF155369 Buthus ma	354	133	4.7	1038	10	BC013496	BC013496 Mus muscu
C 282	133	4.7	437	3	AF155369	AF155369 Buthus ma	355	133	4.7	1044	10	BC049565	BC049565 Mus muscu
C 283	133	4.7	446	3	AF146743	AF146743 Mesobuthu	356	133	4.7	1047	9	BC027974	BC027974 Homo sapi
C 284	133	4.7	480	9	BC055410	BC055410 Homo sapi	357	133	4.7	1048	9	BC063640	BC063640 Homo sapi
C 285	133	4.7	481	6	CQ524400	CQ524400 Sequence	358	133	4.7	1054	10	BC049758	BC049758 Mus muscu
C 286	133	4.7	481	9	BC070219	BC070219 Homo sapi	359	133	4.7	1085	10	BC049634	BC049634 Mus muscu
C 287	133	4.7	501	6	CQ527244	CQ527244 Sequence	360	133	4.7	1071	9	AF078844	AF078844 Homo sapi
C 288	133	4.7	508	9	BC017744	BC017744 Homo sapi	361	133	4.7	1071	9	BSM805733	BSM805733 Homo sapi
C 289	133	4.7	525	9	BC034020	BC034020 Homo sapi	362	133	4.7	1080	9	BC022354	BC022354 Homo sapi
C 290	133	4.7	532	10	BC049701	BC049701 Mus muscu	363	133	4.7	1081	10	BC049719	BC049719 Mus muscu
C 291	133	4.7	565	6	CQ526051	CQ526051 Sequence	364	133	4.7	1084	9	BC026265	BC026265 Homo sapi
C 292	133	4.7	570	6	CQ527266	CQ527266 Sequence	365	133	4.7	1090	5	BC066372	BC066372 Dario rer
C 293	133	4.7	615	10	BC043668	BC043668 Mus muscu	366	133	4.7	1090	9	BC049543	BC049543 Mus muscu
C 294	133	4.7	658	6	BD275413	BD275413 50 Human	367	133	4.7	1093	9	BC043577	BC043577 Homo sapi
C 295	133	4.7	664	10	BC061046	BC061046 Mus muscu	368	133	4.7	1100	10	BC061092	BC061092 Mus muscu
C 296	133	4.7	675	10	BC059112	BC059112 Rattus no	369	133	4.7	1109	10	BC063150	BC063150 Rattus no
C 297	133	4.7	676	10	BC049769	BC049769 Mus muscu	370	133	4.7	1115	10	BC049678	BC049678 Mus muscu
C 298	133	4.7	679	9	BC052814	BC052814 Homo sapi	371	133	4.7	1119	9	BC070137	BC070137 Homo sapi
C 299	133	4.7	686	10	BC060302	BC060302 Mus muscu	372	133	4.7	1122	10	BC049644	BC049644 Mus muscu
C 300	133	4.7	686	10	BC064030	BC064030 Rattus no	373	133	4.7	1124	9	BC025950	BC025950 Homo sapi
C 301	133	4.7	691	5	BC071138	BC071138 Xenopus l	374	133	4.7	1137	10	BC062232	BC062232 Rattus no
C 302	133	4.7	701	5	BC075162	BC075162 Xenopus l	375	133	4.7	1159	9	BC043507	BC043507 Homo sapi
C 303	133	4.7	720	8	CNS01D7J	CNS01D7J Botrytis	376	133	4.7	1173	10	BC061094	BC061094 Mus muscu
C 304	133	4.7	732	5	AY522586	AY522586 Oreochrom	377	133	4.7	1175	5	BC049447	BC049447 Dario rer
C 305	133	4.7	733	9	BC009801	BC009801 Homo sapi	378	133	4.7	1200	5	BC077122	BC077122 Dario rer
C 306	133	4.7	738	9	BSM806309	BSM806309 Homo sapi	379	133	4.7	1201	9	BC050586	BC050586 Homo sapi
C 307	133	4.7	746	10	BC061195	BC061195 Mus muscu	380	133	4.7	1219	10	BC049717	BC049717 Mus muscu
C 308	133	4.7	749	9	BC008417	BC008417 Homo sapi	381	133	4.7	1245	10	BC049747	BC049747 Mus muscu
C 309	133	4.7	757	9	BC051791	BC051791 Homo sapi	382	133	4.7	1248	5	BC071085	BC071085 Xenopus l
C 310	133	4.7	758	9	BC062750	BC062750 Homo sapi	383	133	4.7	1250	9	BC051908	BC051908 Homo sapi
C 311	133	4.7	760	6	CQ497632	CQ497632 Sequence	384	133	4.7	1251	10	BC038552	BC038552 Mus muscu

385	133	4.7	1269	9	BC072684	BC072684 Homo sapi	458	133	4.7	1941	9	BC051758	BC051758 Homo sapi
386	133	4.7	1271	9	AF090934	AF090934 Homo sapi	459	133	4.7	1944	9	BC028346	BC028346 Homo sapi
387	133	4.7	1273	10	BC049640	BC049640 Mus muscu	460	133	4.7	1954	6	BD270057	BD270057 Secreted
388	133	4.7	1289	10	BC049691	BC049691 Mus muscu	461	133	4.7	1960	10	BC061459	BC061459 Mus muscu
389	133	4.7	1310	9	BSM807559	BSM807559 Homo sapi	462	133	4.7	1985	10	BC049351	BC049351 Mus muscu
390	133	4.7	1333	10	BC010296	BC010296 Mus muscu	463	133	4.7	1986	10	BC050807	BC050807 Mus muscu
391	133	4.7	1337	3	AY118704	AY118704 Drosophil	464	133	4.7	1990	10	BC042668	BC042668 Mus muscu
392	133	4.7	1343	10	BC061103	BC061103 Mus muscu	465	133	4.7	1993	9	BSM803801	BSM803801 Homo sapi
393	133	4.7	1373	10	BC049731	BC049731 Mus muscu	466	133	4.7	2004	9	BC043556	BC043556 Homo sapi
394	133	4.7	1382	10	BC066858	BC066858 Mus muscu	467	133	4.7	2019	9	BC063758	BC063758 Homo sapi
395	133	4.7	1383	9	BC032432	BC032432 Homo sapi	468	133	4.7	2035	9	BSM807574	BSM807574 Homo sapi
396	133	4.7	1384	10	BC052146	BC052146 Mus muscu	469	133	4.7	2040	9	BSM807056	BSM807056 Homo sapi
397	133	4.7	1405	9	BC044934	BC044934 Homo sapi	470	133	4.7	2048	9	BC044243	BC044243 Homo sapi
398	133	4.7	1409	10	BC049776	BC049776 Mus muscu	471	133	4.7	2054	10	BC039272	BC039272 Mus muscu
399	133	4.7	1416	9	AF090943	AF090943 Homo sapi	472	133	4.7	2073	9	BC068024	BC068024 Homo sapi
400	133	4.7	1419	9	BC032340	BC032340 Homo sapi	473	133	4.7	2098	9	BC017717	BC017717 Homo sapi
401	133	4.7	1430	5	BC064202	BC064202 Xenopus t	474	133	4.7	2104	9	BSM806838	BSM806838 Homo sapi
402	133	4.7	1432	10	BC062239	BC062239 Rattus no	475	133	4.7	2132	9	AB072776	AB072776 Macaca fa
403	133	4.7	1472	9	BC017724	BC017724 Homo sapi	476	133	4.7	2158	5	BC082415	BC082415 Xenopus l
404	133	4.7	1493	9	BC042547	BC042547 Homo sapi	477	133	4.7	2164	10	BC005513	BC005513 Mus muscu
405	133	4.7	1501	5	BC080019	BC080019 Xenopus l	478	133	4.7	2190	9	BC048340	BC048340 Homo sapi
406	133	4.7	1528	9	BC043517	BC043517 Homo sapi	479	133	4.7	2233	9	BC040959	BC040959 Homo sapi
407	133	4.7	1545	10	BC062173	BC062173 Mus muscu	480	133	4.7	2237	3	AK112710	AK112710 Ciona int
408	133	4.7	1549	9	BSM808772	BSM808772 Homo sapi	481	133	4.7	2245	9	BC037547	BC037547 Homo sapi
409	133	4.7	1562	5	BC054239	BC054239 Xenopus l	482	133	4.7	2262	6	AR487911	AR487911 Sequence
410	133	4.7	1568	10	BC048399	BC048399 Mus muscu	483	133	4.7	2280	9	BC047310	BC047310 Homo sapi
411	133	4.7	1576	9	BSM806260	BSM806260 Homo sapi	484	133	4.7	2282	9	BC033689	BC033689 Homo sapi
412	133	4.7	1580	5	BC067146	BC067146 Danio rer	485	133	4.7	2284	9	AB055303	AB055303 Macaca fa
413	133	4.7	1589	9	BC043543	BC043543 Homo sapi	486	133	4.7	2312	9	BSM803723	BSM803723 Homo sapi
414	133	4.7	1598	9	BC013323	BC013323 Homo sapi	487	133	4.7	2321	9	BC058898	BC058898 Homo sapi
415	133	4.7	1606	10	BC051176	BC051176 Mus muscu	488	133	4.7	2328	9	BC043587	BC043587 Homo sapi
416	133	4.7	1610	9	BC064141	BC064141 Homo sapi	489	133	4.7	2334	3	AK116665	AK116665 Ciona int
417	133	4.7	1625	9	BSM806623	BSM806623 Homo sapi	490	133	4.7	2350	5	BC078091	BC078091 Xenopus l
418	133	4.7	1626	9	BC050587	BC050587 Homo sapi	491	133	4.7	2356	10	BC061208	BC061208 Mus muscu
419	133	4.7	1684	10	BC064148	BC064148 Homo sapi	492	133	4.7	2367	10	BC048933	BC048933 Mus muscu
420	133	4.7	1684	10	BC055910	BC055910 Mus muscu	493	133	4.7	2390	9	AF090900	AF090900 Homo sapi
421	133	4.7	1694	9	BC012597	BC012597 Homo sapi	494	133	4.7	2393	5	BC070538	BC070538 Homo sapi
422	133	4.7	1696	6	AR256293	AR256293 Sequence	495	133	4.7	2420	5	BC066695	BC066695 Danio rer
423	133	4.7	1719	10	BC045148	BC045148 Mus muscu	496	133	4.7	2435	9	BC050387	BC050387 Homo sapi
424	133	4.7	1725	9	BSM806934	BSM806934 Homo sapi	497	133	4.7	2439	9	BSM807466	BSM807466 Homo sapi
425	133	4.7	1727	5	BC071446	BC071446 Danio rer	498	133	4.7	2441	3	AK174351	AK174351 Ciona int
426	133	4.7	1727	10	BC050800	BC050800 Mus muscu	499	133	4.7	2447	6	BD190886	BD190886 Secreted
427	133	4.7	1730	9	BC033615	BC033615 Homo sapi	500	133	4.7	2447	6	BD190886	BD190886 Secreted
428	133	4.7	1732	9	BSM806991	BSM806991 Homo sapi	501	133	4.7	2464	9	BSM807471	BSM807471 Homo sapi
429	133	4.7	1740	9	BC042437	BC042437 Homo sapi	502	133	4.7	2501	6	AX598878	AX598878 Sequence
430	133	4.7	1743	9	AB070131	AB070131 Macaca fa	503	133	4.7	2501	6	AX599024	AX599024 Sequence
431	133	4.7	1746	9	BC025377	BC025377 Homo sapi	504	133	4.7	2507	10	BC053747	BC053747 Mus muscu
432	133	4.7	1763	10	BC061098	BC061098 Mus muscu	505	133	4.7	2533	9	BC032304	BC032304 Homo sapi
433	133	4.7	1770	9	BC025717	BC025717 Homo sapi	506	133	4.7	2545	9	BC063430	BC063430 Homo sapi
434	133	4.7	1782	10	BC050802	BC050802 Mus muscu	507	133	4.7	2549	10	BC061563	BC061563 Rattus no
435	133	4.7	1786	9	AB070107	AB070107 Macaca fa	508	133	4.7	2556	9	BSM805953	BSM805953 Homo sapi
436	133	4.7	1788	9	BSM806673	BSM806673 Homo sapi	509	133	4.7	2562	9	AP125949	AP125949 Homo sapi
437	133	4.7	1793	3	AK112657	AK112657 Ciona int	510	133	4.7	2563	9	AP125949	AP125949 Homo sapi
438	133	4.7	1793	9	BC071757	BC071757 Homo sapi	511	133	4.7	2566	6	CQ834011	CQ834011 Sequence
439	133	4.7	1798	6	AR366535	AR366535 Sequence	512	133	4.7	2585	9	BSM805677	BSM805677 Homo sapi
440	133	4.7	1803	9	BSM807650	BSM807650 Homo sapi	513	133	4.7	2593	9	BSM807470	BSM807470 Homo sapi
441	133	4.7	1808	6	AX535019	AX535019 Homo sapi	514	133	4.7	2598	5	BC044109	BC044109 Xenopus l
442	133	4.7	1820	8	BT009533	BT009533 Triticum	515	133	4.7	2612	10	BC053749	BC053749 Mus muscu
443	133	4.7	1827	9	AB070106	AB070106 Macaca fa	516	133	4.7	2621	10	MUSBRED	MUSBRED Mus muscu
444	133	4.7	1835	9	BC040063	BC040063 Homo sapi	517	133	4.7	2627	9	BC027919	BC027919 Homo sapi
445	133	4.7	1853	10	BC052346	BC052346 Mus muscu	518	133	4.7	2648	10	BC031180	BC031180 Mus muscu
446	133	4.7	1876	10	BC053422	BC053422 Mus muscu	519	133	4.7	2666	9	BC027972	BC027972 Homo sapi
447	133	4.7	1877	5	BC066464	BC066464 Danio rer	520	133	4.7	2688	9	BC021087	BC021087 Homo sapi
448	133	4.7	1883	10	BC022165	BC022165 Mus muscu	521	133	4.7	2700	9	BC064849	BC064849 Homo sapi
449	133	4.7	1890	9	BSM807434	BSM807434 Homo sapi	522	133	4.7	2722	9	BSM806004	BSM806004 Homo sapi
450	133	4.7	1906	10	BC063161	BC063161 Rattus no	523	133	4.7	2722	10	BC075615	BC075615 Mus muscu
451	133	4.7	1912	10	BC027060	BC027060 Mus muscu	524	133	4.7	2725	5	BSM07764	BSM07764 Sequence
452	133	4.7	1913	9	BC012362	BC012362 Homo sapi	525	133	4.7	2782	9	BSM803706	BSM803706 Homo sapi
453	133	4.7	1931	10	BC036150	BC036150 Mus muscu	526	133	4.7	2846	9	BSM802834	BSM802834 Homo sapi
454	133	4.7	1933	6	BD270058	BD270058 Secreted	527	133	4.7	2869	9	BSM804689	BSM804689 Homo sapi
455	133	4.7	1933	9	BSM806724	BSM806724 Homo sapi	528	133	4.7	2878	9	BSM805674	BSM805674 Homo sapi
456	133	4.7	1935	5	BC065678	BC065678 Danio rer	529	133	4.7	2909	3	AK116710	AK116710 Ciona int
457	133	4.7	1939	5	BC079974	BC079974 Xenopus l	530	133	4.7	2910	9	BC042070	BC042070 Homo sapi

531	133	4.7	2917	9	BC054514	BC054514 Homo sapi	604	133	4.7	5154	9	BSM805947	BSM805947 Homo sapi
532	133	4.7	2922	6	C0491282	C0491282 Sequence	605	133	4.7	5155	9	BSM805801	BSM805801 Homo sapi
533	133	4.7	2922	9	BC032692	BC032692 Homo sapi	606	133	4.7	5205	9	BSM805958	BSM805958 Homo sapi
534	133	4.7	2929	10	BC053441	BC053441 Mus muscu	607	133	4.7	5355	9	BSM806819	BSM806819 Homo sapi
535	133	4.7	2936	5	BC077828	BC077828 Xenopus l	608	133	4.7	5365	9	BSM807518	BSM807518 Homo sapi
536	133	4.7	2943	10	BC005526	BC005526 Mus muscu	609	133	4.7	5402	9	BSM804677	BSM804677 Homo sapi
537	133	4.7	2968	10	BC058408	BC058408 Mus muscu	610	133	4.7	5439	9	BSM805827	BSM805827 Homo sapi
538	133	4.7	2972	9	BC023549	BC023549 Homo sapi	c 611	133	4.7	5586	6	AX348391	AX348391 Sequence
539	133	4.7	2975	9	BSM804650	BSM804650 Homo sapi	612	133	4.7	5597	10	BC043113	BC043113 Mus muscu
540	133	4.7	2977	5	BC070986	BC070986 Xenopus l	613	133	4.7	5695	10	BC082548	BC082548 Mus muscu
541	133	4.7	3014	9	BSM803702	BSM803702 Homo sapi	614	133	4.7	5703	10	BC054080	BC054080 Mus muscu
542	133	4.7	3030	3	AX116919	AX116919 Ciona int	615	133	4.7	5763	9	BSM808699	BSM808699 Homo sapi
543	133	4.7	3084	10	BC058950	BC058950 Mus muscu	c 616	133	4.7	6134	6	AX458624	AX458624 Sequence
544	133	4.7	3117	10	BC043717	BC043717 Mus muscu	c 617	133	4.7	6161	6	AX345313	AX345313 Sequence
545	133	4.7	3134	9	BSM805794	BSM805794 Homo sapi	618	133	4.7	7216	9	BSM805762	BSM805762 Homo sapi
546	133	4.7	3149	10	BC040763	BC040763 Mus muscu	c 619	133	4.7	7369	6	AX598791	AX598791 Sequence
547	133	4.7	3159	10	BC030921	BC030921 Mus muscu	c 620	133	4.7	7369	6	AX705365	AX705365 Sequence
548	133	4.7	3178	9	BSM803719	BSM803719 Homo sapi	c 621	133	4.7	8079	6	AX356488	AX356488 Sequence
549	133	4.7	3180	10	BC041774	BC041774 Mus muscu	c 622	133	4.7	9580	14	AF054250	AF054250 Hepatitis B
550	133	4.7	3183	9	BC044242	BC044242 Homo sapi	623	133	4.7	9747	9	BSM806689	BSM806689 Homo sapi
551	133	4.7	3189	9	BC002830	BC002830 Homo sapi	c 624	133	4.7	10369	6	AX251057	AX251057 Sequence
552	133	4.7	3226	9	AX189289	AX189289 Homo sapi	c 625	133	4.7	10369	6	AX345294	AX345294 Sequence
553	133	4.7	3232	9	AF090901	AF090901 Homo sapi	c 626	133	4.7	11416	6	AX251758	AX251758 Sequence
554	133	4.7	3245	9	BSM805849	BSM805849 Homo sapi	c 627	133	4.7	11416	6	AX345020	AX345020 Sequence
555	133	4.7	3269	5	BC073066	BC073066 Xenopus l	c 628	133	4.7	11416	6	AX348567	AX348567 Sequence
556	133	4.7	3332	10	BC053922	BC053922 Mus muscu	c 629	133	4.7	11729	6	AX345797	AX345797 Sequence
557	133	4.7	3353	9	BSM803622	BSM803622 Homo sapi	c 630	133	4.7	12007	6	AX345619	AX345619 Sequence
558	133	4.7	3380	9	BSM807223	BSM807223 Homo sapi	c 631	133	4.7	14798	6	AX345934	AX345934 Sequence
559	133	4.7	3394	9	BC050550	BC050550 Homo sapi	c 632	133	4.7	16033	6	AX346306	AX346306 Sequence
560	133	4.7	3482	9	BSM800550	BSM800550 Homo sapi	c 633	133	4.7	16633	6	AX344576	AX344576 Sequence
561	133	4.7	3518	9	BSM807510	BSM807510 Homo sapi	c 634	133	4.7	21354	6	AX251544	AX251544 Sequence
562	133	4.7	3525	10	BC034207	BC034207 Mus muscu	c 635	133	4.7	35962	6	AX598758	AX598758 Sequence
563	133	4.7	3530	10	BC053732	BC053732 Mus muscu	c 636	133	4.7	35962	6	AX598904	AX598904 Sequence
564	133	4.7	3532	9	BSM807372	BSM807372 Homo sapi	c 637	133	4.7	70389	2	AC135853	AC135853 Homo sapi
565	133	4.7	3623	10	BC034092	BC034092 Mus muscu	c 638	133	4.7	193988	2	AC102269	AC102269 Mus muscu
566	133	4.7	3660	10	BC051069	BC051069 Mus muscu	c 639	133	4.7	21273	10	AC104920	AC104920 Mus muscu
567	133	4.7	3681	9	BSM806036	BSM806036 Homo sapi	c 640	133	4.7	349980	6	AX344551	AX344551 Sequence
568	133	4.7	3687	9	BC040431	BC040431 Homo sapi	c 641	133	4.7	349980	6	AX344553	AX344553 Sequence
569	133	4.7	3723	9	BSM808835	BSM808835 Homo sapi	c 642	133	4.7	349980	6	AX344559	AX344559 Sequence
570	133	4.7	3758	9	BSM801755	BSM801755 Homo sapi	c 643	133	4.7	349980	6	AX344566	AX344566 Sequence
571	133	4.7	3795	5	BC066783	BC066783 Xenopus t	c 644	133	4.7	349980	6	AX344572	AX344572 Sequence
572	133	4.7	3883	9	BSM808647	BSM808647 Homo sapi	c 645	132	4.6	549	6	CQ524814	CQ524814 Sequence
573	133	4.7	3924	10	MUSBREDA	L31397 Mus musculu	646	132	4.6	711	9	BC051802	BC051802 Homo sapi
574	133	4.7	3973	6	AX345073	AX345073 Sequence	647	132	4.6	774	10	BC013457	BC013457 Mus muscu
575	133	4.7	4001	6	AX347363	AX347363 Sequence	648	132	4.6	1000	9	BSM806624	BSM806624 Homo sapi
576	133	4.7	4001	6	AX349084	AX349084 Sequence	649	132	4.6	1062	5	BC084361	BC084361 Xenopus l
577	133	4.7	4001	6	AX657851	AX657851 Sequence	650	132	4.6	1257	9	BC043535	BC043535 Homo sapi
578	133	4.7	4001	6	AX659125	AX659125 Sequence	651	132	4.6	1352	3	AX115954	AX115954 Ciona int
579	133	4.7	4043	10	BC020177	BC020177 Mus muscu	652	132	4.6	1383	5	BC056115	BC056115 Xenopus l
580	133	4.7	4062	5	BC070004	BC070004 Dario rer	653	132	4.6	1457	9	BC056863	BC056863 Homo sapi
581	133	4.7	4081	9	BSM807531	BSM807531 Homo sapi	654	132	4.6	1648	9	BSM808551	BSM808551 Homo sapi
582	133	4.7	4086	9	BSM803439	BSM803439 Homo sapi	655	132	4.6	1816	9	BC050396	BC050396 Homo sapi
583	133	4.7	4155	5	BC074405	BC074405 Xenopus l	656	132	4.6	1953	9	AB056420	AB056420 Macaca fa
584	133	4.7	4185	9	BC050532	BC050532 Homo sapi	657	132	4.6	1968	10	BC006016	BC006016 Mus muscu
585	133	4.7	4237	6	BS057918	BS057918 Secreted	658	132	4.6	1983	10	BC005510	BC005510 Mus muscu
586	133	4.7	4286	9	BSM807052	BSM807052 Homo sapi	659	132	4.6	1999	9	BSA242859	BSA242859 Homo sapi
587	133	4.7	4358	10	BC060187	BC060187 Mus muscu	660	132	4.6	2009	3	AX116580	AX116580 Ciona int
588	133	4.7	4389	10	BC058345	BC058345 Mus muscu	661	132	4.6	2027	9	BC063512	BC063512 Homo sapi
589	133	4.7	4413	10	BC053035	BC053035 Mus muscu	662	132	4.6	2394	6	AR374733	AR374733 Sequence
590	133	4.7	4421	10	BC042512	BC042512 Mus muscu	663	132	4.6	2514	9	BC044863	BC044863 Homo sapi
591	133	4.7	4436	10	BC058961	BC058961 Mus muscu	664	132	4.6	2752	9	BSM806735	BSM806735 Homo sapi
592	133	4.7	4457	10	BC070435	BC070435 Mus muscu	665	132	4.6	2943	9	BSM803526	BSM803526 Homo sapi
593	133	4.7	4494	10	BC063058	BC063058 Mus muscu	666	132	4.6	3006	9	BC039068	BC039068 Homo sapi
594	133	4.7	4562	9	BSM805779	BSM805779 Homo sapi	667	132	4.6	4942	9	BSM808887	BSM808887 Homo sapi
595	133	4.7	4574	9	BSM803437	BSM803437 Homo sapi	668	132	4.6	6719	9	BSM803507	BSM803507 Sequence
596	133	4.7	4619	9	BSM806714	BSM806714 Homo sapi	c 669	132	4.6	6775	6	AX458643	AX458643 Sequence
597	133	4.7	4636	10	BC057352	BC057352 Mus muscu	c 670	132	4.6	8900	6	CQ806977	CQ806977 Sequence
598	133	4.7	4661	5	BC068849	BC068849 Xenopus l	c 671	132	4.6	8900	6	CQ807251	CQ807251 Sequence
599	133	4.7	4725	9	BC040525	BC040525 Homo sapi	672	132	4.6	13054	2	AC149986	AC149986 Strongylo
600	133	4.7	4726	9	BSM808819	BSM808819 Homo sapi	673	131	4.6	358	6	CQ671266	CQ671266 Sequence
601	133	4.7	4828	9	BSM808886	BSM808886 Homo sapi	c 674	131	4.6	1083	9	BSM800551	BSM800551 Homo sapi
602	133	4.7	4838	10	BC082542	BC082542 Mus muscu	675	131	4.6	1094	9	BC039173	BC039173 Homo sapi
603	133	4.7	4946	9	BSM805863	BSM805863 Homo sapi	676	131	4.6	1138	10	BC062234	BC062234 Rattus no



677	131	4.6	1150	5	BC066608	BC066608 Danilo rer	750	128	4.5	1433	3	AK174181	AK174181 Ciona int
678	131	4.6	1372	9	BC024221	BC024221 Homo sapi	751	128	4.5	1456	5	BC077897	BC077897 Xenopus l
679	131	4.6	1414	10	BC049767	BC049767 Mus muscu	752	128	4.5	1560	9	BC032420	BC032420 Homo sapi
680	131	4.6	1788	9	BC044944	BC044944 Homo sapi	753	128	4.5	1715	5	BC067176	BC067176 Danilo rer
681	131	4.6	1941	5	BC053250	BC053250 Danilo rer	754	128	4.5	1728	9	AB070110	AB070110 Macaca fa
682	131	4.6	1985	3	AY118692	AY118692 Drosophila	755	128	4.5	1773	9	BC037559	BC037559 Homo sapi
683	131	4.6	2116	9	BC034379	BC034379 Homo sapi	756	128	4.5	1812	10	BC055113	BC055113 Mus muscu
684	131	4.6	2207	10	BC066857	BC066857 Mus muscu	757	128	4.5	1838	10	BC083573	BC083573 Rattus no
685	131	4.6	2313	10	BC021410	BC021410 Mus muscu	758	128	4.5	1889	9	BC073841	BC073841 Homo sapi
686	131	4.6	2395	9	AF090903	AF090903 Homo sapi	759	128	4.5	1905	9	BC032703	BC032703 Homo sapi
687	131	4.6	2827	6	CQ491125	CQ491125 Sequence	760	128	4.5	1913	3	AY069281	AY069281 Drosophila
688	131	4.6	2827	6	CQ496990	CQ496990 Sequence	761	128	4.5	1985	6	BD172402	BD172402 Secreted
689	131	4.6	3255	9	HSM803224	AL831898 Homo sapi	762	128	4.5	1985	6	BD172721	BD172721 Secreted
690	131	4.6	3383	9	HSM803701	AL832393 Homo sapi	763	128	4.5	1985	6	BD173040	BD173040 Secreted
691	131	4.6	3916	10	BC018439	BC018439 Mus muscu	764	128	4.5	1985	6	BD173359	BD173359 Secreted
692	131	4.6	4670	9	AF104032	AF104032 Homo sapi	765	128	4.5	1985	6	BD175393	BD175393 Secretory
693	131	4.6	4744	5	BC066770	BC066770 Xenopus l	766	128	4.5	1985	6	BD275145	BD275145 48 Human
694	131	4.6	8712	6	AX344694	AX344694 Sequence	767	128	4.5	1985	6	CQ881212	CQ881212 Sequence
695	131	4.6	31656	2	AC149363	AC149363 Phakopsor	768	128	4.5	1985	6	AR410771	AR410771 Sequence
696	130	4.6	547	9	BC070202	BC070202 Homo sapi	769	128	4.5	1985	6	AR439135	AR439135 Sequence
697	130	4.6	687	10	BC049765	BC049765 Mus muscu	770	128	4.5	1985	6	AR473155	AR473155 Sequence
698	130	4.6	967	9	HSM802777	AL390167 Homo sapi	771	128	4.5	1985	6	AR527141	AR527141 Sequence
699	130	4.6	1078	9	BC035314	BC035314 Homo sapi	772	128	4.5	1985	6	AR566174	AR566174 Sequence
700	130	4.6	1166	9	BC043545	BC043545 Homo sapi	773	128	4.5	1985	6	AX375960	AX375960 Sequence
701	130	4.6	1408	10	BC048693	BC048693 Mus muscu	774	128	4.5	1985	6	AX697621	AX697621 Sequence
702	130	4.6	1447	6	AR237880	AR237880 Sequence	775	128	4.5	1985	6	BD075542	BD075542 Secretory
703	130	4.6	1468	10	BC068202	BC068202 Rattus no	776	128	4.5	1985	9	AV358500	AV358500 Homo sapi
704	130	4.6	1489	9	AB048953	AB048953 Macaca fa	777	128	4.5	2030	9	BC063602	BC063602 Homo sapi
705	130	4.6	1738	6	AR560934	AR560934 Sequence	778	128	4.5	2178	6	AX099370	AX099370 Sequence
706	130	4.6	1738	8	BT009079	BT009079 Triticum	779	128	4.5	2245	9	HSM803715	AL832407 Homo sapi
707	130	4.6	1770	9	BC063419	BC063419 Homo sapi	780	128	4.5	2265	10	BC051639	BC051639 Mus muscu
708	130	4.6	1872	9	BC038952	BC038952 Homo sapi	781	128	4.5	2287	9	BC044220	BC044220 Homo sapi
709	130	4.6	1945	5	BC077411	BC077411 Xenopus l	782	128	4.5	2500	10	BC058946	BC058946 Mus muscu
710	130	4.6	2316	10	BC064469	BC064469 Mus muscu	783	128	4.5	2508	10	BC079036	BC079036 Rattus no
711	130	4.6	2905	3	AK174395	AK174395 Ciona int	784	128	4.5	2607	5	BC054610	BC054610 Danilo rer
712	130	4.6	3399	9	BC063840	BC063840 Homo sapi	785	128	4.5	2674	6	AR183261	AR183261 Sequence
713	130	4.6	3582	10	BC053927	BC053927 Mus muscu	786	128	4.5	2674	6	AR456323	AR456323 Sequence
c 714	130	4.6	349980	6	AX344570	AX344570 Sequence	787	128	4.5	3300	9	BC011656	BC011656 Homo sapi
c 715	130	4.6	34980	6	AX344571	AX344571 Sequence	788	128	4.5	3375	9	BC038406	BC038406 Homo sapi
716	129	4.5	502	6	CQ525917	CQ525917 Sequence	789	128	4.5	3454	9	HSM802993	AL713659 Homo sapi
717	129	4.5	661	10	BC051629	BC051629 Mus muscu	790	128	4.5	61940	2	AC109312	AC109312 Homo sapi
718	129	4.5	681	5	BC055187	BC055187 Danilo rer	791	127	4.5	127	6	BD021987	BD021987 Secreted
719	129	4.5	972	10	BC049738	BC049738 Mus muscu	792	127	4.5	474	6	CQ522390	CQ522390 Sequence
720	129	4.5	1051	6	AR164814	AR164814 Sequence	793	127	4.5	490	6	CQ523744	CQ523744 Sequence
721	129	4.5	1051	6	AR490614	AR490614 Sequence	794	127	4.5	569	6	BD223440	BD223440 94 human
722	129	4.5	1051	6	AR532388	AR532388 Sequence	795	127	4.5	569	6	AR243074	AR243074 Sequence
723	129	4.5	1339	9	BC016710	BC016710 Homo sapi	796	127	4.5	569	6	AR404255	AR404255 Sequence
724	129	4.5	1615	9	AF218014	AF218014 Homo sapi	797	127	4.5	580	10	BC006049	BC006049 Mus muscu
725	129	4.5	1711	9	BC032509	BC032509 Homo sapi	798	127	4.5	607	5	BC049055	BC049055 Danilo rer
726	129	4.5	1994	3	AK116078	AK116078 Ciona int	799	127	4.5	977	9	BC051846	BC051846 Homo sapi
727	129	4.5	2090	9	BC049196	BC049196 Homo sapi	800	127	4.5	981	9	BC041179	BC041179 Homo sapi
728	129	4.5	2548	9	BC040371	BC040371 Homo sapi	801	127	4.5	1012	10	BC049579	BC049579 Mus muscu
729	129	4.5	2604	8	BT009473	BT009473 Triticum	802	127	4.5	1128	9	BC071732	BC071732 Homo sapi
730	129	4.5	2610	9	BC038448	BC038448 Homo sapi	803	127	4.5	1156	5	BC049488	BC049488 Danilo rer
731	129	4.5	2612	9	BC063856	BC063856 Homo sapi	804	127	4.5	1175	9	BC049386	BC049386 Homo sapi
732	129	4.5	2915	10	BC061479	BC061479 Mus muscu	805	127	4.5	1265	9	BC033301	BC033301 Homo sapi
733	129	4.5	4606	10	BC058089	BC058089 Mus muscu	806	127	4.5	1280	9	BC047365	BC047365 Homo sapi
c 734	129	4.5	4684	6	AX344730	AX344730 Sequence	807	127	4.5	1445	9	BC063545	BC063545 Homo sapi
c 735	129	4.5	6577	6	AX251920	AX251920 Sequence	808	127	4.5	1462	10	BC060618	BC060618 Mus muscu
c 736	129	4.5	6577	6	AX346258	AX346258 Sequence	809	127	4.5	1743	10	BC051150	BC051150 Mus muscu
c 737	129	4.5	6577	6	AX348993	AX348993 Sequence	810	127	4.5	1756	9	BC069223	BC069223 Homo sapi
738	128	4.5	510	9	BC070217	BC070217 Homo sapi	811	127	4.5	1793	10	BC062171	BC062171 Mus muscu
739	128	4.5	579	6	CQ526842	CQ526842 Sequence	812	127	4.5	1850	9	BC040123	BC040123 Homo sapi
740	128	4.5	612	10	BC061085	BC061085 Mus muscu	813	127	4.5	1882	5	BC068036	BC068036 Xenopus t
741	128	4.5	705	9	HSM800237	AL049452 Homo sapi	814	127	4.5	1978	9	BC012750	BC012750 Homo sapi
742	128	4.5	720	10	BC061086	BC061086 Mus muscu	815	127	4.5	2029	10	BC050265	BC050265 Mus muscu
743	128	4.5	763	9	BC040916	BC040916 Homo sapi	816	127	4.5	2035	9	BC063696	BC063696 Homo sapi
744	128	4.5	878	6	AX482482	AX482482 Sequence	817	127	4.5	2039	10	BC050804	BC050804 Mus muscu
745	128	4.5	1119	9	BC071717	BC071717 Homo sapi	818	127	4.5	2139	5	BC054626	BC054626 Danilo rer
c 746	128	4.5	1328	8	AJ840631	AJ840631 Arabidops	819	127	4.5	2247	9	BC009648	BC009648 Homo sapi
747	128	4.5	1329	9	AF544398	AF544398 Homo sapi	820	127	4.5	2337	9	HSM800876	AL110221 Homo sapi
748	128	4.5	1402	9	BC040630	BC040630 Homo sapi	821	127	4.5	2530	9	BC036868	BC036868 Homo sapi
749	128	4.5	1429	10	BC022900	BC022900 Mus muscu	822	127	4.5	2690	5	BC077100	BC077100 Danilo rer

823	127	4.5	2728	5	BC081323	BC081323 Xenopus t	896	125	4.4	2633	9	HSM804701	AL833388 Homo sapi
824	127	4.5	2840	5	BC056558	BC056558 Danio rer	897	125	4.4	2641	9	BC020219	BC020219 Homo sapi
825	127	4.5	3341	9	BC032308	BC032308 Homo sapi	898	125	4.4	2661	10	BC026137	BC026137 Mus muscu
826	127	4.5	3446	9	HSM802955	AL713742 Homo sapi	899	125	4.4	2709	10	BC054846	BC054846 Mus muscu
827	127	4.5	4180	10	BC042645	BC042645 Mus muscu	900	125	4.4	2750	10	BC084264	BC084264 Xenopus l
828	127	4.5	4438	10	BC067016	BC067016 Mus muscu	901	125	4.4	2924	6	AX683129	AX683129 Sequence
829	127	4.5	4459	9	HSM804634	AL833321 Homo sapi	902	125	4.4	2924	10	S68736	S68736 Rattus sp.
830	127	4.5	4818	9	HSM807492	BX647348 Homo sapi	903	125	4.4	3626	9	BC012147	BC012147 Homo sapi
831	127	4.5	5251	10	BC065072	BC065072 Mus muscu	904	125	4.4	4124	3	AK112284	AK112284 Ciona int
832	127	4.5	6976	9	HSM808639	BX648491 Homo sapi	905	125	4.4	4169	10	BC053919	BC053919 Mus muscu
833	126	4.4	299	6	C0669036	C0669036 Sequence	c 906	125	4.4	6112	6	AX345565	AX345565 Sequence
834	126	4.4	407	6	C0522526	C0522526 Sequence	c 907	124	4.4	237	6	AX284920	AX284920 Sequence
835	126	4.4	439	6	C0518358	C0518358 Sequence	908	124	4.4	332	6	C0523998	C0523998 Sequence
836	126	4.4	602	9	BC008488	BC008488 Homo sapi	909	124	4.4	743	6	C0526797	C0526797 Sequence
837	126	4.4	674	6	AR283453	AR283453 Sequence	910	124	4.4	605	10	BC049606	BC049606 Mus muscu
838	126	4.4	674	6	AR344221	AR344221 Sequence	911	124	4.4	870	5	BD231669	BD231669 31 human
839	126	4.4	674	6	AR351422	AR351422 Sequence	912	124	4.4	1073	5	BC084065	BC084065 Xenopus l
840	126	4.4	674	6	AR454002	AR454002 Sequence	913	124	4.4	1092	10	BC005748	BC005748 Mus muscu
841	126	4.4	674	6	AR561590	AR561590 Sequence	914	124	4.4	1164	8	BT009497	BT009497 Tricicum
842	126	4.4	674	6	AX282972	AX282972 Sequence	915	124	4.4	1205	9	BC039058	BC039058 Homo sapi
843	126	4.4	674	6	AX303145	AX303145 Sequence	916	124	4.4	1287	3	BT009948	BT009948 Drosophil
844	126	4.4	720	10	BC083088	BC083088 Mus muscu	917	124	4.4	1331	10	BC030915	BC030915 Mus muscu
845	126	4.4	935	10	BC061157	BC061157 Mus muscu	918	124	4.4	1347	10	BC008980	BC008980 Mus muscu
846	126	4.4	1004	9	BC043536	BC043536 Homo sapi	919	124	4.4	1426	5	BC054250	BC054250 Xenopus l
847	126	4.4	1073	9	BC032697	BC032697 Homo sapi	920	124	4.4	1627	9	BC039584	BC039584 Homo sapi
848	126	4.4	1232	10	BC060554	BC060554 Rattus no	921	124	4.4	1665	9	BC041446	BC041446 Homo sapi
849	126	4.4	1350	10	BC072695	BC072695 Rattus no	922	124	4.4	1976	9	BC040113	BC040113 Homo sapi
850	126	4.4	1414	10	BC005487	BC005487 Mus muscu	923	124	4.4	2082	6	AR059958	AR059958 Sequence
851	126	4.4	1457	6	BD231695	BD231695 31 human	924	124	4.4	2085	5	BC077186	BC077186 Xenopus l
852	126	4.4	1487	6	AY423736	AY423736 Tachyglos	925	124	4.4	2150	9	BC025715	BC025715 Homo sapi
853	126	4.4	1527	5	BC064182	BC064182 Xenopus t	926	124	4.4	2212	10	BC046775	BC046775 Mus muscu
854	126	4.4	1588	9	BC070183	BC070183 Homo sapi	927	124	4.4	2320	10	BC046962	BC046962 Mus muscu
855	126	4.4	1608	9	AY358187	AY358187 Homo sapi	928	124	4.4	2465	9	BC013348	BC013348 Homo sapi
856	126	4.4	1706	5	BC082351	BC082351 Xenopus l	929	124	4.4	2754	10	BC066817	BC066817 Mus muscu
857	126	4.4	1775	5	BC053257	BC053257 Danio rer	930	124	4.4	2759	10	BC055046	BC055046 Mus muscu
858	126	4.4	1781	5	BC064253	BC064253 Xenopus t	931	124	4.4	3082	10	BC046972	BC046972 Mus muscu
859	126	4.4	1817	10	BC083562	BC083562 Rattus no	932	124	4.4	3110	10	BC057617	BC057617 Mus muscu
860	126	4.4	2150	6	C0882012	C0882012 Sequence	933	124	4.4	3251	5	BC074658	BC074658 Xenopus t
861	126	4.4	2261	6	C0882010	C0882010 Sequence	934	124	4.4	3307	9	BC025714	BC025714 Homo sapi
862	126	4.4	2270	9	HSM806047	BX537526 Homo sapi	935	124	4.4	3328	10	BC005512	BC005512 Mus muscu
863	126	4.4	2350	9	BC063427	BC063427 Homo sapi	936	124	4.4	3345	9	BC041132	BC041132 Homo sapi
864	126	4.4	2377	8	AY080711	AY080711 Arabidops	937	124	4.4	3499	10	BC007476	BC007476 Mus muscu
865	126	4.4	2578	9	AB049758	AB049758 Homo sapi	938	124	4.4	3686	10	BC043709	BC043709 Mus muscu
866	126	4.4	2790	9	BC048292	BC048292 Homo sapi	939	124	4.4	6251	10	BC050823	BC050823 Mus muscu
867	126	4.4	2841	10	BC045601	BC045601 Mus muscu	940	123	4.3	300	6	BD213699	BD213699 Novel hum
868	126	4.4	2946	5	BC076976	BC076976 Xenopus t	941	123	4.3	500	9	BC070218	BC070218 Homo sapi
869	126	4.4	3050	5	BC066571	BC066571 Danio rer	942	123	4.3	515	6	C0522671	C0522671 Sequence
870	126	4.4	3326	9	HSM808512	BX648364 Homo sapi	943	123	4.3	516	6	C0524041	C0524041 Sequence
871	126	4.4	4651	9	BC042656	BC042656 Homo sapi	944	123	4.3	585	6	C0526237	C0526237 Sequence
872	126	4.4	5277	9	HSM808645	BX648497 Homo sapi	945	123	4.3	586	6	C0524455	C0524455 Sequence
873	125	4.4	458	10	BC061002	BC061002 Mus muscu	946	123	4.3	1076	10	BC062802	BC062802 Rattus no
874	125	4.4	547	6	C0526009	C0526009 Sequence	947	123	4.3	1108	9	BC063631	BC063631 Homo sapi
875	125	4.4	580	6	C0526169	C0526169 Sequence	948	123	4.3	1348	9	BC070154	BC070154 Homo sapi
876	125	4.4	633	5	BC057512	BC057512 Danio rer	949	123	4.3	1501	10	BC039998	BC039998 Mus muscu
877	125	4.4	1065	10	BC049675	BC049675 Mus muscu	950	123	4.3	1690	9	BC049211	BC049211 Homo sapi
878	125	4.4	1130	10	BC043698	BC043698 Mus muscu	951	123	4.3	1722	5	BC063371	BC063371 Xenopus t
879	125	4.4	1359	5	BC053194	BC053194 Danio rer	952	123	4.3	1959	9	BC043548	BC043548 Homo sapi
880	125	4.4	1397	6	C0491382	C0491382 Sequence	953	123	4.3	2000	9	BC063423	BC063423 Homo sapi
881	125	4.4	1470	9	BC072387	BC072387 Homo sapi	954	123	4.3	2105	5	BC075571	BC075571 Xenopus t
882	125	4.4	1499	9	BC042195	BC042195 Homo sapi	955	123	4.3	2557	9	BC042875	BC042875 Homo sapi
883	125	4.4	1517	9	BC016152	BC016152 Homo sapi	956	123	4.3	2611	9	BC041438	BC041438 Homo sapi
884	125	4.4	1651	10	BC024872	BC024872 Mus muscu	957	123	4.3	2679	10	BC006021	BC006021 Mus muscu
885	125	4.4	1760	9	BC051807	BC051807 Homo sapi	958	123	4.3	2920	3	AK174466	AK174466 Ciona int
886	125	4.4	1765	9	BC063438	BC063438 Homo sapi	959	123	4.3	2922	3	AF479582	AF479582 Boophilus
887	125	4.4	1805	9	AB070053	AB070053 Macaca fa	960	123	4.3	3038	9	HSM806221	BX538051 Homo sapi
888	125	4.4	1880	6	C0769491	C0769491 Sequence	961	123	4.3	4064	10	BC072632	BC072632 Mus muscu
889	125	4.4	1985	5	BC053414	BC053414 Danio rer	962	123	4.3	45685	2	AC087168	AC087168 Homo sapi
890	125	4.4	2005	9	BC013372	BC013372 Homo sapi	963	122	4.3	144	6	BD138840	BD138840 Secreted
891	125	4.4	2012	9	AY125488	AY125488 Homo sapi	964	122	4.3	144	6	I89947	I89947 Sequence 26
892	125	4.4	2161	6	C0414527	C0414527 Sequence	965	122	4.3	144	6	BD005387	BD005387 Secreted
893	125	4.4	2165	5	BC054602	BC054602 Danio rer	966	122	4.3	263	6	CQ663258	CQ663258 Sequence
894	125	4.4	2178	9	BC046358	BC046358 Homo sapi	967	122	4.3	317	6	C0526915	C0526915 Sequence
895	125	4.4	2314	5	BC068218	BC068218 Xenopus t	968	122	4.3	323	6	C0524910	C0524910 Sequence

969	122	4.3	472	6	CQ525172 Sequence	1042	121	4.3	3487	10	BC016095	BC016095 Mus muscu
970	122	4.3	487	10	BC069220 Mus muscu	1043	121	4.3	3491	5	BC059285	BC059285 Xenopus l
971	122	4.3	539	6	CQ523463 Sequence	1044	121	4.3	3498	5	BC065688	BC065688 Danio rer
972	122	4.3	543	6	CQ524637 Sequence	1045	121	4.3	3983	9	BSM803572	AL833265 Homo sapi
973	122	4.3	847	9	BC053571 Homo sapi	1046	121	4.3	4498	10	BC075723	BC075723 Homo sapi
974	122	4.3	894	9	BC044257 Homo sapi	1047	121	4.3	4679	9	BSM808418	BC044257 Homo sapi
975	122	4.3	942	5	BC049498 Homo sapi	1048	121	4.3	4829	10	BC060175	BC060175 Mus muscu
976	122	4.3	1027	9	BC041442 Homo sapi	1049	121	4.3	4969	9	BSM806817	BC041442 Homo sapi
977	122	4.3	1034	9	AK026865 Homo sapi	1050	120	4.2	319	6	CQ670102	BC0670102 Sequence
978	122	4.3	1132	6	BD131068 Secreted	1051	120	4.2	412	6	CQ522434	CQ522434 Sequence
979	122	4.3	1319	9	BC003683 Homo sapi	1052	120	4.2	543	10	BC055944	BC055944 Mus muscu
980	122	4.3	1319	9	BC015490 Homo sapi	1053	120	4.2	608	5	BC075124	BC075124 Xenopus l
981	122	4.3	1331	6	CQ776637 Sequence	1054	120	4.2	791	5	BC077926	BC077926 Xenopus l
982	122	4.3	1461	9	AB048964 Macaca fa	1055	120	4.2	997	9	BC047943	BC047943 Homo sapi
983	122	4.3	1556	9	BC042072 Homo sapi	1056	120	4.2	1155	9	BC036792	BC036792 Homo sapi
984	122	4.3	1630	9	BC039130 Homo sapi	1057	120	4.2	1233	10	BC058696	BC058696 Mus muscu
985	122	4.3	1661	9	BC025753 Homo sapi	1058	120	4.2	1257	10	BC071264	BC071264 Mus muscu
986	122	4.3	1690	9	BC011595 Homo sapi	1059	120	4.2	1286	10	BC062175	BC062175 Mus muscu
987	122	4.3	1789	9	BC070134 Homo sapi	1060	120	4.2	1637	6	AX460089	AX460089 Sequence
988	122	4.3	1846	9	BC038379 Homo sapi	1061	120	4.2	1660	9	BC032309	BC032309 Homo sapi
989	122	4.3	1930	5	BC066725 Danio rer	1062	120	4.2	1691	3	AF044679	AF044679 Leishmani
990	122	4.3	2080	10	BC013564 Mus muscu	1063	120	4.2	1692	8	BT009528	BT009528 Triticum
991	122	4.3	2094	9	BC044310 Homo sapi	1064	120	4.2	1719	3	AK116650	AK116650 Ciona int
992	122	4.3	2173	5	BC068406 Homo sapi	1065	120	4.2	1762	9	AF258575	AF258575 Homo sapi
993	122	4.3	2246	9	BC051820 Homo sapi	1066	120	4.2	1810	9	BSM805776	BSM805776 Homo sapi
994	122	4.3	2421	10	BC061106 Mus muscu	1067	120	4.2	1876	9	BC071731	BC071731 Homo sapi
995	122	4.3	2734	5	BC076749 Xenopus l	1068	120	4.2	1923	9	AB093671	AB093671 Macaca fa
996	122	4.3	2788	9	AF111847 Homo sapi	1069	120	4.2	1940	9	BSM807445	BSM807445 Homo sapi
997	122	4.3	2840	10	BC052769 Mus muscu	1070	120	4.2	1946	9	BSM808123	BSM808123 Homo sapi
998	122	4.3	2986	5	BC084243 Xenopus l	1071	120	4.2	1958	10	BC023841	BC023841 Mus muscu
999	122	4.3	3045	9	BSM808843 Sequence	1072	120	4.2	2064	10	BC053424	BC053424 Mus muscu
1000	122	4.3	3353	6	AX086952 Sequence	1073	120	4.2	2084	9	AB072761	AB072761 Macaca fa
1001	122	4.3	3640	9	BSM806825 Homo sapi	1074	120	4.2	2196	9	BSM805743	BSM805743 Homo sapi
1002	122	4.3	3850	10	BC063749 Mus muscu	1075	120	4.2	2216	5	BC054636	BC054636 Danio rer
c1003	122	4.3	5216	6	AX281348 Sequence	1076	120	4.2	2265	9	BC063477	BC063477 Homo sapi
c1004	122	4.3	5216	6	AX345249 Sequence	1077	120	4.2	2367	9	BSM801757	BSM801757 Homo sapi
1005	122	4.3	5325	9	BSM806205 Homo sapi	1078	120	4.2	2415	9	BC028002	BC028002 Homo sapi
c1006	122	4.3	6794	6	AX251872 Sequence	1079	120	4.2	2630	9	BC038222	BC038222 Homo sapi
c1007	122	4.3	6794	6	AX344260 Sequence	1080	120	4.2	2683	10	BC052924	BC052924 Mus muscu
c1008	122	4.3	6794	6	AX348651 Sequence	1081	120	4.2	2780	10	BC021914	BC021914 Mus muscu
c1009	122	4.3	349980	6	AX344554 Sequence	1082	120	4.2	3401	9	BC040376	BC040376 Homo sapi
c1010	122	4.3	349980	6	AX344555 Sequence	1083	120	4.2	3686	10	BC023773	BC023773 Mus muscu
1011	121	4.3	125	6	CQ677274 Sequence	1084	120	4.2	3856	9	BSM805531	AL834437 Homo sapi
1012	121	4.3	267	6	CQ525163 Sequence	1085	120	4.2	3997	6	AX086658	AX086658 Sequence
1013	121	4.3	544	6	CQ524776 Sequence	1086	120	4.2	4670	9	BC027849	BC027849 Homo sapi
1014	121	4.3	671	5	BC082915 Sequence	1087	120	4.2	5599	10	BC049182	BC049182 Mus muscu
1015	121	4.3	743	10	BC034898 Mus muscu	1088	120	4.2	7240	9	BSM808174	BSM808174 Homo sapi
1016	121	4.3	766	8	AF531371 Gossypium	1089	119	4.2	119	6	AX099495	AX099495 Sequence
1017	121	4.3	793	9	BC018189 Homo sapi	1090	119	4.2	119	6	BD063978	BD063978 Secreted
1018	121	4.3	861	10	BC049709 Mus muscu	1091	119	4.2	452	6	CQ527434	CQ527434 Sequence
1019	121	4.3	872	6	AX068322 Sequence	1092	119	4.2	484	6	CQ526160	CQ526160 Sequence
1020	121	4.3	1117	8	AF243375 Glycine m	1093	119	4.2	528	6	CQ526616	CQ526616 Sequence
1021	121	4.3	1400	9	BC063708 Homo sapi	1094	119	4.2	533	6	CQ527387	CQ527387 Sequence
1022	121	4.3	1591	9	BC050659 Homo sapi	1095	119	4.2	539	10	BC031454	BC031454 Mus muscu
1023	121	4.3	1591	10	AB041801 Mus muscl	1096	119	4.2	549	10	BC048536	BC048536 Mus muscu
1024	121	4.3	1601	9	BC050451 Homo sapi	1097	119	4.2	633	10	BC059147	BC059147 Rattus no
1025	121	4.3	1653	8	BT009403 Triticum	1098	119	4.2	653	10	BC039566	BC039566 Mus muscu
1026	121	4.3	1725	9	BC028081 Homo sapi	1099	119	4.2	706	10	BC055114	BC055114 Mus muscu
1027	121	4.3	1913	9	BC030546 Homo sapi	1100	119	4.2	772	6	BD191024	BD191024 Secreted
1028	121	4.3	1933	9	BSX37929 Homo sapi	1101	119	4.2	899	5	BC060392	BC060392 Xenopus l
1029	121	4.3	1944	9	BC025786 Homo sapi	1102	119	4.2	939	10	BC049689	BC049689 Mus muscu
1030	121	4.3	2006	10	BC083579 Rattus no	1103	119	4.2	1010	10	BC061971	BC061971 Rattus no
1031	121	4.3	2053	9	BC030196 Homo sapi	1104	119	4.2	1191	9	BC014547	BC014547 Homo sapi
1032	121	4.3	2072	9	BC044245 Homo sapi	c1105	119	4.2	1197	8	AJ840663	AJ840663 Arabidops
1033	121	4.3	2190	9	BC063454 Homo sapi	1106	119	4.2	1487	10	BC026303	BC026303 Homo sapi
1034	121	4.3	2325	10	BC051401 Mus muscu	1107	119	4.2	1562	10	BC063181	BC063181 Rattus no
1035	121	4.3	2385	6	BD186882 Nucleic a	1108	119	4.2	1568	5	BC050177	BC050177 Homo rer
1036	121	4.3	2445	9	BC019562 Homo sapi	1109	119	4.2	1632	9	BC040434	BC040434 Homo sapi
1037	121	4.3	2500	9	BC065207 Homo sapi	1110	119	4.2	1650	9	BC036926	BC036926 Homo sapi
1038	121	4.3	2607	9	BC053734 Homo sapi	1111	119	4.2	1650	9	BC063391	BC063391 Homo sapi
1039	121	4.3	2692	3	AK173351 Ciona int	1112	119	4.2	1667	10	BC019215	BC019215 Mus muscu
1040	121	4.3	2747	9	BC025706 Homo sapi	1113	119	4.2	1673	6	BD138829	BD138829 Secreted
1041	121	4.3	2820	10	BC062390 Rattus no	1114	119	4.2	1680	10	AF528194	AF528194 Mus muscu

1115	119	4.2	1842	9	BC024042	BC024042 Homo sapi	1188	118	4.1	4057	10	BC067005	BC067005 Mus muscu
1116	119	4.2	2013	9	AB070201	AB070201 Macaca fa	1189	118	4.1	4298	10	BSM804564	AL833251 Homo sapi
1117	119	4.2	2112	5	BC076765	BC076765 Xenopus l	1190	118	4.1	4306	10	BC059824	BC059824 Mus muscu
1118	119	4.2	2134	5	XLCTCG	X84990 X.laavis Cc	c1192	118	4.1	4990	6	CQ493127	CQ493127 Sequence
1119	119	4.2	2223	5	BC067619	BC067619 Danio rer	c1192	118	4.1	4990	6	CQ493522	CQ493522 Sequence
1120	119	4.2	2355	9	BSM801346	AL133075 Homo sapi	1193	118	4.1	6003	10	AX426535	AX426535 Mus muscu
1121	119	4.2	2360	9	BC063595	BC063595 Homo sapi	c1194	118	4.1	13606	6	AX251315	AX251315 Sequence
1122	119	4.2	2447	9	BC027927	BC027927 Homo sapi	c1195	118	4.1	13606	6	AX278002	AX278002 Sequence
1123	119	4.2	2610	10	BC063267	BC063267 Mus muscu	c1196	118	4.1	13606	6	AX323699	AX323699 Sequence
1124	119	4.2	2686	5	AJ719361	AJ719361 Gallus ga	c1197	118	4.1	13606	6	AX346712	AX346712 Sequence
1125	119	4.2	2740	9	BC053595	BC053595 Homo sapi	c1198	118	4.1	17934	6	AX346621	AX346621 Sequence
1126	119	4.2	2747	9	BSM803601	AL833294 Homo sapi	1199	117	4.1	117	6	I89931	I89931 Sequence 3
1127	119	4.2	2989	9	BSM807541	AX647396 Homo sapi	1200	117	4.1	117	6	BD005371	BD005371 Secreted
1128	119	4.2	3010	6	AX358754	AX358754 Sequence	1201	117	4.1	270	6	CQ655781	CQ655781 Sequence
1129	119	4.2	3010	6	AX362247	AX362247 Sequence	1202	117	4.1	401	3	AF543047	AF543047 Mesobuthu
1130	119	4.2	3030	9	AF058753	AF058753 Homo sapi	1203	117	4.1	409	6	CQ526032	BC060322 Homo sapi
1131	119	4.2	3036	9	AF090896	AF090896 Homo sapi	1204	117	4.1	421	6	CQ526039	CQ526039 Sequence
1132	119	4.2	3315	9	AB056768	AB056768 Macaca fa	1205	117	4.1	527	9	BC032225	BC032225 Homo sapi
1133	119	4.2	3547	5	BC084146	BC084146 Xenopus t	1206	117	4.1	539	10	BC061539	BC061539 Rattus no
1134	119	4.2	3676	10	BC062923	BC062923 Mus muscu	1207	117	4.1	575	6	CQ526566	CQ526566 Sequence
1135	119	4.2	3894	10	BC053925	BC053925 Mus muscu	1208	117	4.1	911	10	BC061126	BC061126 Mus muscu
1136	119	4.2	4851	10	BC062121	BC062121 Mus muscu	1209	117	4.1	959	9	BC031674	BC031674 Homo sapi
1137	119	4.2	5249	9	BSM803431	AL8332124 Homo sapi	1210	117	4.1	1019	10	BC043927	BC043927 Mus muscu
1138	119	4.2	18682	2	AC107855	AC107855 Mus muscu	1211	117	4.1	1243	9	BSM802621	AL162083 Homo sapi
1139	118	4.1	138	6	CQ705290	CQ705290 Sequence	1212	117	4.1	1287	10	BSM61031	BC061031 Mus muscu
1140	118	4.1	360	6	CQ524586	CQ524586 Sequence	1213	117	4.1	1376	6	BD194853	BD194853 86 human
c1141	118	4.1	396	6	AR391210	AR391210 Sequence	1214	117	4.1	1376	6	CQ855181	CQ855181 Sequence
c1142	118	4.1	396	6	AR392915	AR392915 Sequence	1215	117	4.1	1526	9	BC041705	BC041705 Homo sapi
c1143	118	4.1	396	6	AR489645	AR489645 Sequence	1216	117	4.1	1538	5	BC051777	BC051777 Danio rer
c1144	118	4.1	396	6	AR493886	AR493886 Sequence	1217	117	4.1	1555	9	AB063070	AB063070 Macaca fa
c1145	118	4.1	396	6	AX093215	AX093215 Sequence	1218	117	4.1	1656	5	BC064161	BC064161 Xenopus t
1146	118	4.1	410	6	CQ522484	CQ522484 Sequence	1219	117	4.1	1733	6	BD062047	BD062047 Novel tum
1147	118	4.1	514	10	BC061178	BC061178 Mus muscu	1220	117	4.1	1739	9	AK026045	AK026045 Homo sapi
1148	118	4.1	614	8	AF165421	AF165421 Mesembrya	1221	117	4.1	1869	5	BC076804	BC076804 Xenopus l
1149	118	4.1	667	6	BD249950	BD249950 50 human	1222	117	4.1	1894	9	AB063046	AB063046 Macaca fa
1150	118	4.1	681	5	BC071507	BC071507 Danio rer	1223	117	4.1	2009	5	BC074651	BC074651 Xenopus t
1151	118	4.1	723	9	BSM808728	AX648577 Homo sapi	1224	117	4.1	2108	9	AB047801	AB047801 Homo sapi
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1154	118	4.1	762	9	BC070287	BC070287 Homo sapi	1227	117	4.1	2403	9	BSM808752	AX648601 Homo sapi
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1156	118	4.1	1108	10	BC032259	BC032259 Mus muscu	1229	117	4.1	2773	6	AR252502	AR252502 Sequence
1157	118	4.1	1113	9	BC030277	BC030277 Homo sapi	1230	117	4.1	2773	6	AX092302	AX092302 Sequence
1158	118	4.1	1116	9	BC032317	BC032317 Homo sapi	1231	117	4.1	2773	6	AX376082	AX376082 Sequence
1159	118	4.1	1171	9	BC056889	BC056889 Homo sapi	1232	117	4.1	2773	6	AX403291	AX403291 Sequence
1160	118	4.1	1237	5	BC075738	BC075738 Danio rer	1233	117	4.1	2773	9	AY358338	AY358338 Homo sapi
1161	118	4.1	1284	3	AK113775	AK113775 Ciona int	1234	117	4.1	2968	9	BC060758	BC060758 Homo sapi
1162	118	4.1	1448	10	BC052344	BC052344 Mus muscu	1235	117	4.1	3307	10	BC018613	BC018613 Mus muscu
1163	118	4.1	1498	5	BC077743	BC077743 Xenopus l	1236	117	4.1	3310	10	BC061486	BC061486 Mus muscu
1164	118	4.1	1561	9	BC040443	BC040443 Homo sapi	1237	117	4.1	3328	10	BC052770	BC052770 Mus muscu
1165	118	4.1	1612	9	BC044235	BC044235 Homo sapi	1238	117	4.1	3747	10	BC064447	BC064447 Mus muscu
1166	118	4.1	1650	9	AB047615	AB047615 Macaca fa	1239	117	4.1	3937	5	BC068837	BC068837 Xenopus l
1167	118	4.1	1718	9	AK025339	AK025339 Homo sapi	1240	117	4.1	4339	9	AF106862	AF106862 Homo sapi
1168	118	4.1	1738	3	AK112524	AK112524 Ciona int	1241	117	4.1	5339	3	AY119181	AY119181 Drosophil
1169	118	4.1	1924	9	AK026741	AK026741 Homo sapi	c1242	117	4.1	5845	6	AX346564	AX346564 Sequence
1170	118	4.1	1924	9	AK026741	AK026741 Homo sapi	c1243	117	4.1	17137	6	AX345092	AX345092 Sequence
1171	118	4.1	1959	9	BC040005	BC040005 Homo sapi	1244	116	4.1	235	6	CQ677257	CQ677257 Sequence
1172	118	4.1	1975	10	BC052682	BC052682 Mus muscu	1245	116	4.1	268	6	CQ526263	CQ526263 Sequence
1173	118	4.1	2002	6	BC068030	BC068030 Homo sapi	1246	116	4.1	381	3	AF159974	AF159974 Butchur ma
1174	118	4.1	2012	6	AX664375	AX664375 Sequence	1247	116	4.1	472	6	CQ518059	CQ518059 Sequence
1175	118	4.1	2012	10	AF362952	AF362952 Mus muscu	1248	116	4.1	489	6	CQ524523	CQ524523 Sequence
1176	118	4.1	2096	10	BC034131	BC034131 Mus muscu	1249	116	4.1	504	6	CQ526778	CQ526778 Sequence
1177	118	4.1	2138	9	BC067301	BC067301 Homo sapi	1250	116	4.1	515	6	CQ526571	CQ526571 Sequence
1178	118	4.1	2261	10	BC072562	BC072562 Mus muscu	1251	116	4.1	562	10	BC049688	BC049688 Mus muscu
1179	118	4.1	2379	9	AB060887	AB060887 Macaca fa	1252	116	4.1	572	9	BC032439	BC032439 Homo sapi
1180	118	4.1	2462	9	BSM800419	AL050116 Homo sapi	1253	116	4.1	579	6	CQ526139	CQ526139 Sequence
1181	118	4.1	2735	9	BC046366	BC046366 Homo sapi	1254	116	4.1	898	10	BC026633	BC026633 Mus muscu
1182	118	4.1	2891	9	BSM804499	AL833188 Homo sapi	1255	116	4.1	910	10	BC069266	BC069266 Mus muscu
1183	118	4.1	3232	10	BC082299	BC082299 Mus muscu	1256	116	4.1	1081	9	BC043527	BC043527 Homo sapi
1184	118	4.1	3274	9	BSM807371	AX647227 Homo sapi	1257	116	4.1	1107	3	AK173973	AK173973 Ciona int
1185	118	4.1	3294	10	BC053924	BC053924 Mus muscu	1258	116	4.1	1311	5	BC075786	BC075786 Danio rer
1186	118	4.1	3420	10	BC074017	BC074017 Rattus no	1259	116	4.1	1573	9	BSM801268	AL122050 Homo sapi
1187	118	4.1	3914	9	BSM803724	AL832416 Homo sapi	1260	116	4.1	1590	9	BSM803698	AL832390 Homo sapi

1361	116	4.1	1604	9	BC044260	Homo sapi	1334	115	4.0	2477	9	BC034692	Homo sapi
1362	116	4.1	1668	10	BC008187	Mus muscu	1335	115	4.0	2485	10	BC064470	Mus muscu
1363	116	4.1	1732	10	BC033364	Mus muscu	1336	115	4.0	2487	6	BD074862	Secreted
1364	116	4.1	1741	9	AB063008	Macaca fa	1337	115	4.0	2496	6	BD191411	Secreted
1365	116	4.1	1755	9	BC031825	Homo sapi	1338	115	4.0	2765	3	AK115430	Ciona int
1366	116	4.1	1813	6	AR164089	Sequence	1339	115	4.0	2800	9	BC053596	Homo sapi
1367	116	4.1	1886	9	AK025084	Homo sapi	1340	115	4.0	2820	9	BC065198	Homo sapi
1368	116	4.1	1889	9	BC050462	Homo sapi	1341	115	4.0	3002	6	AX354181	Sequence
1369	116	4.1	1925	5	BC066381	Danio rer	1342	115	4.0	3117	9	BC043528	Homo sapi
1370	116	4.1	1973	3	BC022780	Homo sapi	1343	115	4.0	3597	10	BC036180	Mus muscu
1371	116	4.1	2001	3	AK112791	Ciona int	1344	115	4.0	4066	10	BC048824	Mus muscu
1372	116	4.1	2025	10	BC030861	Mus muscu	1345	115	4.0	4255	6	AX346935	Sequence
1373	116	4.1	2026	9	BC022399	Homo sapi	1346	115	4.0	4675	9	BSM803445	Homo sapi
1374	116	4.1	2081	10	BC043712	Mus muscu	1347	115	4.0	5123	10	BC064466	Mus muscu
1375	116	4.1	2095	5	BC067676	Danio rer	1348	115	4.0	5405	10	BC038061	Mus muscu
1376	116	4.1	2130	10	BC062005	Rattus no	1349	115	4.0	5567	10	BC052164	Mus muscu
1377	116	4.1	2230	5	BC078288	Danio rer	1350	115	4.0	6153	6	BD160662	Primer fo
1378	116	4.1	2238	5	BC063964	Danio rer	1351	115	4.0	6153	6	AX884010	Sequence
1379	116	4.1	2511	3	AK174016	Ciona int	1352	115	4.0	6153	9	AK027868	Homo sapi
1380	116	4.1	2577	9	BC050385	Homo sapi	1353	115	4.0	7165	9	BSM803503	Homo sapi
1381	116	4.1	2846	10	BC017647	Mus muscu	1354	115	4.0	24259	6	AX251447	Sequence
1382	116	4.1	2986	9	BSM80768	Homo sapi	1355	115	4.0	173854	2	AC073047	Homo sapi
1383	116	4.1	3000	9	BC036812	Sequence	1356	114	4.0	221	6	CQ685593	Sequence
1384	116	4.1	3002	6	AX571883	Sequence	1357	114	4.0	349	6	CQ410968	Sequence
1385	116	4.1	3059	10	BC051082	Mus muscu	1358	114	4.0	385	6	CQ398297	Sequence
1386	116	4.1	3221	9	BC015893	Homo sapi	1359	114	4.0	385	6	CQ404584	Sequence
1387	116	4.1	3475	5	BSM808741	Homo sapi	1360	114	4.0	436	6	CQ397977	Sequence
1388	116	4.1	3492	5	BC078645	Danio rer	1361	114	4.0	436	6	CQ404269	Sequence
1389	116	4.1	3605	9	BSM808524	Sequence	1362	114	4.0	439	6	CQ525664	Sequence
1390	116	4.1	3747	9	HSU42766	Human neuro	1363	114	4.0	462	6	CQ523723	Sequence
1391	116	4.1	3884	9	BSM806337	Sequence	1364	114	4.0	495	6	CQ398141	Sequence
1392	116	4.1	3930	9	BC027963	Homo sapi	1365	114	4.0	495	6	CQ404428	Sequence
1393	116	4.1	6668	6	AX346598	Sequence	1366	114	4.0	519	6	CQ522478	Sequence
1394	115	4.0	236	6	CQ664217	Sequence	1367	114	4.0	544	6	CQ410812	Sequence
1395	115	4.0	240	6	CQ663206	Sequence	1368	114	4.0	659	9	BC022405	Homo sapi
1396	115	4.0	247	6	CQ524931	Sequence	1369	114	4.0	806	5	CR405924	Gallus ga
1397	115	4.0	297	6	CQ667350	Sequence	1370	114	4.0	822	9	BC006807	Homo sapi
1398	115	4.0	466	11	BV090989	RPMWSEQO	1371	114	4.0	831	6	CQ423554	Sequence
1399	115	4.0	466	11	BV098168	RPMWSEQO	1372	114	4.0	956	5	BC071149	Xenopus l
1300	115	4.0	497	6	CQ526425	Sequence	1373	114	4.0	1265	10	BC026436	Mus muscu
1301	115	4.0	501	6	CQ411817	Sequence	1374	114	4.0	1286	9	BC044234	Homo sapi
1302	115	4.0	556	9	AB055361	Macaca fa	1375	114	4.0	1306	10	BC070474	Mus muscu
1303	115	4.0	780	5	BC051617	Danio rer	1376	114	4.0	1319	9	BC068029	Homo sapi
1304	115	4.0	782	9	BC040860	Homo sapi	1377	114	4.0	1355	9	BC063463	Homo sapi
1305	115	4.0	805	6	CQ395292	Sequence	1378	114	4.0	1495	5	BC074583	Xenopus t
1306	115	4.0	805	6	CQ401630	Sequence	1379	114	4.0	1498	10	BC083575	Rattus no
1307	115	4.0	917	5	BC084108	Xenopus l	1380	114	4.0	1502	9	BC009739	Homo sapi
1308	115	4.0	1044	9	AB019565	Homo sapi	1381	114	4.0	1529	9	BC063597	Homo sapi
1309	115	4.0	1053	10	BC049595	Mus muscu	1382	114	4.0	1619	10	BC058767	Mus muscu
1310	115	4.0	1087	5	BC083541	Danio rer	1383	114	4.0	1646	9	BC051812	Homo sapi
1311	115	4.0	1309	5	BC067650	Danio rer	1384	114	4.0	1680	9	BC053634	Homo sapi
1312	115	4.0	1387	9	BC032568	Homo sapi	1385	114	4.0	1734	6	AX092320	Sequence
1313	115	4.0	1410	5	BC049418	Danio rer	1386	114	4.0	1734	6	AX358902	Sequence
1314	115	4.0	1425	9	BC036851	Homo sapi	1387	114	4.0	1734	6	AX362395	Sequence
1315	115	4.0	1458	10	BC061969	Sequence	1388	114	4.0	1734	6	AX376134	Sequence
1316	115	4.0	1549	10	BC005509	Mus muscu	1389	114	4.0	1734	6	AX403750	Sequence
1317	115	4.0	1619	9	BC043510	Homo sapi	1390	114	4.0	1734	6	AX454564	Sequence
1318	115	4.0	1632	5	BC069370	Danio rer	1391	114	4.0	1734	6	AX491042	Sequence
1319	115	4.0	1641	9	BC043576	Homo sapi	1392	114	4.0	1734	6	AX696983	Sequence
1320	115	4.0	1756	9	BC029848	Homo sapi	1393	114	4.0	1734	9	AX358412	Homo sapi
1321	115	4.0	1904	6	AR528502	Sequence	1394	114	4.0	1767	9	BSM800099	Sequence
1322	115	4.0	1904	6	AX463966	Sequence	1395	114	4.0	1831	6	CQ498497	Sequence
1323	115	4.0	1904	6	AX358614	Homo sapi	1396	114	4.0	1844	6	CQ412894	Sequence
1324	115	4.0	1929	10	BC058811	Mus muscu	1397	114	4.0	1870	9	AK025958	Homo sapi
1325	115	4.0	2205	3	AK115544	Ciona int	1398	114	4.0	1887	10	BC050801	Mus muscu
1326	115	4.0	2210	9	AB066547	Macaca fa	1399	114	4.0	1936	10	BC031408	Mus muscu
1327	115	4.0	2259	9	BC051847	Homo sapi	1400	114	4.0	2000	9	BC039729	Homo sapi
1328	115	4.0	2286	9	BC020211	Homo sapi	1401	114	4.0	2010	10	BC046588	Mus muscu
1329	115	4.0	2344	9	BC050578	Homo sapi	1402	114	4.0	2038	9	BC043591	Homo sapi
1330	115	4.0	2400	5	BC056284	Danio rer	1403	114	4.0	2104	9	BC032371	Homo sapi
1331	115	4.0	2417	9	BSM800967	Sequence	1404	114	4.0	2108	5	BC084490	Xenopus t
1332	115	4.0	2419	9	BC043583	Homo sapi	1405	114	4.0	2135	10	BC017640	Mus muscu
1333	115	4.0	2429	10	BC049167	Homo sapi	1406	114	4.0	2269	6	BD136822	Podocalyx

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1407 114 4.0 2269 6 AR372112 Sequence
1408 114 4.0 2269 9 AF219137 Homo sapi
1409 114 4.0 2277 3 AK116699 Ciona int
1410 114 4.0 2406 9 BC042542 Homo sapi
1411 114 4.0 2404 9 BC042542 Homo sapi
1412 114 4.0 2475 3 AV296116 Homo sapi
1413 114 4.0 2500 9 BC050384 Homo sapi
1414 114 4.0 2601 5 BC072034 Homo sapi
1415 114 4.0 2628 9 BC021085 Homo sapi
1416 114 4.0 2654 3 AK174482 Ciona int
1417 114 4.0 2868 10 BC006583 Mus muscu
1418 114 4.0 3288 10 BC021457 Mus muscu
1419 114 4.0 3501 6 AR528471 Sequence
1420 114 4.0 3501 6 AR463904 Sequence
1421 114 4.0 3502 9 BX647580 Homo sapi
1422 114 4.0 3669 10 BC038376 Mus muscu
1423 114 4.0 4004 9 BC041086 Homo sapi
1424 114 4.0 4064 6 AR526951 Sequence
1425 114 4.0 4064 10 AF438405 Mus muscu
1426 114 4.0 4812 5 BC068296 Homo sapi
1427 114 4.0 8059 5 BC076779 Xenopus l
1428 114 4.0 15954 6 AR344491 Sequence
1429 114 4.0 15954 6 AR348900 Sequence
1430 113 4.0 277 6 CO671217 Sequence
1431 113 4.0 396 6 AR391193 Sequence
1432 113 4.0 396 6 AR392898 Sequence
1433 113 4.0 396 6 AR489628 Sequence
1434 113 4.0 396 6 AR493869 Sequence
1435 113 4.0 396 6 AX093198 Sequence
1436 113 4.0 432 6 CO526159 Sequence
1437 113 4.0 510 6 CO526266 Sequence
1438 113 4.0 579 6 CO525663 Sequence
1439 113 4.0 606 6 CO524188 Sequence
1440 113 4.0 705 10 BC049708 Mus muscu
1441 113 4.0 727 9 BC024701 Homo sapi
1442 113 4.0 843 10 BC026460 Mus muscu
1443 113 4.0 1003 5 BC067645 Danio rer
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DEFINITION Sequence 230 from patent US 6478825.  
ACCESSION AR252533  
VERSION AR252533.1 GI:27300441  
KEYWORDS SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 2846)  
TITLE Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.  
Implant, method of making same and use of the implant for the  
treatment of bone defects  
JOURNAL Patent: US 6478825-A 230 12-NOV-2002;  
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ACCESSION AX092306
VERSION AX092306.1 GI:13444467
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0116318-A 37 08-MAR-2001;
Genentech, Inc. (US)
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DEFINITION Sequence 169 from Patent WO0168848.  
ACCESSION AX376102  
VERSION AX376102.1 GI:19170443  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and  
Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: WO 0168848-A 169 20-SEP-2001;  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Shimkets, R.A. and Fernandes, E.  
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Curagen Corporation (US)  
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## LOCUS

BC038457 2350 bp mRNA linear PRI 26-JUN-2004  
Homo sapiens regeneration associated muscle protease, mRNA (cdna)

## ACCESSION

BC038457

## VERSION

BC038457.1

## KEYWORDS

GI:23620401

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 2350)

## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Shac, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 2350)  
 Strausberg, R.  
 Direct Submission  
 Submitted (04-OCT-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
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 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakealey, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 McDuro, Q.L., Masiello, C., Maekeri, B., Mastrian, S.D., McCloskey, J.C.,  
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 Young, A., Zhang, L.-H. and Green, B.D.  
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VERSION	AR339478.1 GI:33726335		
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SOURCE	Unknown.		
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AUTHORS	Tang, Y. T., Zhou, P. and Drmanac, R. T.		
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RESULT 11
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LOCUS AR339515 2142 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1006 from patent US 6569662.
ACCESSION AR339515
VERSION AR339515.1 GI:33726372
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2142)
AUTHORS Tang,Y.T., Zhou,P. and Drmanac,R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 6569662-A 1006 27-MAY-2003;
FEATURES
source 1..2142
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ORIGIN
Query Match 64.2%; Score 1827; DB 6; Length 2142;
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RESULT 12
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DEFINITION Sequence 2 from patent US 6743613.
ACCESSION AR541687
VERSION AR541687.1 GI:53933727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2259)
AUTHORS Ni,J., Ruben,S.M. and Shi,Y.
TITLE Lysoyl-oxidase HOHEC84 polynucleotides
JOURNAL Patent: US 6743613-A 2 01-JUN-2004;
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ACCESSION BD157134
VERSION BD157134.1 GI:27862892
KEYWORDS JP 2002191363-A/11977.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2784)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
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Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11977 09-JUL-2002;
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DEFINITION Sequence 13201 from Patent EP1074617.
ACCESSION AX878296
VERSION AX878296.1 GI:40033032
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 13201 07-FEB-2001,
Research Association for Biotechnology (JP)
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JOURNAL			
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Db 1758 CCATCTCTGCTGATGCTGACATCGCCATCTCTGAAGCTCTTAGACAAGGCCCGTATCAGCA 1817  
Qy 1746 CCGAGTCCAGCCCATCTGCTCGCTGCAAGTGGGATCTCAGCACTTCTCTCAGGAGT 1805  
Db 1818 CCGAGTCCAGCCCATCTGCTCGCTGCAAGTGGGATCTCAGCACTTCTCTCAGGAGT 1877  
Qy 1806 CCACATCACTGTGCTGGCTGGATGCTCCTGGCAGAGCTGAGGAGCCCTGCTTCAAGA 1865  
Db 1878 CCACATCACTGTGCTGGCTGGATGCTCCTGGCAGAGCTGAGGAGCCCTGCTTCAAGA 1937  
Qy 1866 ACACACACTGCTGCTGGGGTGGTCAAGTGTGGTGGATCTCGCTGCTGTGTGAGGAGCAGC 1925  
Db 1938 ACACACACTGCTGCTGGGGTGGTCAAGTGTGGTGGATCTCGCTGCTGTGTGAGGAGCAGC 1997  
Qy 1926 ATGAGGACCATGGCATCCCAAGTGAAGTCACTGATAAATGTTCTGTGCCAGCTGGGAAC 1985  
Db 1998 ATGAGGACCATGGCATCCCAAGTGAAGTCACTGATAAATGTTCTGTGCCAGCTGGGAAC 2057  
Qy 1986 CCATGCCCCCTTCTGATATCTGCACTGCAAGAGCAGGAGGCATCGCGGCTGTGCTTCC 2045  
Db 2058 CCATGCCCCCTTCTGATATCTGCACTGCAAGAGCAGGAGGCATCGCGGCTGTGCTTCC 2117  
Qy 2046 CCGGACGAGCATCTCTGAGCACGCTGGCATCTGATGGGACTGCTGCTGCTGAGCTGAGTATG 2105  
Db 2118 CCGGACGAGCATCTCTGAGCACGCTGGCATCTGATGGGACTGCTGCTGCTGAGCTGAGTATG 2177  
Qy 2106 ATAAAAATGAGCAGCAGGCTCTCCACTGCTCTCAACAGGCTGCTGCTTTTAAAGACT 2165  
Db 2178 ATAAAAATGAGCAGCAGGCTCTCCACTGCTCTCAACAGGCTGCTGCTTTTAAAGACT 2237  
Qy 2166 GGATTTGAAGAAATATGAAATGAACCATGCTCATGCACTCTCTGAGAGTCTTCTGTAT 2225  
Db 2238 GGATTTGAAGAAATATGAAATGAACCATGCTCATGCACTCTCTGAGAGTCTTCTGTAT 2297  
Qy 2226 ATCCGCTCTGACGTGTGTCATTGCGTGAAGCAGTGTGGGCTCTGAAGTGTGATTTGGCCCTG 2285  
Db 2298 ATCCGCTCTGACGTGTGTCATTGCGTGAAGCAGTGTGGGCTCTGAAGTGTGATTTGGCCCTG 2357  
Qy 2286 TGAACCTTGGCTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAG 2345  
Db 2358 TGAACCTTGGCTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAG 2417  
Qy 2346 ACCTCCATTTGCTGTAGGCTGATGCGGCTCCACTACTAGACAGCCAAATTTGGAAGATGC 2405  
Db 2418 ACCTCCATTTGCTGTAGGCTGATGCGGCTCCACTACTAGACAGCCAAATTTGGAAGATGC 2477  
Qy 2406 CAGGGCTTGAAGAAAGTAAAGTTTCTTCAAGAAAGACCATATACAAAACCTCTCCACTCCA 2465  
Db 2478 CAGGGCTTGAAGAAAGTAAAGTTTCTTCAAGAAAGACCATATACAAAACCTCTCCACTCCA 2537  
Qy 2466 CTGACCTGGTGTCTTCCCAACCTTTCAGTTATACGAATGCGCATCAGCTTGACCCAGGAA 2525  
Db 2538 CTGACCTGGTGTCTTCCCAACCTTTCAGTTATACGAATGCGCATCAGCTTGACCCAGGAA 2596  
Qy 2526 GATCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGA 2585  
Db 2597 GATCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGA 2656  
Qy 2586 CAGCCAGGCGCAGCAGAGCTGGGATGTGTCATGCTTCTGTACATGGCCACAGATACA 2645  
Db 2657 CAGCCAGGCGCAGCAGAGCTGGGATGTGTCATGCTTCTGTACATGGCCACAGATACA 2716  
Qy 2646 GTCTGGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2705  
Db 2717 GTCTGGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2776  
Qy 2706 TGAACCTAC 2713  
|||||

Db 2777 TGAFACTAC 2784

Search completed: May 8, 2005, 15:25:31  
Job time : 8150 secs



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OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 11:26:52 ; Search time 8099 Seconds  
(without alignments)  
17027.231 Million cell updates/sec

Title: US-10-063-692-37

Perfect score: 2846

Sequence: 1 cgcctgggcaccagccggc.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_to.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2846	100.0	2846	6	AR252533 Sequence
2	2846	100.0	2846	6	AX092306 Sequence
3	2846	100.0	2846	6	AX376102 Sequence
4	2846	100.0	2846	6	AX403343 Sequence
5	2846	100.0	2846	9	AY358346 Homo sapi
6	2761.6	97.0	2768	9	AL832391 Homo sapi
7	2636.8	92.6	2784	6	BD157134 Primer fo
8	2636.8	92.6	2784	6	AX878296 Sequence
9	2636.8	92.6	2784	6	BD012234 A novel g
10	2636.8	92.6	2784	9	AK027841 Homo sapi
11	2292.4	80.5	2632	6	AX704692 Sequence
12	2292.4	79.4	2886	6	AR263926 Sequence
13	2223.8	78.1	2350	9	BC038457 Homo sapi
14	2197.6	77.2	2306	6	AX084209 Sequence
15	2197.6	77.2	2306	6	AX133839 Sequence
16	2142.2	75.3	2259	6	AR541687 Sequence
17	2095.8	73.6	2289	6	BD012236 A novel g
18	1988.4	69.9	2144	6	AR339478 Sequence
19	1984.8	69.7	2142	6	AR339515 Sequence

20	1831.4	64.3	2841	10	BC031841	BC031841	Mus muscu	
21	1831.4	64.3	2841	10	BC057685	BC057685	Mus muscu	
22	1722	60.5	1867	6	AX084207	AX084207	Sequence	
23	1692.6	59.5	2244	6	BD012235	A novel g		
24	1667.4	58.6	1669	6	C0723377	Sequence		
25	1084.8	38.1	1088	9	HSMB00511	AL050214	Homo sapi	
26	1070.4	37.6	141818	2	AL133389	AL133389	Homo sapi	
27	1068.8	37.6	208659	2	AC067845	AC067845	Homo sapi	
28	1059.4	37.2	142522	9	AC090625	AC090625	Homo sapi	
c	29	1058.4	37.2	5735	5	BC075430	Xenopus t	
30	648	22.8	705	6	BD150061	Primer fo		
31	648	22.8	705	6	AX869999	Sequence		
c	32	546.4	19.2	217777	2	AC113891	Rattus no	
c	33	546.4	19.2	223330	2	AC096255	Rattus no	
c	34	546.4	19.2	246369	2	AC125707	Rattus no	
c	35	523.6	18.4	188958	10	AL844605	Mouse DNA	
36	479.4	16.8	505	6	AR264001	AL264001	Sequence	
37	421	14.8	421	6	C0723379	Sequence		
38	417.8	14.7	73880	2	AC090728	AC090728	Homo sapi	
c	39	408.2	14.3	532	6	BD155023	Primer fo	
c	40	408.2	14.3	532	6	AX874961	Sequence	
c	41	337	11.8	337	6	AX331347	Sequence	
c	42	337	11.8	337	6	AX331781	Sequence	
43	332	11.7	340	6	BD076812	BD076812	5' EST of	
44	293.4	10.3	106657	9	AL354921	AL354921	human DNA	
45	279.4	9.8	297	6	C0667350	C0667350	Sequence	
46	261.4	9.2	657	5	CR387267	CR387267	Gallus ga	
47	213.6	7.5	369	6	AX395272	AX395272	Sequence	
c	48	181	6.4	208659	2	AC067845	Homo sapi	
c	49	165	5.8	561	11	G91095	G91095	S210P6215RE
50	152	5.3	615	10	BC043668	BC043668	Mus muscu	
51	149.8	5.3	1084	9	BC026265	BC026265	Homo sapi	
52	148.8	5.2	1727	5	BC071446	BD071446	Danio rer	
53	148.2	5.2	920	10	C0277780	BC027780	Mus muscu	
54	147.8	5.2	4574	9	HSB803437	AL832130	Homo sapi	
55	147.6	5.2	4619	9	HSB806714	AX640658	Homo sapi	
56	146.8	5.2	5338	9	HSB808825	BX648674	Homo sapi	
57	146.6	5.2	1132	10	BC060558	BC060558	Rattus no	
58	146	5.1	1200	5	BC077122	BC077122	Danio rer	
59	146	5.1	3723	9	HSB808835	BX648684	Homo sapi	
60	145.8	5.1	446	3	AF146743	AP146743	Mesobuthu	
61	145.8	5.1	1935	5	BC065678	BC065678	Danio rer	
62	145.6	5.1	2005	9	HSB803426	AL832119	Homo sapi	
63	145	5.1	1793	3	AX112657	AK112657	Ciona int	
64	144.8	5.1	935	10	BC049693	BC049693	Mus muscu	
65	144.8	5.1	2688	10	BC021912	BC021912	Mus muscu	
66	144.6	5.1	1100	10	BC061092	BC061092	Mus muscu	
67	144.6	5.1	3482	9	HSB800550	AL050393	Homo sapi	
68	144.4	5.1	2674	10	BC083550	BC083550	Rattus no	
69	144	5.1	381	6	CQ526814	CQ526814	Sequence	
70	144	5.1	883	10	BC049726	BC049726	Mus muscu	
71	144	5.1	1990	10	BC042668	BC042668	Mus muscu	
c	72	144	5.1	4413	10	BC053035	Mus muscu	
73	143.8	5.1	375	6	CQ513063	CQ513063	Sequence	
74	143.8	5.1	818	9	BC026261	BC026261	Homo sapi	
75	143.8	5.1	1999	9	BC020684	BC020684	Homo sapi	
76	143.8	5.1	2245	9	BC037547	BC037547	Homo sapi	
77	143.8	5.1	2441	3	AK174351	AK174351	Ciona int	
78	143.8	5.1	5517	9	HSB807238	BX647094	Homo sapi	
79	143.6	5.0	1137	10	BC062232	BC062232	Rattus no	
80	143.6	5.0	1388	9	BC016332	BC016332	Homo sapi	
81	143.6	5.0	1424	5	BC063367	BC063367	Xenopus t	
82	143.6	5.0	3796	5	BC066783	BC066783	Xenopus t	
83	143.4	5.0	733	9	BC009801	BC009801	Homo sapi	
84	143.4	5.0	1620	10	BC046622	BC046622	Mus muscu	
85	143.4	5.0	3687	9	BC040431	BC040431	Homo sapi	
86	143.2	5.0	1835	9	BC040063	BC040063	Homo sapi	
87	143.2	5.0	2722	9	HSB806004	BX537897	Homo sapi	
88	143.2	5.0	2804	9	HSB807489	BX647345	Homo sapi	
89	143	5.0	701	5	BC075162	BC075162	Xenopus l	
90	143	5.0	3623	10	BC034092	BC034092	Mus muscu	
91	142.8	5.0	819	9	HSB807474	BX647330	Homo sapi	
92	142.8	5.0	887	6	BD260630	BD260630	49 human	

BC031841	Mus muscu
BC057685	Mus muscu
AX084207	Sequence
BD012235	A novel g
C0723377	Sequence
AL050214	Homo sapi
AL133389	Homo sapi
AC067845	Homo sapi
AC090625	Homo sapi
BC075430	Xenopus t
BD150061	Primer fo
AX869999	Sequence
AC113891	Rattus no
AC096255	Rattus no
AC125707	Rattus no
AL844605	Mouse DNA
AR264001	Sequence
C0723379	Sequence
AC090728	Homo sapi
BD155023	Primer fo
AX874961	Sequence
AX331347	Sequence
AX331781	Sequence
BD076812	5' EST of
AL354921	Human DNA
C0667350	Sequence
CR387267	Gallus ga
AX395272	Sequence
AC067845	Homo sapi
G91095	S210P6215RE
BC043668	Mus muscu
BC026265	Homo sapi
BC071446	Danio rer
C0277780	Mus muscu
AL832130	Homo sapi
BX40658	Homo sapi
BX48674	Homo sapi
BC060558	Rattus no
BC077122	Danio rer
AF146743	Mesobuthu
BC065678	Danio rer
AL832119	Homo sapi
AK112657	Ciona int
BC049693	Mus muscu
BC021912	Mus muscu
BC061092	Mus muscu
AL050393	Homo sapi
C0526814	Sequence
BC049726	Mus muscu
BC042668	Mus muscu
BC053035	Mus muscu
C0513063	Sequence
BC026261	Homo sapi
BC020684	Homo sapi
BC037547	Homo sapi
AX174351	Ciona int
BX647094	Homo sapi
BC062232	Rattus no
BC016332	Homo sapi
BC063367	Xenopus t
BC066783	Xenopus t
BC009801	Homo sapi
BC046622	Mus muscu
BC040431	Homo sapi
BC040063	Homo sapi
BX537897	Homo sapi
BX647345	Homo sapi
BC075162	Xenopus 1
BC034092	Mus muscu
BX647330	Homo sapi
BD260630	49 human



93	142.8	5.0	3380	9	HS807223	BX647079 Homo sapi	166	141	5.0	4154	9	HS803629	AL832322 Homo sapi
94	142.6	5.0	1175	5	BC049447	BC049447 Danilo ter	167	141	5.0	4562	9	HS805779	BX537704 Homo sapi
95	142.6	5.0	1409	10	BC049776	BC049776 Mus muscu	c 168	141	5.0	223538	2	BC087150	BC087150 Mus muscu
96	142.6	5.0	2822	6	CQ491282	CQ491282 Sequence	169	140.8	4.9	502	6	CQ525917	CQ525917 Sequence
97	142.6	5.0	3014	9	HS803702	AL832394 Homo sapi	170	140.8	4.9	676	10	BC049769	BC049769 Mus muscu
98	142.4	5.0	1057	3	AY588476	AY588476 Ciona int	171	140.8	4.9	897	10	BC049625	BC049625 Mus muscu
99	142.4	5.0	1912	10	BC027060	BC027060 Mus muscu	172	140.8	4.9	1694	9	BC012597	BC012597 Homo sapi
100	142.4	5.0	1959	10	BC060504	BC060504 Mus muscu	173	140.8	4.9	1696	6	AR256293	AR256293 Sequence
101	142.4	5.0	2167	10	BC028325	BC028325 Mus muscu	174	140.8	4.9	2319	9	HS805518	AL834428 Homo sapi
102	142.4	5.0	2329	9	HS805883	BX537499 Homo sapi	175	140.8	4.9	7609	9	HS807874	AL834728 Homo sapi
103	142.4	5.0	3870	9	HS808069	BX537527 Homo sapi	c 176	140.8	4.9	8079	6	AX356488	AX356488 Sequence
104	142.2	5.0	544	6	CQ524776	CQ524776 Sequence	177	140.6	4.9	601	5	BC082926	BC082926 Xenopus l
105	142.2	5.0	2173	9	HS806315	BX538120 Homo sapi	178	140.6	4.9	837	9	S78214	S78214 APC-tumor s
106	142.2	5.0	2975	9	HS804650	AL833337 Homo sapi	179	140.6	4.9	1018	9	BC022044	BC022044 Homo sapi
107	142	5.0	705	10	BC059084	BC059084 Mus muscu	180	140.6	4.9	1472	9	BC017724	BC017724 Homo sapi
108	142	5.0	854	5	BC084189	BC084189 Xenopus t	181	140.6	4.9	1500	5	XLNAXATP	Y11587 X.laevis mR
109	142	5.0	909	10	BC035323	BC035323 Mus muscu	182	140.6	4.9	1562	5	BC054239	BC054239 Xenopus l
110	142	5.0	970	10	BC049752	BC049752 Mus muscu	183	140.6	4.9	1860	9	BC058897	BC058897 Homo sapi
111	142	5.0	1080	9	BC022354	BC022354 Homo sapi	184	140.6	4.9	2201	5	BC068355	BC068355 Danilo ter
112	142	5.0	1201	9	BC050586	BC050586 Homo sapi	185	140.6	4.9	2439	9	HS807466	BX647322 Homo sapi
113	142	5.0	1696	5	BC067590	BC067590 Danilo ter	186	140.6	4.9	2549	10	BC061563	BC061563 Rattus no
114	142	5.0	2190	9	BC048340	BC048340 Homo sapi	187	140.6	4.9	2612	10	BC053749	BC053749 Mus muscu
115	142	5.0	2533	9	BC032304	BC032304 Homo sapi	188	140.6	4.9	2684	9	HS805935	BX537504 Homo sapi
116	142	5.0	3269	5	BC073066	BC073066 Xenopus l	189	140.6	4.9	2688	9	BC021087	BC021087 Homo sapi
117	142	5.0	3660	10	BC051069	BC051069 Mus muscu	190	140.6	4.9	2809	9	HS802470	AL157431 Homo sapi
118	142	5.0	12178	10	AP466694	AP466694 Rattus no	191	140.6	4.9	3226	9	AV189289	AV189289 Homo sapi
119	141.8	5.0	1333	10	BC010296	BC010296 Mus muscu	c 192	140.6	4.9	15954	6	AX344491	AX344491 Sequence
120	141.6	5.0	691	5	BC071138	BC071138 Xenopus l	c 193	140.6	4.9	15954	6	AX348900	AX348900 Sequence
121	141.6	5.0	805	10	BC063183	BC063183 Rattus no	194	140.4	4.9	1175	10	BC049596	BC049596 Mus muscu
122	141.6	5.0	1100	9	BC063599	BC063599 Homo sapi	195	140.4	4.9	1265	10	BC061243	BC061243 Mus muscu
123	141.6	5.0	1159	9	BC043507	BC043507 Homo sapi	196	140.4	4.9	1319	9	BC034528	BC034528 Homo sapi
124	141.6	5.0	1343	10	BC061103	BC061103 Mus muscu	197	140.4	4.9	1377	5	BC063336	BC063336 Xenopus t
125	141.6	5.0	2039	9	HS806781	BX640711 Homo sapi	198	140.4	4.9	1405	9	BC044934	BC044934 Homo sapi
126	141.6	5.0	2214	9	HS807772	BX647626 Homo sapi	199	140.4	4.9	2350	5	BC078091	BC078091 Xenopus l
127	141.6	5.0	2237	10	BC059191	BC059191 Mus muscu	200	140.4	4.9	2390	9	AF090900	AF090900 Homo sapi
128	141.6	5.0	3724	5	BC068927	BC068927 Xenopus l	201	140.4	4.9	2869	9	HS804689	AL833376 Homo sapi
129	141.6	5.0	8392	6	AX346392	AX346392 Sequence	202	140.4	4.9	3159	10	BC030921	BC030921 Mus muscu
130	141.6	5.0	11416	6	AX251758	AX251758 Sequence	203	140.4	4.9	4362	9	HS805498	AL834414 Homo sapi
131	141.6	5.0	11416	6	AX345020	AX345020 Sequence	204	140.4	4.9	4385	9	HS806219	BX538049 Homo sapi
132	141.6	5.0	11416	6	AX348567	AX348567 Sequence	205	140.4	4.9	4494	10	BC063058	BC063058 Mus muscu
133	141.6	5.0	16033	6	AX346306	AX346306 Sequence	206	140.4	4.9	4828	9	HS808886	BX648735 Homo sapi
134	141.6	5.0	1081	10	BC049719	BC049719 Mus muscu	207	140.4	4.9	6644	6	E23356	E23356 Virus vecto
135	141.4	5.0	1409	5	BC064261	BC064261 Xenopus t	208	140.4	4.9	7372	6	E23357	E23357 Virus vecto
136	141.4	5.0	1883	10	BC022165	BC022165 Mus muscu	209	140.4	4.9	7797	6	E23355	E23355 Virus vecto
137	141.4	5.0	1946	5	BC077411	BC077411 Xenopus l	210	140.4	4.9	7996	6	E23359	E23359 Virus vecto
138	141.4	5.0	2194	10	BC031202	BC031202 Mus muscu	c 211	140.4	4.9	9747	9	HS806689	BX640841 Homo sapi
139	141.4	5.0	2250	5	BC061708	BC061708 Danilo ter	c 212	140.4	4.9	11729	6	AX345797	AX345797 Sequence
140	141.4	5.0	2562	9	HS808661	BX648513 Homo sapi	213	140.2	4.9	260	6	CQ695445	CQ695445 Sequence
141	141.4	5.0	2878	9	HS805674	BX537379 Homo sapi	214	140.2	4.9	397	3	AF135818	AF135818 Mesobuthu
142	141.2	5.0	480	9	BC055410	BC055410 Homo sapi	215	140.2	4.9	812	10	BC061144	BC061144 Mus muscu
143	141.2	5.0	532	10	BC049701	BC049701 Mus muscu	216	140.2	4.9	848	5	BC062495	BC062495 Xenopus t
144	141.2	5.0	824	9	BC070291	BC070291 Homo sapi	217	140.2	4.9	860	9	BC039722	BC039722 Homo sapi
145	141.2	5.0	1038	10	BC013496	BC013496 Mus muscu	218	140.2	4.9	942	9	BC043511	BC043511 Homo sapi
146	141.2	5.0	1090	10	BC049543	BC049543 Mus muscu	219	140.2	4.9	1054	10	BC049758	BC049758 Mus muscu
147	141.2	5.0	1332	10	BC060992	BC060992 Mus muscu	220	140.2	4.9	1763	10	BC061098	BC061098 Mus muscu
148	141.2	5.0	1448	10	BC052344	BC052344 Mus muscu	221	140.2	4.9	1960	10	BC061459	BC061459 Mus muscu
149	141.2	5.0	1626	9	BC050587	BC050587 Homo sapi	222	140.2	4.9	1993	9	HS803801	AL832493 Homo sapi
150	141.2	5.0	1806	9	BC025776	BC025776 Homo sapi	223	140.2	4.9	2054	10	BC039272	BC039272 Mus muscu
151	141.2	5.0	1986	10	BC050807	BC050807 Mus muscu	224	140.2	4.9	2202	10	BC052362	BC052362 Mus muscu
152	141.2	5.0	2284	9	AB055303	AB055303 Macaca fa	225	140.2	4.9	2316	10	BC064469	BC064469 Mus muscu
153	141.2	5.0	2593	9	HS807470	BX647326 Homo sapi	226	140	4.9	240	6	I48979	I48979 Sequence 6
154	141.2	5.0	2724	9	HS806666	BX641033 Homo sapi	227	140	4.9	749	9	BC008417	BC008417 Homo sapi
155	141.2	5.0	3245	9	HS805849	BX537493 Homo sapi	228	140	4.9	760	6	CQ497632	CQ497632 Sequence
156	141.2	5.0	4725	9	BC040525	BC040525 Homo sapi	229	140	4.9	760	9	BC040885	BC040885 Homo sapi
157	141.2	5.0	6775	6	AX458643	AX458643 Sequence	230	140	4.9	889	10	BC049685	BC049685 Mus muscu
158	141.2	5.0	8900	6	CQ806977	CQ806977 Sequence	231	140	4.9	1093	9	BC043577	BC043577 Homo sapi
159	141.2	5.0	8900	6	CQ807251	CQ807251 Sequence	232	140	4.9	1119	9	BC070137	BC070137 Homo sapi
160	141	5.0	705	9	HS800237	AL049452 Homo sapi	233	140	4.9	1139	9	HS807844	BX647698 Homo sapi
161	141	5.0	1568	10	BC048399	BC048399 Mus muscu	234	140	4.9	1273	10	BC049640	BC049640 Mus muscu
162	141	5.0	2172	9	AB096991	AB096991 Macaca fa	235	140	4.9	1549	9	HS808772	BX648621 Homo sapi
163	141	5.0	2627	9	BC027919	BC027919 Homo sapi	236	140	4.9	1603	6	CQ490224	CQ490224 Sequence
164	141	5.0	2972	9	BC023549	BC023549 Homo sapi	237	140	4.9	1603	6	CQ491236	CQ491236 Sequence
165	141	5.0	3454	9	HS802993	AL713659 Homo sapi	238	140	4.9	1603	6	CQ496086	CQ496086 Sequence

239	140	4.9	1503	6	CQ497104	Sequence	CQ497104	Sequence	312	139.2	4.9	1271	9	AF090934	Homo sapi	
240	140	4.9	1727	10	BC050800	BC050800 Mus muscu	BC050800 Mus muscu	BC050800 Mus muscu	313	139.2	4.9	1271	9	BC043542	Homo sapi	
241	140	4.9	1793	9	BC071757	Homo sapi	BC071757 Homo sapi	BC071757 Homo sapi	314	139.2	4.9	1786	9	AB070107	Macaca fa	
242	140	4.9	3305	10	BC040407	Mus muscu	BC040407 Mus muscu	BC040407 Mus muscu	315	139.2	4.9	1827	9	AB070106	Macaca fa	
243	140	4.9	3332	10	BC053922	Mus muscu	BC053922 Mus muscu	BC053922 Mus muscu	316	139.2	4.9	1891	9	HSM807589	Homo sapi	
244	140	4.9	3358	9	HSM803467	Homo sapi	AL832160 Homo sapi	AL832160 Homo sapi	317	139.2	4.9	1944	9	BC028346	Homo sapi	
245	140	4.9	3373	6	AX345073	Sequence	AX345073 Sequence	AX345073 Sequence	318	139.2	4.9	2604	8	BT009473	Triticum	
c	246	140	4.9	4389	10	BC058345	Mus muscu	BC058345 Mus muscu	319	139.2	4.9	2986	9	HSM807768	Homo sapi	
c	247	140	4.9	5439	9	HSM805827	Sequence	AX537489 Homo sapi	320	139.2	4.9	4237	6	BD057918	Secreted	
c	248	140	4.9	40324	6	AX458633	Sequence	AX458633 Sequence	321	139.2	4.9	21354	6	AX251544	Sequence	
249	139.8	4.9	525	9	BC034020	Homo sapi	BC034020 Homo sapi	BC034020 Homo sapi	322	139	4.9	439	6	C0525664	Sequence	
250	139.8	4.9	738	9	HSM806309	Homo sapi	AX538116 Homo sapi	AX538116 Homo sapi	323	139	4.9	758	9	BC062750	Homo sapi	
251	139.8	4.9	757	9	BC051791	Homo sapi	BC051791 Homo sapi	BC051791 Homo sapi	324	139	4.9	819	10	BC064002	Mus muscu	
252	139.8	4.9	881	10	BC049733	Mus muscu	BC049733 Mus muscu	BC049733 Mus muscu	325	139	4.9	911	10	BC061108	Mus muscu	
253	139.8	4.9	973	9	BC043578	Homo sapi	BC043578 Homo sapi	BC043578 Homo sapi	326	139	4.9	1181	10	BC049768	Mus muscu	
254	139.8	4.9	1030	5	BC054286	Xenopus l	BC054286 Xenopus l	BC054286 Xenopus l	327	139	4.9	1652	9	BC028121	Homo sapi	
255	139.8	4.9	1037	10	BC061131	Mus muscu	BC061131 Mus muscu	BC061131 Mus muscu	328	139	4.9	1661	9	BC025755	Homo sapi	
256	139.8	4.9	1047	9	BC027974	Homo sapi	BC027974 Homo sapi	BC027974 Homo sapi	329	139	4.9	1684	9	BC064148	Homo sapi	
257	139.8	4.9	1416	9	AF090943	Homo sapi	AF090943 Homo sapi	AF090943 Homo sapi	330	139	4.9	1788	9	HSM806673	Homo sapi	
258	139.8	4.9	1457	9	BC056863	Homo sapi	BC056863 Homo sapi	BC056863 Homo sapi	331	139	4.9	2058	6	BD276055	48 Human	
259	139.8	4.9	1500	9	BC056861	Homo sapi	BC056861 Homo sapi	BC056861 Homo sapi	332	139	4.9	2312	9	HSM803723	Homo sapi	
260	139.8	4.9	1576	9	HSM806260	Homo sapi	AX538080 Homo sapi	AX538080 Homo sapi	333	139	4.9	2334	3	AK116665	Ciona int	
261	139.8	4.9	1598	9	BC013323	Homo sapi	BC013323 Homo sapi	BC013323 Homo sapi	334	139	4.9	3230	9	BC063118	Homo sapi	
262	139.8	4.9	1606	10	BC055176	Mus muscu	BC055176 Mus muscu	BC055176 Mus muscu	335	139	4.9	5365	9	HSM807518	Homo sapi	
263	139.8	4.9	2040	9	HSM807056	Homo sapi	AX640916 Homo sapi	AX640916 Homo sapi	c	336	139	4.9	5845	6	AX346564	Sequence
264	139.8	4.9	2235	9	BC022267	Homo sapi	BC022267 Homo sapi	BC022267 Homo sapi	337	139	4.9	6719	9	HSM803507	Homo sapi	
265	139.8	4.9	2280	9	BC047310	Homo sapi	BC047310 Homo sapi	BC047310 Homo sapi	c	338	139	4.9	7306	6	AX346539	Sequence
266	139.8	4.9	2356	10	BC061208	Mus muscu	BC061208 Mus muscu	BC061208 Mus muscu	c	339	139	4.9	12007	6	AX345619	Sequence
267	139.8	4.9	2832	10	BC052176	Mus muscu	BC052176 Mus muscu	BC052176 Mus muscu	c	340	139	4.9	34980	6	AX344553	Sequence
268	139.8	4.9	3005	10	BC032271	Mus muscu	BC032271 Mus muscu	BC032271 Mus muscu	341	138.8	4.9	685	10	BC049720	Mus muscu	
269	139.8	4.9	3080	9	HSM807488	Homo sapi	AX647344 Homo sapi	AX647344 Homo sapi	342	138.8	4.9	936	6	BD107846	36 Human	
270	139.8	4.9	3645	10	BC062916	Mus muscu	BC062916 Mus muscu	BC062916 Mus muscu	343	138.8	4.9	1044	10	BC049565	Mus muscu	
271	139.8	4.9	4043	10	BC020177	Mus muscu	BC020177 Mus muscu	BC020177 Mus muscu	344	138.8	4.9	1084	9	BC022290	Homo sapi	
272	139.8	4.9	4518	9	HSM802971	Homo sapi	AL713745 Homo sapi	AL713745 Homo sapi	345	138.8	4.9	1124	9	BC025950	Homo sapi	
273	139.8	4.9	5205	9	HSM805958	Homo sapi	AX537507 Homo sapi	AX537507 Homo sapi	346	138.8	4.9	1248	5	BC071085	Xenopus l	
274	139.6	4.9	490	6	CQ525211	Sequence	CQ525211 Sequence	CQ525211 Sequence	347	138.8	4.9	1250	9	BC051908	Homo sapi	
275	139.6	4.9	901	10	BC0553108	Mus muscu	BC0553108 Mus muscu	BC0553108 Mus muscu	348	138.8	4.9	1251	10	BC038552	Mus muscu	
276	139.6	4.9	971	10	BC030946	Mus muscu	BC030946 Mus muscu	BC030946 Mus muscu	349	138.8	4.9	1384	10	BC052146	Mus muscu	
277	139.6	4.9	1782	10	BC050802	Mus muscu	BC050802 Mus muscu	BC050802 Mus muscu	350	138.8	4.9	1625	9	HSM806623	Homo sapi	
278	139.6	4.9	2302	5	BC079972	Homo sapi	BC079972 Xenopus l	BC079972 Xenopus l	351	138.8	4.9	1877	5	BC066464	Danio rer	
279	139.6	4.9	2499	9	HSM801350	Homo sapi	AL133016 Homo sapi	AL133016 Homo sapi	352	138.8	4.9	2035	9	HSM807574	Homo sapi	
280	139.6	4.9	2777	5	BC063344	Xenopus t	BC063344 Xenopus t	BC063344 Xenopus t	353	138.8	4.9	2244	9	HSM807352	Homo sapi	
c	281	139.6	4.9	3001	6	CQ787448	Sequence	CQ787448 Sequence	354	138.8	4.9	2453	9	HSM807676	Homo sapi	
282	139.6	4.9	3180	10	BC041774	Mus muscu	BC041774 Mus muscu	BC041774 Mus muscu	355	138.8	4.9	2507	10	BC053747	Homo sapi	
283	139.6	4.9	3353	9	HSM803622	Mus muscu	AL832315 Homo sapi	AL832315 Homo sapi	356	138.8	4.9	2730	9	BC053349	Homo sapi	
284	139.6	4.9	4436	10	BC050961	Mus muscu	BC050961 Mus muscu	BC050961 Mus muscu	357	138.8	4.9	2782	9	HSM803706	Homo sapi	
285	139.6	4.9	5359	10	BC054082	Mus muscu	BC054082 Mus muscu	BC054082 Mus muscu	358	138.8	4.9	2943	10	BC005526	Mus muscu	
286	139.6	4.9	6458	9	HSM806837	Mus muscu	AX641067 Homo sapi	AX641067 Homo sapi	359	138.8	4.9	2977	5	BC070986	Xenopus l	
287	139.4	4.9	667	6	BD249950	50 human	BD249950 50 human	BD249950 50 human	360	138.8	4.9	3178	9	HSM803719	Homo sapi	
288	139.4	4.9	686	10	BC064030	Rattus no	BC064030 Rattus no	BC064030 Rattus no	361	138.8	4.9	3394	9	BC050550	Homo sapi	
289	139.4	4.9	1080	9	BC063605	Homo sapi	BC063605 Homo sapi	BC063605 Homo sapi	362	138.8	4.9	4838	10	BC082542	Mus muscu	
290	139.4	4.9	1122	10	BC049644	Mus muscu	BC049644 Mus muscu	BC049644 Mus muscu	363	138.8	4.9	5155	9	HSM805801	Homo sapi	
291	139.4	4.9	1124	3	AK174947	Ciona int	AK174947 Ciona int	AK174947 Ciona int	c	364	138.8	4.9	15832	6	AX277943	Sequence
292	139.4	4.9	1906	10	BC063161	Rattus no	BC063161 Rattus no	BC063161 Rattus no	c	365	138.8	4.9	15832	6	AX23630	Sequence
293	139.4	4.9	1974	10	BC083571	Rattus no	BC083571 Rattus no	BC083571 Rattus no	c	366	138.6	4.9	309	6	CQ513146	Sequence
294	139.4	4.9	2004	9	BC043556	Homo sapi	BC043556 Homo sapi	BC043556 Homo sapi	367	138.6	4.9	746	10	BC061195	Mus muscu	
295	139.4	4.9	2046	9	HSM808718	Homo sapi	AX648570 Homo sapi	AX648570 Homo sapi	368	138.6	4.9	789	9	BC061900	Homo sapi	
296	139.4	4.9	2132	9	AB072776	Macaca fa	AB072776 Macaca fa	AB072776 Macaca fa	369	138.6	4.9	893	6	CQ472917	Sequence	
297	139.4	4.9	2420	5	BC066695	Danio rer	BC066695 Danio rer	BC066695 Danio rer	c	370	138.6	4.9	1000	10	BC038055	Mus muscu
298	139.4	4.9	2470	10	BC027800	Mus muscu	BC027800 Mus muscu	BC027800 Mus muscu	371	138.6	4.9	1373	10	BC049731	Mus muscu	
299	139.4	4.9	2648	10	BC031180	Mus muscu	BC031180 Mus muscu	BC031180 Mus muscu	372	138.6	4.9	1610	9	BC064141	Homo sapi	
300	139.4	4.9	2846	9	HSM802834	Homo sapi	AL442082 Homo sapi	AL442082 Homo sapi	373	138.6	4.9	1876	10	BC053422	Mus muscu	
301	139.4	4.9	2910	9	BC042070	Homo sapi	BC042070 Homo sapi	BC042070 Homo sapi	374	138.6	4.9	1985	5	BC053414	Danio rer	
302	139.4	4.9	3084	10	BC058950	Mus muscu	BC058950 Mus muscu	BC058950 Mus muscu	375	138.6	4.9	1985	10	BC049351	Mus muscu	
303	139.4	4.9	3134	9	HSM805794	Homo sapi	AX537718 Homo sapi	AX537718 Homo sapi	376	138.6	4.9	1995	10	BC050759	Mus muscu	
304	139.4	4.9	4116	9	HSM807269	Homo sapi	AX647125 Homo sapi	AX647125 Homo sapi	377	138.6	4.9	2098	9	BC017717	Homo sapi	
305	139.4	4.9	5695	10	BC082548	Mus muscu	BC082548 Mus muscu	BC082548 Mus muscu	378	138.6	4.9	2321	9	BC058898	Homo sapi	
306	139.4	4.9	25673	2	AC087146	Sequence	AC087146 Mus muscu	AC087146 Mus muscu	379	138.6	4.9	2815	9	BC038597	Homo sapi	
c	307	139.4	4.9	349980	6	AX344573	Sequence	AX344573 Sequence	380	138.6	4.9	2886	10	BC025599	Mus muscu	
308	139.2	4.9	658	6	BD275413	50 Human	BD275413 50 Human	BD275413 50 Human	381	138.6	4.9	3189	9	BC002830	Homo sapi	
309	139.2	4.9	1062	5	BC084361	Xenopus l	BC084361 Xenopus l	BC084361 Xenopus l	382	138.6	4.9	3502	9	HSM807726	Homo sapi	
310	139.2	4.9	1071	9	AF078844	Homo sapi	AF078844 Homo sapi	AF078844 Homo sapi	383	138.6	4.9	4155	5	BC074405	Xenopus l	
311	139.2	4.9	1129	10	BC060535	Rattus no	BC060535 Rattus no	BC060535 Rattus no	384	138.6	4.9					

385	138.6	4.9	4946	9	HSM805863	138	4.8	113515	6	AX347076	Sequence	
386	138.6	4.9	5344	9	HSM807425	138	4.8	349980	6	AX344559	Sequence	
387	138.6	4.9	7216	9	HSM805762	138	4.8	349980	6	AX344565	Sequence	
C 388	138.6	4.9	14006	6	AX346860	138	4.8	349980	6	AX344572	Sequence	
C 389	138.4	4.9	396	6	AR391230	462	137.8	4.8	384	3	AF155365	Butus ma
C 390	138.4	4.9	396	6	AR392935	463	137.8	4.8	437	3	AF155369	Butus ma
C 391	138.4	4.9	396	6	AR489665	464	137.8	4.8	596	9	BC008387	Homo sapi
C 392	138.4	4.9	396	6	AR493906	465	137.8	4.8	675	10	BC059112	Rattus no
C 393	138.4	4.9	396	6	AX093235	466	137.8	4.8	686	10	BC060302	Mus muscu
394	138.4	4.9	704	10	BC049749	467	137.8	4.8	879	9	BC007021	Mus muscu
395	138.4	4.9	863	10	BC061014	468	137.8	4.8	1219	10	BC049717	Mus muscu
396	138.4	4.9	935	3	AK174210	469	137.8	4.8	1493	9	BC042547	Homo sapi
397	138.4	4.9	1080	10	BC049655	470	137.8	4.8	1770	9	BC025717	Homo sapi
398	138.4	4.9	1493	9	BC032462	471	137.8	4.8	1798	6	AR366535	Sequence
399	138.4	4.9	1671	10	BC022180	472	137.8	4.8	2464	9	HSM807471	Sequence
400	138.4	4.9	2030	10	BC058229	473	137.8	4.8	2770	9	HSM807752	Sequence
401	138.4	4.9	2553	10	BC061558	C 474	137.8	4.8	4316	6	CQ806814	Sequence
402	138.4	4.9	4259	9	HSM805206	C 475	137.8	4.8	4316	6	AX795752	Sequence
403	138.4	4.9	4421	10	BC042512	C 476	137.8	4.8	4316	6	AX822260	Sequence
404	138.4	4.9	4930	9	HSM803373	C 477	137.8	4.8	4316	6	AX825900	Sequence
405	138.4	4.9	4940	9	HSM806769	C 478	137.8	4.8	4636	10	BC057352	Sequence
406	138.4	4.9	5402	9	HSM804677	C 479	137.8	4.8	5195	6	AX345823	Sequence
C 407	138.4	4.9	6486	6	AX458534	480	137.8	4.8	5355	9	HSM806819	Sequence
C 408	138.4	4.9	7369	6	AX598791	C 481	137.8	4.8	6944	6	AX347467	Sequence
C 409	138.4	4.9	7369	6	AX705365	C 482	137.8	4.8	6944	6	AX349188	Sequence
C 410	138.4	4.9	10369	6	AX251057	C 483	137.8	4.8	6944	6	AX657867	Sequence
C 411	138.4	4.9	10369	6	AX345294	C 484	137.8	4.8	6944	6	AX659141	Sequence
C 412	138.4	4.9	70389	2	AC135853	C 485	137.8	4.8	73778	6	AX344575	Sequence
413	138.4	4.9	153567	2	AC087145	C 486	137.6	4.8	406	6	CQ397829	Sequence
C 414	138.4	4.9	212273	10	AC104920	C 487	137.6	4.8	406	6	CQ404124	Sequence
C 415	138.2	4.9	351	6	CQ410508	488	137.6	4.8	556	6	CQ508215	Sequence
416	138.2	4.9	625	10	BC059134	489	137.6	4.8	556	6	CQ510257	Sequence
417	138.2	4.9	687	10	BC049765	490	137.6	4.8	556	6	CQ511753	Sequence
418	138.2	4.9	788	5	BC072244	491	137.6	4.8	809	6	BD252094	47 secret
419	138.2	4.9	794	9	BC058920	492	137.6	4.8	845	9	BC044653	Homo sapi
420	138.2	4.9	940	10	BC060548	493	137.6	4.8	873	6	AX780227	Sequence
421	138.2	4.9	1289	10	BC049691	494	137.6	4.8	1071	9	HSM805733	Sequence
422	138.2	4.9	1382	10	BC066858	495	137.6	4.8	1433	3	AX174181	Ciona int
423	138.2	4.9	1500	10	BC049755	496	137.6	4.8	1433	5	BC082836	Xenopus l
424	138.2	4.9	1954	6	BD270057	497	137.6	4.8	1802	9	AB071113	Macaca fa
425	138.2	4.9	2621	10	MUSBRD	498	137.6	4.8	1933	9	HSM806724	Homo sapi
426	138.2	4.9	3149	10	BC040763	499	137.6	4.8	2003	9	BC051760	Homo sapi
427	138.2	4.9	3275	6	BD237099	500	137.6	4.8	2439	10	BC061540	Rattus no
428	138.2	4.9	3275	6	AR225499	501	137.6	4.8	2556	9	HSM805953	Sequence
429	138.2	4.9	3275	6	AR562922	502	137.6	4.8	2917	9	BC054514	Homo sapi
430	138.2	4.9	3275	6	AX321620	503	137.6	4.8	2986	5	BC084243	Xenopus l
431	138.2	4.9	3518	9	HSM807510	C 504	137.6	4.8	6171	6	AX345690	Sequence
432	138.2	4.9	3564	10	BC065123	C 505	137.6	4.8	431	9	BC070144	Homo sapi
433	138.2	4.9	3924	10	MUSBRD	506	137.4	4.8	664	10	BC061046	Mus muscu
434	138.2	4.9	4286	9	HSM807052	507	137.4	4.8	720	10	BC083088	Mus muscu
435	138.2	4.9	4345	9	HSM808518	508	137.4	4.8	749	10	BC060563	Rattus no
436	138.2	4.9	5154	9	HSM805947	509	137.4	4.8	760	9	BC032326	Homo sapi
437	138.2	4.9	5280	10	BC052198	510	137.4	4.8	953	10	BC049732	Mus muscu
438	138.2	4.9	5763	9	HSM808699	511	137.4	4.8	1109	10	BC063150	Rattus no
C 439	138.2	4.9	6436	6	AX345583	512	137.4	4.8	1381	5	BC063358	Xenopus t
C 440	138.2	4.9	349980	6	AX344558	513	137.4	4.8	1432	10	BC062239	Rattus no
441	138	4.8	1173	10	BC061094	514	137.4	4.8	1820	8	BT009533	Triticum
442	138	4.8	1464	9	IR2005397	515	137.4	4.8	2387	10	BC048933	Homo sapi
443	138	4.8	1589	9	BC043543	516	137.4	4.8	2545	9	BC063430	Homo sapi
444	138	4.8	1725	9	HSM806934	517	137.4	4.8	5241	6	AX252153	Sequence
445	138	4.8	1740	9	BC042437	518	137.4	4.8	5241	6	AX348924	Sequence
446	138	4.8	2073	9	BC068024	519	137.4	4.8	2909	3	AX116710	Ciona int
447	138	4.8	2158	5	BC082415	520	137.4	4.8	2936	5	BC077828	Xenopus l
448	138	4.8	2329	10	BC050816	521	137.4	4.8	3006	9	BC039068	Homo sapi
449	138	4.8	2700	9	BC064849	522	137.4	4.8	3117	10	BC043717	Mus muscu
450	138	4.8	2789	10	BC026672	523	137.4	4.8	3183	9	BC044242	Homo sapi
451	138	4.8	2929	10	BC053441	C 524	137.4	4.8	5241	6	AX252153	Sequence
C 452	138	4.8	3001	6	BC0787464	C 525	137.4	4.8	5241	6	AX348924	Sequence
453	138	4.8	3532	9	HSM807372	C 526	137.4	4.8	22723	2	AC141526	Rattus no
454	138	4.8	4457	10	BC070435	527	137.2	4.8	539	10	BC061539	Rattus no
455	138	4.8	5395	9	BC078662	528	137.2	4.8	932	9	BC043537	Homo sapi
456	138	4.8	5627	9	HSM807499	529	137.2	4.8	950	9	BC063550	Homo sapi
C 457	138	4.8	8946	6	AX345813	530	137.2	4.8	1001	10	BC049605	Mus muscu

531	137.2	4.8	1115	10	BC049678	BC049678 Mus muscu	604	136.6	4.8	2262	6	AR487911	Sequence	
532	137.2	4.8	1119	9	BC071717	BC071717 Homo sapi	605	136.6	4.8	2271	9	AB056809	Macaca fa	
533	137.2	4.8	1267	10	BC049715	BC049715 Mus muscu	606	136.6	4.8	2282	9	BC033689	Homo sapi	
534	137.2	4.8	1684	10	BC055910	BC055910 Mus muscu	607	136.6	4.8	2328	9	BC043587	Homo sapi	
535	137.2	4.8	1808	6	AX535019	AX535019 Sequence	608	136.6	4.8	2666	9	BC027972	Homo sapi	
536	137.2	4.8	1966	9	HSB808069	AX535019 Sequence	609	136.6	4.8	2991	9	BC030556	Homo sapi	
537	137.2	4.8	2019	10	BC063758	BC063758 Mus muscu	610	136.6	4.8	3141	3	AX116783	Ciona int	
538	137.2	4.8	2104	9	HSB806838	BC063758 Mus muscu	611	136.6	4.8	3375	10	BC060187	Homo sapi	
539	137.2	4.8	3883	9	HSB808647	BC063758 Mus muscu	612	136.6	4.8	4358	10	BC060187	Homo sapi	
540	137.2	4.8	4726	9	HSB808819	BC063758 Mus muscu	613	136.6	4.8	4942	9	HSB80887	Homo sapi	
c	541	137.2	4.8	12177	6	AX345553	AX345553 Sequence	614	136.6	4.8	5703	10	BC054080	Mus muscu
542	137	4.8	497	6	CQ526425	CQ526425 Sequence	c	615	136.6	4.8	11394	6	AX323608	Sequence
543	137	4.8	732	5	AY522586	AY522586 Oreochrom	c	616	136.6	4.8	34980	6	AX344551	Sequence
544	137	4.8	865	10	BC060948	BC060948 Mus muscu	617	136.6	4.8	510	9	BC070217	Homo sapi	
545	137	4.8	900	10	BC049654	BC049654 Mus muscu	618	136.4	4.8	516	6	CQ524041	Sequence	
546	137	4.8	910	10	BC049687	BC049687 Mus muscu	c	619	136.4	4.8	539	6	CQ410791	Sequence
547	137	4.8	1222	9	BC035237	BC035237 Homo sapi	620	136.4	4.8	549	10	BC048536	Mus muscu	
548	137	4.8	1368	10	BC0383654	BC0383654 Rattus no	621	136.4	4.8	645	3	AY168768	Branchios	
549	137	4.8	1383	9	BC032432	BC032432 Homo sapi	622	136.4	4.8	679	9	BC052814	Homo sapi	
550	137	4.8	1493	9	HSB805897	BC032432 Homo sapi	623	136.4	4.8	699	10	BC049621	Mus muscu	
551	137	4.8	1730	9	BC033615	BC033615 Homo sapi	624	136.4	4.8	705	10	BC049708	Mus muscu	
552	137	4.8	1890	9	HSB807434	BC033615 Homo sapi	625	136.4	4.8	827	10	BC049739	Mus muscu	
553	137	4.8	2039	10	BC050804	BC050804 Mus muscu	626	136.4	4.8	970	10	BC061464	Mus muscu	
554	137	4.8	2447	6	AR079032	AR079032 Sequence	627	136.4	4.8	1030	10	BC049544	Mus muscu	
555	137	4.8	2447	6	BD190886	BD190886 Secreted	628	136.4	4.8	1048	9	BC063640	Homo sapi	
556	137	4.8	2598	5	BC044109	BC044109 Xenopus 1	629	136.4	4.8	1580	5	BC067146	Danio rer	
557	137	4.8	2752	9	HSB806735	BC044109 Homo sapi	630	136.4	4.8	1762	9	AF258575	Homo sapi	
558	137	4.8	3232	9	AF090901	AF090901 Homo sapi	631	136.4	4.8	1931	10	BC036150	Mus muscu	
559	137	4.8	6172	6	AX281462	AX281462 Sequence	632	136.4	4.8	1941	9	BC051758	Homo sapi	
560	137	4.8	65326	2	AC124815	AC124815 Mus muscu	633	136.4	4.8	2521	10	BC026021	Mus muscu	
561	137	4.8	191531	2	AC113984	AC113984 Mus muscu	c	634	136.4	4.8	4316	6	CQ807088	Sequence
562	136.8	4.8	570	6	CQ527266	CQ527266 Sequence	c	635	136.4	4.8	4316	6	AX795868	Sequence
563	136.8	4.8	589	10	BC049706	BC049706 Mus muscu	c	636	136.4	4.8	4316	6	AX822388	Sequence
564	136.8	4.8	1017	10	BC049561	BC049561 Mus muscu	c	637	136.4	4.8	4316	6	AX826028	Sequence
565	136.8	4.8	1591	9	HSB807298	BC049561 Mus muscu	c	638	136.4	4.8	4659	9	HSB806121	Homo sapi
566	136.8	4.8	1640	9	ASB070034	BC049561 Mus muscu	c	639	136.4	4.8	5368	6	AX344691	Sequence
567	136.8	4.8	1743	10	BC051150	AB070034 Macaca fa	c	640	136.4	4.8	5586	6	AX348391	Sequence
568	136.8	4.8	1746	9	BC025377	BC051150 Mus muscu	c	641	136.4	4.8	24259	6	AX251448	Sequence
569	136.8	4.8	1803	9	HSB807650	BC025377 Homo sapi	c	642	136.4	4.8	31656	2	AC149363	Phakopsor
570	136.8	4.8	1885	9	HSB807866	BC025377 Homo sapi	643	136.2	4.8	459	6	CQ522436	Sequence	
571	136.8	4.8	1913	3	AX069281	AX069281 Drosophil	644	136.2	4.8	481	6	CQ524400	Sequence	
572	136.8	4.8	2217	9	AX073932	BC073932 Homo sapi	645	136.2	4.8	828	10	BC049756	Mus muscu	
573	136.8	4.8	2313	10	BC021410	BC021410 Mus muscu	646	136.2	4.8	890	8	AY735693	Arabidopp	
574	136.8	4.8	2835	9	BC068211	BC068211 Homo sapi	647	136.2	4.8	1038	9	BC038366	Homo sapi	
575	136.8	4.8	3525	10	BC034207	BC034207 Mus muscu	648	136.2	4.8	1245	10	BC049747	Mus muscu	
576	136.8	4.8	3530	10	BC053732	BC053732 Mus muscu	649	136.2	4.8	1430	5	BC064202	Xenopus t	
577	136.8	4.8	4081	9	HSB807531	BC053732 Mus muscu	650	136.2	4.8	1657	10	BC057688	Mus muscu	
578	136.8	4.8	4597	10	BC043113	BC043113 Mus muscu	651	136.2	4.8	1719	10	BC054148	Mus muscu	
c	579	136.8	4.8	6161	6	AX345313	AX345313 Sequence	652	136.2	4.8	1887	10	BC050801	Mus muscu
580	136.8	4.8	6192	6	AX251440	AX251440 Sequence	653	136.2	4.8	2048	9	BC044243	Homo sapi	
581	136.8	4.8	7369	6	AX598937	AX598937 Sequence	654	136.2	4.8	2370	10	BC034555	Mus muscu	
c	582	136.8	4.8	7369	6	AX705387	AX705387 Sequence	655	136.2	4.8	2776	10	BC034120	Mus muscu
583	136.8	4.8	15528	6	A93016	A93016 Sequence 4	656	136.2	4.8	2968	10	BC058408	Mus muscu	
584	136.8	4.8	15528	12	FEAVGEN	Y07862 Cloning vec	657	136.2	4.8	3329	10	BC054371	Mus muscu	
585	136.6	4.8	212	6	CQ677317	CQ677317 Sequence	658	136.2	4.8	4661	5	BC068849	Xenopus 1	
586	136.6	4.8	368	10	BC049735	BC049735 Mus muscu	659	136.2	4.8	4753	10	BC058514	Mus muscu	
587	136.6	4.8	394	6	CQ481688	CQ481688 Sequence	660	136.2	4.8	5249	9	HSB803431	Sequence	
588	136.6	4.8	408	6	CQ502830	CQ502830 Sequence	c	661	136.2	4.8	5387	6	AX344633	Sequence
589	136.6	4.8	408	6	CQ511687	CQ511687 Sequence	c	662	136.2	4.8	24259	6	AX251447	Sequence
590	136.6	4.8	484	6	CQ526160	CQ526160 Sequence	663	136	4.8	138	6	CQ705290	Sequence	
591	136.6	4.8	661	10	BC051629	BC051629 Mus muscu	664	136	4.8	481	9	BC070219	Homo sapi	
592	136.6	4.8	907	10	BC064826	BC064826 Mus muscu	665	136	4.8	671	5	BC082915	Xenopus 1	
593	136.6	4.8	1017	10	BC034217	BC034217 Mus muscu	666	136	4.8	1024	9	BC012602	Homo sapi	
594	136.6	4.8	1065	10	BC049634	BC049634 Mus muscu	667	136	4.8	1419	9	BC032340	Homo sapi	
595	136.6	4.8	1150	5	BC066608	BC066608 Danio rer	668	136	4.8	1500	3	AX174058	Ciona int	
596	136.6	4.8	1182	10	BC049567	BC049567 Mus muscu	669	136	4.8	1913	9	BC012362	Homo sapi	
597	136.6	4.8	1310	9	HSB807559	BC049567 Homo sapi	670	136	4.8	2435	9	BC050387	Homo sapi	
598	136.6	4.8	1414	10	BC049767	BC049767 Mus muscu	671	136	4.8	2725	5	BC077764	Sequence	
599	136.6	4.8	1501	5	BC080019	BC080019 Xenopus 1	672	136	4.8	3030	3	AX116919	Ciona int	
600	136.6	4.8	1545	10	BC062173	BC062173 Mus muscu	c	673	136	4.8	34980	6	AX344566	Sequence
601	136.6	4.8	1647	9	HSB806060	BC062173 Homo sapi	674	135.8	4.8	396	6	CQ525748	Sequence	
602	136.6	4.8	2016	10	BC063147	BC063147 Rattus no	675	135.8	4.8	508	9	BC017744	Homo sapi	
603	136.6	4.8	2233	9	BC040959	BC040959 Homo sapi	c	676	135.8	4.8	549	6	CQ524814	Sequence

677	135.8	4.8	711	9	BC051802	BC051802 Homo sapi	C 750	135.2	4.8	9580	14	AF054250	AF054250 Hepatitis
678	135.8	4.8	781	10	BC049734	BC049734 Mus muscu	C 751	135.2	4.8	349980	6	AX344563	AX344563 Sequence
679	135.8	4.8	1035	10	BC055104	BC055104 Mus muscu	752	135	4.7	240	6	C0663206	C0663206 Sequence
680	135.8	4.8	1528	9	BC043317	BC043317 Homo sapi	C 753	135	4.7	417	6	C0477248	C0477248 Sequence
681	135.8	4.8	1832	5	BC084269	BC084269 Xenopus l	754	135	4.7	612	10	BC061085	BC061085 Mus muscu
682	135.8	4.8	1939	5	BC079974	BC079974 Xenopus l	755	135	4.7	1329	9	AF544398	AF544398 Homo sapi
683	135.8	4.8	2074	9	BC014433	BC014433 Homo sapi	756	135	4.7	1872	9	BC038952	BC038952 Homo sapi
684	135.8	4.8	2081	9	HS080627	BX537592 Homo sapi	757	135	4.7	1933	6	BD270058	BD270058 Secreted
685	135.8	4.8	2112	5	BC076765	BC076765 Xenopus l	758	135	4.7	3255	9	HS080322	AL831898 Homo sapi
686	135.8	4.8	2116	9	BC034379	BC034379 Homo sapi	759	135	4.7	6163	10	BC052150	BC052150 Mus muscu
C 687	135.8	4.8	2501	6	AX598878	AX598878 Sequence	760	134.8	4.7	515	6	C0522671	C0522671 Sequence
C 688	135.8	4.8	2501	6	AX599024	AX599024 Sequence	761	134.8	4.7	547	9	BC070202	BC070202 Homo sapi
C 689	135.8	4.8	2612	9	BC063856	BC063856 Homo sapi	762	134.8	4.7	1090	5	BC066372	BC066372 Danio rer
C 690	135.8	4.8	4001	6	AX347363	AX347363 Sequence	763	134.8	4.7	1793	10	BC062171	BC062171 Mus muscu
C 691	135.8	4.8	4001	6	AX349084	AX349084 Sequence	764	134.8	4.7	1812	10	BC055113	BC055113 Mus muscu
C 692	135.8	4.8	4001	6	AX657851	AX657851 Sequence	765	134.8	4.7	2511	3	AK174016	AK174016 Ciona int
C 693	135.8	4.8	4001	6	AX659125	AX659125 Sequence	766	134.8	4.7	2905	3	AK174395	AK174395 Ciona int
C 694	135.8	4.8	4265	9	HS080760	BX647458 Homo sapi	767	134.8	4.7	3422	9	HS080592	BX537826 Homo sapi
C 695	135.8	4.8	4863	9	HS080808	BX648657 Homo sapi	768	134.8	4.7	173854	2	AC073047	AC073047 Homo sapi
C 696	135.8	4.8	5306	6	AX345413	AX345413 Sequence	769	134.8	4.7	349980	6	AX344570	AX344570 Sequence
C 697	135.8	4.8	6134	6	AX458624	AX458624 Sequence	C 770	134.6	4.7	360	6	C0527206	C0527206 Sequence
C 698	135.8	4.8	7061	6	AX251886	AX251886 Sequence	C 771	134.6	4.7	391	6	C0476273	C0476273 Sequence
C 699	135.8	4.8	7061	6	AX345898	AX345898 Sequence	772	134.6	4.7	579	6	C0526842	C0526842 Sequence
C 700	135.8	4.8	7061	6	AX348679	AX348679 Sequence	773	134.6	4.7	887	9	AB125184	AB125184 Macaca fa
C 701	135.8	4.8	14798	6	AX345934	AX345934 Sequence	774	134.6	4.7	981	9	BC041179	BC041179 Homo sapi
C 702	135.8	4.8	14920	6	AX344738	AX344738 Sequence	775	134.6	4.7	1562	10	BC063181	BC063181 Rattus no
C 703	135.8	4.8	16633	6	AX344576	AX344576 Sequence	776	134.6	4.7	1853	10	BC052346	BC052346 Mus muscu
C 704	135.8	4.8	17934	6	AX346621	AX346621 Sequence	777	134.6	4.7	3181	5	BC070985	BC070985 Xenopus l
C 705	135.8	4.8	35962	6	AX598758	AX598758 Sequence	778	134.6	4.7	6976	9	HS080863	BX648491 Homo sapi
C 706	135.8	4.8	39662	6	AX598904	AX598904 Sequence	779	134.6	4.7	13054	2	AC149986	AC149986 Strongylo
C 707	135.8	4.8	66993	2	AC138074	AC138074 Homo sapi	C 780	134.6	4.7	45685	2	AC087168	AC087168 Homo sapi
C 708	135.8	4.8	110000	8	CR382134 <sup>12</sup>	Continuation (13 o	C 781	134.4	4.7	416	6	C0484252	C0484252 Sequence
C 709	135.8	4.8	193988	2	AC102269	AC102269 Mus muscu	C 782	134.4	4.7	608	6	C0398119	C0398119 Sequence
C 710	135.6	4.8	800	10	BC034163	BC034163 Mus muscu	C 783	134.4	4.7	608	6	C0404407	C0404407 Sequence
C 711	135.6	4.8	831	6	C0423554	CQ423554 Sequence	784	134.4	4.7	766	8	AF531371	AF531371 Gossypium
C 712	135.6	4.8	1053	10	BC049595	BC049595 Mus muscu	785	134.4	4.7	2237	3	AK112710	AK112710 Ciona int
C 713	135.6	4.8	1459	6	BD270519	BD270519 Novel mai	786	134.4	4.7	2548	9	BC040371	BC040371 Homo sapi
C 714	135.6	4.8	1459	6	AX494847	AX494847 Sequence	787	134.4	4.7	2922	9	BC032692	BC032692 Homo sapi
C 715	135.6	4.8	1459	6	AX046603	AX046603 Sequence	788	134.4	4.7	2943	9	HS080352	AL832219 Homo sapi
C 716	135.6	4.8	1985	3	AX118692	AX118692 Drosophil	C 789	134.4	4.7	11097	6	AX826974	AX826974 Sequence
C 717	135.6	4.8	2395	9	AF090903	AF090903 Homo sapi	C 790	134.4	4.7	240657	2	AC111675	AC111675 Rattus no
C 718	135.6	4.8	2585	9	HS080567	BX537382 Homo sapi	C 791	134.4	4.7	349980	6	AX344554	AX344554 Sequence
C 719	135.6	4.8	2915	10	BC061479	BC061479 Mus muscu	C 792	134.4	4.7	501	6	AX344555	AX344555 Sequence
C 720	135.6	4.8	6484	6	AX344730	AX344730 Sequence	C 793	134.2	4.7	501	6	C0527244	C0527244 Sequence
C 721	135.6	4.8	9095	6	AX458545	AX458545 Sequence	C 794	134.2	4.7	720	8	CNS01D7J	AL116471 Botrytis
C 722	135.6	4.8	15649	6	AX348976	AX348976 Sequence	C 795	134.2	4.7	1269	9	BC072684	BC072684 Homo sapi
C 723	135.6	4.8	40862	6	AX346974	AX346974 Sequence	796	134.2	4.7	1770	9	BC063419	BC063419 Homo sapi
C 724	135.4	4.8	412	6	C0522434	CQ522434 Sequence	797	134.2	4.7	1933	9	HS080604	BX537929 Homo sapi
C 725	135.4	4.8	774	10	BC013457	BC013457 Mus muscu	C 798	134.2	4.7	1953	9	AB056420	AB056420 Macaca fa
C 726	135.4	4.8	859	9	BC043551	BC043551 Homo sapi	C 799	134.2	4.7	7657	6	AX278022	AX278022 Sequence
C 727	135.4	4.8	872	6	AX068322	AX068322 Sequence	C 800	134.2	4.7	7657	6	AX346924	AX346924 Sequence
C 728	135.4	4.8	1004	10	BC025458	BC025458 Mus muscu	C 801	134.2	4.7	9814	6	AX344425	AX344425 Sequence
C 729	135.4	4.8	1198	10	BC033305	BC033305 Mus muscu	C 802	134.2	4.7	37973	6	AX347098	AX347098 Sequence
C 730	135.4	4.8	1648	9	HS080851	BX648403 Homo sapi	C 803	134.2	4.7	63365	2	AC087437	AC087437 Homo sapi
C 731	135.4	4.8	1732	9	HS080691	BX648074 Homo sapi	C 804	134.2	4.7	75689	2	AC018536	AC018536 Homo sapi
C 732	135.4	4.8	1743	9	AB070131	AB070131 Macaca fa	C 805	134.2	4.7	349980	6	AX344567	AX344567 Sequence
C 733	135.4	4.8	2026	9	BC022399	BC022399 Homo sapi	C 806	134	4.7	472	6	C0525172	C0525172 Sequence
C 734	135.4	4.8	2027	9	BC063512	BC063512 Homo sapi	C 807	134	4.7	756	6	CQ393155	CQ393155 Sequence
C 735	135.4	4.8	2371	9	HS080592	BX537833 Homo sapi	C 808	134	4.7	756	6	CQ405433	CQ405433 Sequence
C 736	135.4	4.8	2563	9	AF125949	AF125949 Homo sapi	C 809	134	4.7	844	9	BC009571	BC009571 Homo sapi
C 737	135.4	4.8	3186	5	BC068331	BC068331 Danio rer	C 810	134	4.7	1339	9	BC016710	BC016710 Homo sapi
C 738	135.4	4.8	3758	9	HS080175	AL136787 Homo sapi	C 811	134	4.7	1701	9	BC071665	BC071665 Homo sapi
C 739	135.4	4.8	3836	9	BC063854	BC063854 Homo sapi	C 812	134	4.7	1742	9	HS080667	BX640624 Homo sapi
C 740	135.4	4.8	4086	9	HS080343	AL832132 Homo sapi	C 813	134	4.7	2207	10	BC066857	BC066857 Mus muscu
C 741	135.2	4.8	385	6	C0522393	CQ522393 Sequence	C 814	134	4.7	2610	9	BC038448	BC038448 Homo sapi
C 742	135.2	4.8	522	6	C0518047	CQ518047 Sequence	C 815	134	4.7	2734	5	BC076749	BC076749 Xenopus l
C 743	135.2	4.8	682	10	BC049545	BC049545 Mus muscu	C 816	134	4.7	3274	9	HS080737	BX647227 Homo sapi
C 744	135.2	4.8	1138	10	BC062234	BC062234 Rattus no	C 817	134	4.7	3916	10	BC018439	BC018439 Mus muscu
C 745	135.2	4.8	1963	10	BC083817	BC083817 Rattus no	C 818	134	4.7	4062	5	BC070004	BC070004 Danio rer
C 746	135.2	4.8	1999	9	HS082485	AJ742859 Homo sapi	C 819	134	4.7	5152	6	AX453070	AX453070 Sequence
C 747	135.2	4.8	2394	6	AX374733	AX374733 Sequence	C 820	134	4.7	5152	6	AX281182	AX281182 Sequence
C 748	135.2	4.8	2789	3	AK114441	AK114441 Ciona int	C 821	134	4.7	8899	6	AX345739	AX345739 Sequence
C 749	135.2	4.8	3681	9	HS080603	BX537922 Homo sapi	C 822	134	4.7	8899	6	AX348461	AX348461 Sequence

C-823	134	4.7	64789	2	AC0838339	AC083839	Homo sapi	C 896	133	4.7	6794	6	AX251872	Sequence
C 824	134	4.7	165563	2	AC083752	AC083752	Mus muscu	C 897	133	4.7	6794	6	AX344260	Sequence
825	133.8	4.7	474	6	CQ522390	CQ522390	Sequence	C 898	133	4.7	6794	6	AX348651	Sequence
826	133.8	4.7	500	9	BC070218	BC070218	Homo sapi	C 899	133	4.7	14568	6	AX345132	Sequence
827	133.8	4.7	761	11	CNS06KKG	AL042998 T7 end of		C 900	132.8	4.7	420	6	CQ476954	Sequence
C 828	133.8	4.7	817	6	CQ423543	CQ423543	Sequence	C 901	132.8	4.7	1078	9	BC035314	Sequence
C 829	133.8	4.7	859	9	AC026608	AC026608	Homo sapi	C 902	132.8	4.7	1142	8	AJ840525	Sequence
C 830	133.8	4.7	874	6	CQ414670	CQ414670	Sequence	C 903	132.8	4.7	1456	5	BC077897	Sequence
C 831	133.8	4.7	931	10	BC049725	BC049725	Mus muscu	C 904	132.8	4.7	1456	5	BC060616	Sequence
C 832	133.8	4.7	1197	8	AJ840663	AJ840663	Arabidops	C 905	132.8	4.7	1982	3	AK112713	Ciona int
C 833	133.8	4.7	1328	8	AJ840631	AJ840631	Arabidops	C 906	132.8	4.7	1983	10	BC005510	Mus muscu
C 834	133.8	4.7	2030	9	BC063602	BC063602	Homo sapi	C 907	132.8	4.7	1985	6	BD172402	Secreted
835	133.8	4.7	2566	6	CQ834011	CQ834011	Sequence	C 908	132.8	4.7	1985	6	BD172721	Secreted
C 836	133.8	4.7	3341	9	BC032308	BC032308	Homo sapi	C 909	132.8	4.7	1985	6	BD173040	Secreted
C 837	133.8	4.7	6115	6	AX346703	AX346703	Sequence	C 910	132.8	4.7	1985	6	BD173359	Secreted
C 838	133.8	4.7	8712	6	AX344694	AX344694	Sequence	C 911	132.8	4.7	1985	6	BD175393	Secretory
C 839	133.8	4.7	61940	2	AC109312	AC109312	Homo sapi	C 912	132.8	4.7	1985	6	CQ881212	Sequence
C 840	133.8	4.7	64767	2	AC102701	AC102701	Mus muscu	C 913	132.8	4.7	1985	6	AR410771	Sequence
841	133.8	4.7	133276	2	AC087147	AC087147	Homo sapi	C 914	132.8	4.7	1985	6	AR439135	Sequence
842	133.8	4.7	167711	2	AC007629	AC007629	Mus muscu	C 915	132.8	4.7	1985	6	AR473155	Sequence
843	133.6	4.7	562	10	BC049688	BC049688	Mus muscu	C 916	132.8	4.7	1985	6	AR527141	Sequence
844	133.6	4.7	763	9	BC040916	BC040916	Homo sapi	C 917	132.8	4.7	1985	6	AR566174	Sequence
845	133.6	4.7	967	9	HSN802777	AL390167	Homo sapi	C 918	132.8	4.7	1985	6	AX375960	Sequence
846	133.6	4.7	1352	3	AK115954	AK115954	Ciona int	C 919	132.8	4.7	1985	6	AX697621	Sequence
847	133.6	4.7	1408	10	BC048693	BC048693	Mus muscu	C 920	132.8	4.7	1985	6	BD075542	Secretory
848	133.6	4.7	1788	9	BC044944	BC044944	Homo sapi	C 921	132.8	4.7	1985	9	AX358500	Homo sapi
849	133.6	4.7	1816	9	BC050396	BC050396	Homo sapi	C 922	132.8	4.7	6668	6	AX346598	Sequence
850	133.6	4.7	1889	9	HSN805887	BS537794	Homo sapi	C 923	132.8	4.7	11097	6	AX826972	Sequence
851	133.6	4.7	2178	6	AC099370	AC099370	Sequence	C 924	132.8	4.7	12138	6	AX346530	Sequence
852	133.6	4.7	2514	9	BC044863	BC044863	Homo sapi	C 925	132.8	4.7	12138	6	AX348420	Sequence
853	133.6	4.7	2841	9	BC020219	BC020219	Homo sapi	C 926	132.6	4.7	602	9	BC008488	Homo sapi
854	133.6	4.7	3375	9	BC038406	BC038406	Homo sapi	C 927	132.6	4.7	972	10	BC049738	Mus muscu
C 855	133.6	4.7	6025	6	AX277881	AX277881	Sequence	C 928	132.6	4.7	1590	9	HSN803698	Homo sapi
C 856	133.6	4.7	56153	6	AX251552	AX251552	Sequence	C 929	132.6	4.7	1634	9	HSN807708	Homo sapi
857	133.6	4.7	213641	2	AC114620	AC114620	Mus muscu	C 930	132.6	4.7	2679	10	BC006021	Mus muscu
858	133.4	4.7	202	6	BD190570	BD190570	Secretory	C 931	132.6	4.7	2827	6	CQ491125	Sequence
859	133.4	4.7	358	6	CQ671266	AC099441	Sequence	C 932	132.6	4.7	2827	6	CQ496990	Sequence
860	133.4	4.7	565	6	CQ526051	CQ526051	Sequence	C 933	132.6	4.7	5586	6	AX339195	Sequence
861	133.4	4.7	597	6	AX187052	AX187052	Sequence	C 934	132.6	4.7	5586	6	AX345551	Sequence
C 862	133.4	4.7	621	6	AX187131	AX187131	Sequence	C 935	132.6	4.7	5893	6	AX345761	Sequence
C 863	133.4	4.7	1083	9	HSN800561	AL080060	Homo sapi	C 936	132.6	4.7	6171	6	AX345691	Sequence
C 864	133.4	4.7	1756	9	BC069223	BC069223	Homo sapi	C 937	132.6	4.7	34980	6	AX344571	Sequence
865	133.4	4.7	1941	10	BC053250	BC049624	Mus muscu	C 938	132.4	4.7	1000	9	HSN806624	Homo sapi
866	133.4	4.7	2164	10	BC005513	BC053250	Danio rer	C 939	132.4	4.7	1012	10	BC049579	Mus muscu
867	133.4	4.7	2790	9	BC048292	BC005513	Mus muscu	C 940	132.4	4.7	1073	5	BC084065	Sequence
868	133.2	4.7	1372	9	BC024221	BC048292	Homo sapi	C 941	132.4	4.7	1468	10	BC068202	Sequence
869	133.2	4.7	1383	5	BC056115	BC024221	Homo sapi	C 942	132.4	4.7	2417	9	HSN800967	Sequence
870	133.2	4.7	1737	9	BC056115	BC056115	Xenopus l	C 943	132.4	4.7	2500	10	BC058946	Mus muscu
871	133.2	4.7	1756	9	BC069223	BC069223	Homo sapi	C 944	132.4	4.7	2607	5	BC054610	Danio rer
C 872	133.2	4.7	8186	6	AX344682	AX344682	Sequence	C 945	132.4	4.7	2788	9	AF111847	Homo sapi
C 873	133.2	4.7	9021	6	AX347134	AX347134	Sequence	C 946	132.4	4.7	3383	9	HSN803701	Homo sapi
C 874	133.2	4.7	9021	6	AX347134	AX347134	Sequence	C 947	132.4	4.7	3491	5	BC059285	Sequence
C 875	133.2	4.7	9021	6	AX347426	AX347426	Sequence	C 948	132.4	4.7	4169	10	BC063919	Mus muscu
C 876	133.2	4.7	9021	6	AX348462	AX348462	Sequence	C 949	132.4	4.7	4969	9	HSN806817	Homo sapi
C 877	133.2	4.7	9021	6	AX349147	AX349147	Sequence	C 950	132.4	4.7	61155	2	AC074069	Homo sapi
C 878	133.2	4.7	9021	6	AX657808	AX657808	Sequence	C 951	132.2	4.6	539	6	CQ523463	Sequence
C 879	133.2	4.7	9021	6	AX659082	AX659082	Sequence	C 952	132.2	4.6	878	6	AX482482	Sequence
C 880	133.2	4.7	203657	2	AX927302	AX927302	Danio rer	C 953	132.2	4.6	1359	5	BC053194	Danio rer
881	133.2	4.7	231972	2	AC068055	AC068055	Homo sapi	C 954	132.2	4.6	2161	6	CQ414527	Sequence
C 882	133.2	4.7	340089	2	AC104922	AC104922	Mus muscu	C 955	132	4.6	390	6	CQ410737	Sequence
C 883	133.2	4.7	349980	6	AX344560	AX344560	Sequence	C 956	132	4.6	545	6	AX185705	Sequence
C 884	133	4.7	425	6	CQ506214	CQ506214	Sequence	C 957	132	4.6	681	5	BC055187	Danio rer
C 885	133	4.7	587	9	HSN337540	AJ337540	Homo sapi	C 958	132	4.6	1166	9	BC043545	Homo sapi
886	133	4.7	656	10	BC049555	BC049555	Mus muscu	C 959	132	4.6	2009	3	AK116580	Ciona int
C 887	133	4.7	843	6	CQ484198	CQ484198	Sequence	C 960	132	4.6	2350	9	BC063427	Homo sapi
888	133	4.7	1257	9	BC043535	BC043535	Homo sapi	C 961	132	4.6	71532	2	AC023655	Sequence
889	133	4.7	1337	3	AX118704	AX118704	Drosophill	C 962	132	4.6	200124	2	AC111061	Mus muscu
890	133	4.7	1489	9	AB048953	AB048953	Macaca fa	C 963	131.8	4.6	329	6	CQ518231	Sequence
891	133	4.7	2090	9	BC049196	BC049196	Homo sapi	C 964	131.8	4.6	768	9	CQ432402	Sequence
892	133	4.7	2216	5	BC054636	BC054636	Danio rer	C 965	131.8	4.6	1094	9	BC039173	Homo sapi
893	133	4.7	2293	5	BC070538	BC070538	Xenopus l	C 966	131.8	4.6	1661	9	BC025753	Homo sapi
894	133	4.7	2722	10	BC075615	BC075615	Mus muscu	C 967	131.8	4.6	2674	6	AR183261	Sequence
895	133	4.7	4185	9	BC050532	BC050532	Homo sapi	C 968	131.8	4.6	2674	6	AR456323	Sequence



969	131.8	4.6	3345	9	BC041132	Homo sapi	1042	130.6	4.6	1560	9	BC032420	Homo sapi
970	131.8	4.6	4670	9	AF104032	Homo sapi	1043	130.6	4.6	1985	5	BD275145	48 Human
971	131.6	4.6	308	6	CQ517578	Sequence	1044	130.6	4.6	2690	5	BC077100	Danio rer
972	131.6	4.6	720	10	BC061086	Mus muscu	1045	130.6	4.6	5165	6	CQ413028	Sequence
973	131.6	4.6	1051	6	AR164814	Sequence	c1046	130.6	4.6	9770	6	AX344934	Sequence
974	131.6	4.6	1051	6	AR490614	Sequence	1047	130.6	4.6	132374	2	AC026503	Homo sapi
975	131.6	4.6	1051	6	AR532388	Sequence	1048	130.6	4.6	420	6	CQ526488	Sequence
976	131.6	4.6	1728	9	AB070110	Macaca fa	1049	130.4	4.6	466	6	CQ526037	Sequence
977	131.6	4.6	1773	9	BC037559	Homo sapi	c1050	130.4	4.6	668	6	CQ397705	Sequence
c	978	131.6	6668	6	AX346599	Sequence	c1051	130.4	4.6	668	6	CQ404002	Sequence
979	131.6	4.6	189682	2	AC107855	Mus muscu	c1052	130.4	4.6	749	9	HS4336745	Homo sapi
980	131.4	4.6	351	6	CQ526060	Sequence	1053	130.4	4.6	1665	9	BC041446	Homo sapi
981	131.4	4.6	453	6	CQ524875	Sequence	1054	130.4	4.6	1738	6	AR560934	Sequence
982	131.4	4.6	586	6	CQ524455	Sequence	1055	130.4	4.6	1738	8	BT009079	Triticum
983	131.4	4.6	2165	5	BC054602	Danio rer	1056	130.4	4.6	3399	9	BC063840	Homo sapi
984	131.4	4.6	2747	9	BC025706	Homo sapi	1057	130.4	4.6	3582	10	BC053927	Mus muscu
985	131.4	4.6	4606	10	BC058089	Mus muscu	c1058	130.4	4.6	8607	6	AR453095	Sequence
986	131.4	4.6	58890	2	AC110050	Homo sapi	c1059	130.4	4.6	8607	6	AX281207	Sequence
987	131.4	4.6	126038	2	AC016068	Homo sapi	c1060	130.4	4.6	8607	6	AX356478	Sequence
988	131.4	4.6	173585	2	AC021113	Homo sapi	c1061	130.4	4.6	9547	6	AX346406	Sequence
989	131.2	4.6	490	6	CQ523744	Sequence	c1062	130.4	4.6	45210	2	AC087043	Homo sapi
990	131.2	4.6	543	6	CQ524637	Sequence	c1063	130.4	4.6	57121	2	AC084255	Homo sapi
991	131.2	4.6	1232	10	BC060554	Rattus no	c1064	130.4	4.6	193988	2	AC102269	Mus muscu
992	131.2	4.6	1673	6	AX772808	Sequence	c1065	130.2	4.6	510	6	CQ399174	Sequence
993	131.2	4.6	1775	5	BC053257	Danio rer	c1066	130.2	4.6	510	6	CQ405452	Sequence
994	131.2	4.6	1882	5	BC068036	Xenopus t	1067	130.2	4.6	561	10	BC049674	Mus muscu
995	131.2	4.6	2000	9	BC063423	Homo sapi	1068	130.2	4.6	2270	9	HS806047	Homo sapi
996	131.2	4.6	2080	10	BC013564	Mus muscu	1069	130.2	4.6	2728	5	BC081123	Xenopus t
997	131.2	4.6	3050	5	BC066571	Danio rer	1070	130	4.6	407	6	CQ522526	Sequence
998	131.2	4.6	3640	9	HS806825	Homo sapi	1071	130	4.6	1265	9	BC033301	Homo sapi
999	131.2	4.6	4744	5	BC066770	Xenopus l	1072	130	4.6	1715	5	BC067176	Danio rer
c1000	131.2	4.6	147499	2	AX178788	Canis fam	1073	130	4.6	2246	5	BC051820	Homo sapi
c1001	131	4.6	383	6	CQ502211	Sequence	c1074	130	4.6	56857	2	AC021917	Homo sapi
c1002	131	4.6	383	6	CQ511079	Sequence	c1075	130	4.6	91034	2	AC025911	Mus muscu
1003	131	4.6	423	6	CQ523358	Sequence	1076	130	4.6	26970	2	AC098406	Rattus no
c1004	131	4.6	470	6	CQ514078	Sequence	c1077	129.8	4.6	173	6	AX185626	Sequence
c1005	131	4.6	498	6	CQ481059	Sequence	1078	129.8	4.6	1156	5	BC049488	Danio rer
1006	131	4.6	5243	6	CQ525654	Sequence	1079	129.8	4.6	2029	10	BC050265	Mus muscu
1007	131	4.6	1743	9	HS802621	Homo sapi	1080	129.8	4.6	2709	10	BC054846	Mus muscu
1008	131	4.6	1348	9	BC070154	Homo sapi	1081	129.8	4.6	2759	10	BC055046	Mus muscu
1009	131	4.6	3420	10	BC074017	Rattus no	1082	129.8	4.6	3300	9	BC011656	Homo sapi
1010	131	4.6	3626	9	BC012147	Homo sapi	1083	129.8	4.6	3326	9	HS808512	Homo sapi
c1011	131	4.6	4180	10	BC042645	Mus muscu	1084	129.8	4.6	3850	10	BC063749	Sequence
c1012	131	4.6	5198	6	AX345181	Sequence	c1085	129.8	4.6	141003	2	AC016463	Homo sapi
c1013	131	4.6	5750	6	AX251465	Sequence	1086	129.6	4.6	1128	9	BC071732	Homo sapi
c1014	131	4.6	5750	6	AX346910	Sequence	1087	129.6	4.6	1175	9	BC049386	Homo sapi
c1015	131	4.6	6027	6	AX344764	Sequence	1088	129.6	4.6	1287	3	BT009948	Drosophil
c1016	131	4.6	6577	6	AX251920	Sequence	1089	129.6	4.6	1397	6	CQ491382	Sequence
c1017	131	4.6	6577	6	AX346258	Sequence	1090	129.6	4.6	1402	9	BC040630	Homo sapi
c1018	131	4.6	6577	6	AX348993	Sequence	1091	129.6	4.6	1487	4	AY423736	Tachyglis
c1019	131	4.6	68280	2	AC116016	Homo sapi	1092	129.6	4.6	2247	9	BC009648	Homo sapi
c1020	131	4.6	71778	6	AX344562	Sequence	1093	129.6	4.6	3038	9	HS806221	Homo sapi
c1021	131	4.6	173224	2	AC116813	Sequence	1094	129.6	4.6	5277	9	HS8086645	Homo sapi
1022	131	4.6	263319	2	AC125258	Mus muscu	c1095	129.6	4.6	8342	6	AX345403	Sequence
c1023	131	4.6	349980	6	AX344561	Sequence	1096	129.6	4.6	211348	2	EX927237	Danio rer
c1024	130.8	4.6	364	6	CQ399251	Sequence	1097	129.4	4.5	603	6	CQ526797	Sequence
c1025	130.8	4.6	364	6	CQ405529	Sequence	c1098	129.4	4.5	743	9	HS4335471	Homo sapi
1026	130.8	4.6	1447	6	AR237880	Sequence	1099	129.4	4.5	1130	10	BC043698	Mus muscu
1027	130.8	4.6	1651	10	BC024872	Sequence	1100	129.4	4.5	1429	10	BC022900	Mus muscu
1028	130.8	4.6	1850	9	BC040123	Homo sapi	1101	129.4	4.5	1499	9	BC042195	Homo sapi
1029	130.8	4.6	1905	9	BC032703	Homo sapi	1102	129.4	4.5	1711	9	BC032509	Homo sapi
1030	130.8	4.6	2053	9	BC030196	Homo sapi	1103	129.4	4.5	1760	9	BC051807	Homo sapi
1031	130.8	4.6	2265	10	BC051639	Mus muscu	1104	129.4	4.5	1789	9	BC070134	Homo sapi
1032	130.8	4.6	2336	5	BC072340	Xenopus l	1105	129.4	4.5	1946	9	HS8080123	Homo sapi
1033	130.8	4.6	3941	9	HS80803636	Homo sapi	1106	129.4	4.5	1994	3	AK116078	Ciona int
c1034	130.8	4.6	7906	6	AX277935	Sequence	1107	129.4	4.5	2150	6	CQ882012	Sequence
c1035	130.8	4.6	7906	6	AX323622	Sequence	1108	129.4	4.5	2261	6	CQ882010	Sequence
c1036	130.8	4.6	7906	6	AX344771	Sequence	1109	129.4	4.5	2287	9	BC044220	Homo sapi
c1037	130.6	4.6	501	6	CQ411817	Sequence	1110	129.4	4.5	2367	9	HS8081757	Homo sapi
1038	130.6	4.6	580	10	BC006049	Mus muscu	1111	129.4	4.5	2508	10	BC079036	Rattus no
1039	130.6	4.6	870	6	BD231669	31 human	1112	129.4	4.5	2610	10	BC063267	Mus muscu
1040	130.6	4.6	977	9	BC051846	Homo sapi	1113	129.4	4.5	2922	3	AF479582	Boophilus
1041	130.6	4.6	1280	9	BC047365	Homo sapi	1114	129.4	4.5	4651	9	BC042656	Homo sapi



c1115	129.4	4.5	4990	6	CQ493127	Sequence	1188	128.4	4.5	1976	9	BC040113	Homo sapi
c1116	129.4	4.5	4990	6	CQ493522	Sequence	1189	128.4	4.5	1976	9	BC012750	Homo sapi
c1117	129.4	4.5	5908	6	AX251914	Sequence	1190	128.4	4.5	1990	9	AK000212	Homo sapi
c1118	129.4	4.5	5908	6	AX277930	Sequence	c1191	128.4	4.5	113515	6	AX347077	Sequence
c1119	129.4	4.5	5908	6	AX323617	Sequence	1192	128.2	4.5	299	6	CQ669036	Sequence
c1120	129.4	4.5	6112	6	AX345565	Sequence	1193	128.2	4.5	335	10	BC048511	Mus muscu
c1121	129.4	4.5	6338	6	AX346028	Sequence	c1194	128.2	4.5	385	6	CQ398297	Sequence
c1122	129.4	4.5	7058	6	AX348438	Sequence	c1195	128.2	4.5	385	6	CQ404584	Sequence
c1123	129.4	4.5	8298	6	AX344783	Sequence	1196	128.2	4.5	1004	9	BC043536	Homo sapi
c1124	129.4	4.5	9268	6	AX346503	Sequence	1197	128.2	4.5	1350	10	BC072695	Rattus no
c1125	129.4	4.5	9515	6	AX277997	Sequence	1198	128.2	4.5	1846	9	BC038379	Homo sapi
c1126	129.4	4.5	9515	6	AX323694	Sequence	1199	128.2	4.5	2035	9	BC063696	Homo sapi
c1127	129.4	4.5	9515	6	AX344837	Sequence	1200	128.2	4.5	2085	5	BC077186	Xenopus l
1128	129.4	4.5	185292	2	BX957342	Danio rer	1201	128.2	4.5	2139	5	BC054626	Danio rer
1129	129.2	4.5	267	6	CQ525163	Sequence	1202	128.2	4.5	2633	9	AL833388	Homo sapi
1130	129.2	4.5	567	6	CQ527262	Sequence	1203	128.2	4.5	2946	5	BC076976	Xenopus t
1131	129.2	4.5	1926	5	BC084091	Sequence	c1204	128.2	4.5	6960	6	AX347301	Sequence
1132	129.2	4.5	2840	5	BC056558	Danio rer	c1205	128.2	4.5	62359	2	AC116167	Homo sapi
1133	129.2	4.5	3110	10	BC057617	Sequence	1206	128	4.5	504	6	CQ526419	Sequence
c1134	129.2	4.5	70511	2	AC091083	Sequence	1207	128	4.5	539	6	CQ526970	Sequence
c1135	129.2	4.5	257700	2	AC147391	Pan trogl	1208	128	4.5	606	6	CQ524188	Sequence
1136	129	4.5	247	6	CQ677559	Sequence	1209	128	4.5	1347	10	BC008980	Mus muscu
1137	129	4.5	317	6	CQ526915	Sequence	1210	128	4.5	1469	6	BD260697	50 human
1138	129	4.5	1414	10	BC005487	Mus muscu	1211	128	4.5	1470	9	BC072387	Homo sapi
1139	129	4.5	1527	5	BC064182	Xenopus t	1212	128	4.5	1627	9	BC039584	Homo sapi
1140	129	4.5	1615	9	AF218014	Homo sapi	1213	128	4.5	2002	9	BC068030	Homo sapi
1141	129	4.5	1817	10	BC083562	Sequence	1214	128	4.5	2212	10	BC046775	Mus muscu
1142	129	4.5	2630	9	BC038222	Homo sapi	1215	128	4.5	2500	9	BC065207	Mus muscu
1143	129	4.5	3446	9	HSN802955	Sequence	1216	128	4.5	2754	10	BC066817	Homo sapi
c1144	129	4.5	145992	2	CR339064	Danio rer	1217	128	4.5	3060	6	AR252731	Sequence
1145	128.8	4.5	208	6	CQ677600	Sequence	1218	128	4.5	3060	6	AX055476	Sequence
1146	128.8	4.5	373	6	CQ526228	Sequence	1219	128	4.5	3060	6	AX089948	Sequence
1147	128.8	4.5	471	6	CQ515907	Sequence	1220	128	4.5	3060	6	AX358962	Sequence
1148	128.8	4.5	1010	10	BC061971	Rattus no	1221	128	4.5	3060	6	AX362455	Sequence
1149	128.8	4.5	1011	9	BC020756	Homo sapi	1222	128	4.5	3060	6	AX403617	Sequence
1150	128.8	4.5	1462	10	BC006018	Mus muscu	1223	128	4.5	3060	6	AX454694	Sequence
1151	128.8	4.5	1588	9	BC070183	Sequence	1224	128	4.5	3060	6	AX491172	Sequence
1152	128.8	4.5	1706	5	BC082351	Xenopus l	c1225	128	4.5	81120	2	AC022851	Homo sapi
1153	128.8	4.5	1838	10	BC083573	Rattus no	1226	127.8	4.5	223	6	CQ523534	Sequence
1154	128.8	4.5	2245	9	HSN803715	Sequence	1227	127.8	4.5	439	6	CQ518358	Sequence
1155	128.8	4.5	3251	5	BC074658	Xenopus t	1228	127.8	4.5	535	6	CQ471891	Sequence
1156	128.8	4.5	3894	10	BC053925	Mus muscu	c1229	127.8	4.5	660	8	CNS01C1X	Botrytis
c1157	128.8	4.5	109082	2	AC026133	Sequence	1230	127.8	4.5	935	10	BC061157	Arabidops
c1158	128.8	4.5	258622	2	AC020877	Mus muscu	c1231	127.8	4.5	1306	8	AJ840640	Arabidops
1159	128.6	4.5	319	6	CQ523998	Sequence	1232	127.8	4.5	1408	9	BC065718	Homo sapi
1160	128.6	4.5	332	6	CQ523998	Sequence	1233	127.8	4.5	1765	9	BC063438	Homo sapi
c1161	128.6	4.5	360	6	CQ427909	Sequence	1234	127.8	4.5	1880	6	CQ769491	Sequence
c1162	128.6	4.5	363	6	CQ397318	Sequence	1235	127.8	4.5	2445	9	BC019562	Homo sapi
c1163	128.6	4.5	363	6	CQ403817	Sequence	1236	127.8	4.5	2530	9	BC036868	Homo sapi
1164	128.6	4.5	527	10	BC049658	Mus muscu	c1237	127.8	4.5	2750	5	BC084264	Xenopus l
1165	128.6	4.5	607	5	BC049055	Danio rer	1238	127.8	4.5	3223	6	CQ806938	Sequence
c1166	128.6	4.5	768	6	CQ432391	Sequence	c1239	127.8	4.5	3223	6	CQ807212	Sequence
1167	128.6	4.5	1076	10	BC062802	Rattus no	1240	127.8	4.5	3307	9	BC025714	Homo sapi
1168	128.6	4.5	1205	9	BC039058	Homo sapi	c1241	127.8	4.5	67776	2	AC101220	Mus muscu
1169	128.6	4.5	1426	5	BC054250	Xenopus l	c1242	127.8	4.5	83440	2	AC024285	Homo sapi
1170	128.6	4.5	1567	9	HSN806640	Homo sapi	c1243	127.8	4.5	301026	2	BX004844	Danio rer
1171	128.6	4.5	1608	9	AY358187	Homo sapi	1244	127.6	4.5	674	6	AR283453	Sequence
1172	128.6	4.5	1690	9	BC049211	Homo sapi	1245	127.6	4.5	674	6	AR344221	Sequence
1173	128.6	4.5	1722	5	BC063371	Xenopus t	1246	127.6	4.5	674	6	AR351422	Sequence
1174	128.6	4.5	2085	9	BC029120	Homo sapi	1247	127.6	4.5	674	6	AR454002	Sequence
1175	128.6	4.5	2337	9	HSN800876	Sequence	1248	127.6	4.5	674	6	AR561590	Sequence
1176	128.6	4.5	2377	8	AY080711	Arabidops	1249	127.6	4.5	674	6	AX282972	Sequence
1177	128.6	4.5	3676	10	BC062923	Mus muscu	1250	127.6	4.5	674	6	AX303145	Sequence
1178	128.6	4.5	4818	9	HSN807492	Homo sapi	1251	127.6	4.5	745	10	BC049606	Mus muscu
1179	128.4	4.5	458	10	BC061002	Mus muscu	1252	127.6	4.5	2661	10	BC026137	Mus muscu
1180	128.4	4.5	569	6	BD223440	94 human	1253	127.6	4.5	3856	9	HSN805531	Sequence
1181	128.4	4.5	569	6	AR243074	Sequence	c1254	127.6	4.5	8305	6	AX346470	Sequence
1182	128.4	4.5	569	6	AR404255	Sequence	1255	127.6	4.5	56993	2	AC084077	Homo sapi
1183	128.4	4.5	633	5	BC057512	Danio rer	c1256	127.6	4.5	60565	2	AC023852	Homo sapi
1184	128.4	4.5	806	5	CR405924	Gallus ga	1257	127.4	4.5	807	6	CQ428748	Sequence
1185	128.4	4.5	816	6	CQ486689	Sequence	1258	127.4	4.5	839	9	BC043574	Homo sapi
1186	128.4	4.5	1065	10	BC049675	Mus muscu	c1259	127.4	4.5	840	8	CNS018QK	Botrytis
1187	128.4	4.5	1889	9	BC073841	Homo sapi	1260	127.4	4.5	1027	9	BC041442	Homo sapi

1261	127.4	4.5	1319	9	BC015490	BC015490 Homo sapi
1262	127.4	4.5	1321	6	C0776637	C0776637 Sequence
1263	127.4	4.5	1931	9	AB093671	AB093671 Macaca fa
1264	127.4	4.5	3686	10	BC043709	BC043709 Mus muscu
1265	127.4	4.5	4298	9	HSN804564	HSN804564
1266	127.4	4.5	4438	10	BC067016	BC067016 Homo sapi
1267	127.4	4.5	4829	10	BC060175	BC060175 Mus muscu
1268	127.4	4.5	5251	10	BC065072	BC065072 Mus muscu
c1269	127.4	4.5	13606	6	AX2511315	AX2511315 Sequence
c1270	127.4	4.5	13606	6	AX278002	AX278002 Sequence
c1271	127.4	4.5	13606	6	AX323699	AX323699 Sequence
c1272	127.4	4.5	13606	6	AX346712	AX346712 Sequence
1273	127.4	4.5	164288	2	AC128949	AC128949 Rattus no
1274	127.4	4.5	284160	2	AC107858	AC107858 Mus muscu
1275	127.2	4.5	466	6	C0522677	C0522677 Sequence
1276	127.2	4.5	1400	9	BC063708	BC063708 Homo sapi
1277	127.2	4.5	3499	10	BC007476	BC007476 Mus muscu
1278	127.2	4.5	3501	5	BC076842	BC076842 Xenopus l
1279	127.2	4.5	4124	3	AK112284	AK112284 Ciona int
1280	127.2	4.5	33825	2	AC111154	AC111154 Homo sapi
c1281	127.2	4.5	63363	2	AC068364	AC068364 Homo sapi
c1282	127.2	4.5	73885	2	AC025307	AC025307 Homo sapi
c1283	127.2	4.5	81358	2	AC023330	AC023330 Homo sapi
1284	127.2	4.5	110000	8	CR382131	Continuation (4 of
1285	127.2	4.5	167728	2	AC115889	AC115889 Mus muscu
c1286	127.2	4.5	178802	2	AC140116	AC140116 Rattus no
c1287	127.2	4.5	22962	2	AC079520	AC079520 Mus muscu
1288	127	4.5	127	6	BD021987	BD021987 Secreted
1289	127	4.5	421	6	C0526039	C0526039 Sequence
1290	127	4.5	481	6	C0525180	C0525180 Sequence
1291	127	4.5	885	3	AK174656	AK174656 Ciona int
1292	127	4.5	1445	9	BC063545	BC063545 Homo sapi
1293	127	4.5	1805	9	AB070053	AB070053 Macaca fa
1294	127	4.5	1842	9	BC024042	BC024042 Homo sapi
1295	127	4.5	1959	9	BC043548	BC043548 Homo sapi
1296	127	4.5	2150	9	BC025715	BC025715 Homo sapi
1297	127	4.5	2178	9	BC046358	BC046358 Homo sapi
1298	127	4.5	2557	9	HSN042875	HSN042875 Homo sapi
1299	127	4.5	2591	9	BC031188	BC031188 Homo sapi
1300	126.8	4.5	547	6	C0526009	C0526009 Sequence
c1301	126.8	4.5	606	6	C0503221	C0503221 Sequence
c1302	126.8	4.5	606	6	C0512068	C0512068 Sequence
c1303	126.8	4.5	870	6	C0482086	C0482086 Sequence
1304	126.8	4.5	948	10	BC031142	BC031142 Mus muscu
1305	126.8	4.5	1034	9	AK026865	AK026865 Homo sapi
1306	126.8	4.5	1286	10	BC062175	BC062175 Mus muscu
1307	126.8	4.5	2320	10	BC046962	BC046962 Mus muscu
1308	126.8	4.5	4064	10	BC072632	BC072632 Mus muscu
c1309	126.8	4.5	6485	6	AX251313	AX251313 Sequence
c1310	126.8	4.5	6485	6	AX346710	AX346710 Sequence
c1311	126.8	4.5	123257	2	AC010694	AC010694 Drosophil
c1312	126.8	4.5	143585	2	AC013349	AC013349 Homo sapi
c1313	126.8	4.5	156550	2	AC015830	AC015830 Homo sapi
1314	126.8	4.5	256944	2	AC138343	AC138343 Mus muscu
1315	126.6	4.4	323	6	C05224910	C05224910 Sequence
1316	126.6	4.4	488	6	C0522468	C0522468 Sequence
c1317	126.6	4.4	656	9	HSN337512	HSN337512 Homo sapi
c1318	126.6	4.4	696	6	C0422213	C0422213 Sequence
1319	126.6	4.4	1591	9	BC050659	BC050659 Homo sapi
1320	126.6	4.4	1690	9	BC011595	BC011595 Homo sapi
1321	126.6	4.4	1781	5	BC064253	BC064253 Xenopus t
1322	126.6	4.4	1993	3	AK112520	AK112520 Ciona int
1323	126.6	4.4	2230	5	BC078288	BC078288 Homo sapi
1324	126.6	4.4	2240	5	BC084150	BC084150 Xenopus t
1325	126.6	4.4	2368	9	BC063595	BC063595 Homo sapi
1326	126.6	4.4	2578	9	AB049758	AB049758 Homo sapi
1327	126.6	4.4	2924	6	AX683129	AX683129 Sequence
1328	126.6	4.4	2924	10	S68736	S68736 Rattus sp.
1329	126.6	4.4	3669	10	BC038376	BC038376 Mus muscu
c1330	126.6	4.4	58571	2	AC023309	AC023309 Homo sapi
c1331	126.6	4.4	154314	2	BX901927	BX901927 Dantio rer
1332	126.4	4.4	247	6	C0524931	C0524931 Sequence
1333	126.4	4.4	263	6	C0663258	C0663258 Sequence
1334	126.4	4.4	861	10	BC049709	BC049709 Mus muscu
1335	126.4	4.4	919	5	BC079985	BC079985 Xenopus l
1336	126.4	4.4	1280	9	BC063439	BC063439 Homo sapi
1337	126.4	4.4	1410	5	BC049418	BC049418 Dantio rer
1338	126.4	4.4	2072	9	BC044245	BC044245 Homo sapi
1339	126.4	4.4	2106	5	BC075571	BC075571 Xenopus t
1340	126.4	4.4	2314	5	BC068218	BC068218 Homo sapi
1341	126.4	4.4	2355	9	HSN01346	HSN01346 Homo sapi
1342	126.4	4.4	2415	9	BC028002	BC028002 Homo sapi
1343	126.4	4.4	2421	10	BC061106	BC061106 Mus muscu
1344	126.4	4.4	2607	9	BC053734	BC053734 Homo sapi
1345	126.4	4.4	2611	9	BC041438	BC041438 Homo sapi
1346	126.4	4.4	3036	9	AF090896	AF090896 Homo sapi
1347	126.4	4.4	3082	10	BC046972	BC046972 Mus muscu
1348	126.4	4.4	3401	9	BC040376	BC040376 Homo sapi
1349	126.4	4.4	3487	10	BC016095	BC016095 Mus muscu
c1350	126.4	4.4	9963	6	AX345596	AX345596 Sequence
c1351	126.4	4.4	34980	6	AX344550	AX344550 Sequence
c1352	126.2	4.4	414	6	CQ397915	CQ397915 Sequence
c1353	126.2	4.4	414	6	CQ404208	CQ404208 Sequence
1354	126.2	4.4	452	6	CQ527434	CQ527434 Sequence
1355	126.2	4.4	585	6	CQ526237	CQ526237 Sequence
1356	126.2	4.4	997	9	BC047943	BC047943 Homo sapi
1357	126.2	4.4	1073	9	BC032697	BC032697 Homo sapi
1358	126.2	4.4	1568	5	BC050177	BC050177 Dantio rer
1359	126.2	4.4	1886	9	AK025084	AK025084 Homo sapi
1360	126.2	4.4	2064	10	BC053424	BC053424 Mus muscu
1361	126.2	4.4	2692	3	AK173351	AK173351 Ciona int
1362	126.2	4.4	2773	6	AR252502	AR252502 Sequence
1363	126.2	4.4	2773	6	AX092302	AX092302 Sequence
1364	126.2	4.4	2773	6	AX376082	AX376082 Sequence
1365	126.2	4.4	2773	6	AX403291	AX403291 Sequence
1366	126.2	4.4	2773	9	AV358338	AV358338 Homo sapi
1367	126.2	4.4	2920	3	AK174466	AK174466 Ciona int
1368	126.2	4.4	3203	5	BC077358	BC077358 Xenopus l
1369	126.2	4.4	3547	5	BC084146	BC084146 Xenopus t
1370	126.2	4.4	5599	10	BC049182	BC049182 Mus muscu
1371	126.2	4.4	227370	2	AC116888	AC116888 Mus muscu
1372	126.2	4.4	321708	2	AC087142	AC087142 Mus muscu
1373	126	4.4	464	6	CQ523466	CQ523466 Sequence
1374	126	4.4	519	6	CQ522478	CQ522478 Sequence
1375	126	4.4	528	10	BC049628	BC049628 Mus muscu
c1376	126	4.4	644	9	HSN331225	HSN331225 Homo sapi
1377	126	4.4	1457	6	BD231695	BD231695 31 human
1378	126	4.4	1801	14	SCU78817	SCU78817 Saccharomyc
1379	126	4.4	2081	10	BC043712	BC043712 Mus muscu
1380	126	4.4	2108	5	BC084490	BC084490 Xenopus t
1381	126	4.4	2406	9	BC017107	BC017107 Homo sapi
1382	126	4.4	2642	5	BC068637	BC068637 Xenopus l
1383	126	4.4	2767	10	BC014695	BC014695 Mus muscu
1384	126	4.4	2841	10	BC045601	BC045601 Mus muscu
1385	125.8	4.4	300	6	BD213699	BD213699 Novel hum
1386	125.8	4.4	381	3	AF159974	AF159974 Buthus ma
1387	125.8	4.4	487	10	BC069220	BC069220 Mus muscu
1388	125.8	4.4	510	6	CQ526266	CQ526266 Sequence
1389	125.8	4.4	700	5	BC051617	BC051617 Dantio rer
1390	125.8	4.4	793	9	BC018189	BC018189 Homo sapi
1391	125.8	4.4	847	9	BC053571	BC053571 Homo sapi
1392	125.8	4.4	1319	9	BC003683	BC003683 Homo sapi
1393	125.8	4.4	1331	10	BC030915	BC030915 Mus muscu
1394	125.8	4.4	1650	9	AB047615	AB047615 Macaca fa
1395	125.8	4.4	1706	3	AK112205	AK112205 Ciona int
1396	125.8	4.4	1719	3	AK116650	AK116650 Ciona int
1397	125.8	4.4	2082	6	AR059958	AR059958 Sequence
1398	125.8	4.4	2190	9	BC063454	BC063454 Homo sapi
1399	125.8	4.4	3498	5	BC065688	BC065688 Dantio rer
c1400	125.8	4.4	17721	6	AX346631	AX346631 Dictyoste
c1401	125.8	4.4	151802	3	AC114263	AC114263 Dictyoste
1402	125.8	4.4	172105	2	AC021197	AC021197 Homo sapi
1403	125.6	4.4	360	6	CQ524586	CQ524586 Sequence
c1404	125.6	4.4	384	6	CQ395463	CQ395463 Sequence
c1405	125.6	4.4	384	6	CQ401799	CQ401799 Sequence
1406	125.6	4.4	1164	8	BT009497	BT009497 Triticum

1407	125.6	4.4	2223	5	BC067619	BC067619	Danio rer	1480	124.6	4.4	299	6	CQ0404070	CQ0404070	Sequence
1408	125.6	4.4	2735	9	BC046366	BC046366	Homo sapi	1481	124.6	4.4	503	6	CQ524887	CQ524887	Sequence
1409	125.6	4.4	8234	6	AX346551	AX346551	Sequence	1482	124.6	4.4	534	6	AX284254	AX284254	Sequence
1410	125.6	4.4	74119	2	AC036177	AC036177	Homo sapi	1483	124.6	4.4	743	10	BC034898	BC034898	Mus muscu
1411	125.6	4.4	114897	2	AP003624	AP003624	Oryza sat	1484	124.6	4.4	860	9	BC038839	BC038839	Homo sapi
1412	125.6	4.4	134867	2	AC013788	AC013788	Homo sapi	1485	124.6	4.4	1368	9	AB069989	AB069989	Macaca fa
1413	125.6	4.4	220752	2	AC129776	AC129776	Mus muscu	1486	124.6	4.4	1612	9	BC044235	BC044235	Homo sapi
1414	125.4	4.4	270	6	CQ655781	CQ655781	Sequence	1487	124.6	4.4	2173	5	BC068406	BC068406	Danio rer
1415	125.4	4.4	506	6	CQ518031	CQ518031	Sequence	1488	124.6	4.4	3914	9	HSB803724	HSB803724	Homo sapi
1416	125.4	4.4	791	5	BC077926	BC077926	Xenopus l	1489	124.6	4.4	8059	5	BC076779	BC076779	Xenopus l
1417	125.4	4.4	1894	9	AB063046	AB063046	Macaca fa	1490	124.6	4.4	12669	6	AX252150	AX252150	Sequence
1418	125.4	4.4	2430	10	BC067202	BC067202	Mus muscu	1491	124.6	4.4	12669	6	AX344518	AX344518	Sequence
1419	125.4	4.4	6251	10	BC050823	BC050823	Mus muscu	1492	124.6	4.4	12669	6	AX348921	AX348921	Sequence
1420	125.4	4.4	110000	2	AL954350.4	Continuation (5 of		1493	124.6	4.4	155316	2	AC114646	AC114646	Mus muscu
1421	125.4	4.4	202872	2	AC016160	AC016160	Homo sapi	1494	124.6	4.4	194180	2	AC069140	AC069140	Homo sapi
1422	125.4	4.4	234081	3	PFMALAP2	AL035475	Plasmodiu	1495	124.6	4.4	217621	2	BX901924	BX901924	Danio rer
1423	125.2	4.4	237	6	AX284920	AX284920	Sequence	1496	124.4	4.4	367	6	CQ417446	CQ417446	Sequence
1424	125.2	4.4	328	6	CQ524509	CQ524509	Sequence	1497	124.4	4.4	410	6	CQ522484	CQ522484	Sequence
1425	125.2	4.4	403	6	CQ527098	CQ527098	Sequence	1498	124.4	4.4	607	6	CQ526845	CQ526845	Sequence
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1428	125.2	4.4	472	6	CQ518059	CQ518059	Sequence								
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1431	125.2	4.4	1501	10	BC039998	BC039998	Mus muscu								
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1434	125.2	4.4	3997	6	AX086658	AX086658	Sequence								
1435	125.2	4.4	4498	10	BC075723	BC075723	Mus muscu								
1436	125.2	4.4	16167	6	AX281418	AX281418	Sequence								
1437	125.2	4.4	16167	6	AX345985	AX345985	Sequence								
1438	125.2	4.4	16167	6	AX348686	AX348686	Sequence								
1439	125.2	4.4	50978	2	AC084751	AC084751	Homo sapi								
1440	125.2	4.4	198907	2	AC109232	AC109232	Mus muscu								
1441	125.2	4.4	289973	2	AC135678	AC135678	Rattus no								
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1443	125	4.4	580	6	CQ526169	CQ526169	Sequence								
1444	125	4.4	622	6	CQ427774	CQ427774	Sequence								
1445	125	4.4	1092	10	BC005748	BC005748	Mus muscu								
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1449	125	4.4	1975	10	BC052682	BC052682	Mus muscu								
1450	125	4.4	2005	9	BC013372	BC013372	Homo sapi								
1451	125	4.4	2012	9	AY125488	AY125488	Homo sapi								
1452	125	4.4	2683	10	BC052924	BC052924	Mus muscu								
1453	125	4.4	2820	10	BC062390	BC062390	Rattus no								
1454	125	4.4	3983	9	HSB803572	HSB803572	Homo sapi								
1455	125	4.4	4083	10	BC075708	BC075708	Mus muscu								
1456	125	4.4	5325	9	HSB806205	HSB806205	Homo sapi								
1457	125	4.4	52359	2	AC010772	AC010772	Homo sapi								
1458	125	4.4	174384	2	AC009524	AC009524	Homo sapi								
1459	124.8	4.4	221	6	CQ685593	CQ685593	Sequence								
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1462	124.8	4.4	447	6	CQ526217	CQ526217	Sequence								
1463	124.8	4.4	726	9	HSB327951	AJ327951	Homo sapi								
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1465	124.8	4.4	1108	10	BC0332259	BC0332259	Mus muscu								
1466	124.8	4.4	1630	9	BC039130	BC039130	Homo sapi								
1467	124.8	4.4	1653	8	BT009403	BT009403	Triticum								
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1469	124.8	4.4	2196	9	HSB805743	HSB805743	Homo sapi								
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1472	124.8	4.4	3485	5	BC084302	BC084302	Xenopus l								
1473	124.8	4.4	3686	10	BC023773	BC023773	Mus muscu								
1474	124.8	4.4	4727	5	BC070018	BC070018	Danio rer								
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1476	124.6	4.4	268	6	CQ506876	CQ506876	Sequence								
1477	124.6	4.4	291	6	CQ398062	CQ398062	Sequence								
1478	124.6	4.4	291	6	CQ404353	CQ404353	Sequence								
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## ALIGNMENTS

LOCUS	2846 bp	DNA	linear	PAT 20-DEC-2002
RESULT 1	AR252533	Sequence 230 from patent US 6478825.		
DEFINITION	AR252533			
ACCESSION	AR252533			
VERSION	AR252533.1	GI:27300441		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 2846)			
AUTHORS	Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.			
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects			
JOURNAL	Patent: US 6478825-A 230 12-NOV-2002;			
FEATURES	Location/Qualifiers			
source	1..2846			
ORIGIN	/organism="unknown"			
	/mol_type="genomic DNA"			
Query Match	100.0%;	Score 2846;	DB 6;	Length 2846;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2846;	Conservative	0;	Mismatches	0;
			Indels	0;
Gaps	0;			
Qy	1	CGCTCGGCACACGCGCGCAAGGATGGAGCTGGGTTGCTGGAGCGCAGTTGGGGCTCAC	60	
Db	1	CGCTCGGCACACGCGCGCAAGGATGGAGCTGGGTTGCTGGAGCGCAGTTGGGGCTCAC	60	
Qy	61	TTTTTCTTCAGCTCCTTCTTCATCTCGTCTCTGCCAAGAGATACACAGTCATTAATGAAGC	120	
Db	61	TTTTTCTTCAGCTCCTTCTTCATCTCGTCTCTGCCAAGAGATACACAGTCATTAATGAAGC	120	
Qy	121	CTGCCCTGGAGCAGATGGATATATCATGTGTGGGAGTGTGTGAATATGATCAGATTGA	180	
Db	121	CTGCCCTGGAGCAGATGGATATATCATGTGTGGGAGTGTGTGAATATGATCAGATTGA	180	
Qy	181	GTGGCTGTGCCCCGGAAGAGGAGTGTGGGTTATACCATCCCTCTGCTGCAGGAATGA	240	
Db	181	GTGGCTGTGCCCCGGAAGAGGAGTGTGGGTTATACCATCCCTCTGCTGCAGGAATGA	240	
Qy	241	GGAGAAATGAGTGTGACTCTCGCTGATCCACCCAGGTTGTACCATCTTTGAAAACTCGAA	300	
Db	241	GGAGAAATGAGTGTGACTCTCGCTGATCCACCCAGGTTGTACCATCTTTGAAAACTCGAA	300	
Qy	301	GAGCTGCCGAAATGGCTCATGCGGGGGTACCTTGTGATGACTTCTATGTGAGGGGTTCTA	360	

Db 301 GAGCTGCCAAATGGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 360  
Qy 361 CTGTGCAGATGCCGAGCAGGCTGTGTAACGAGGAGACTGCGATGCGATGTGGCAGGTTCT 420  
Db 361 CTGTGCAGATGCCGAGCAGGCTGTGTAACGAGGAGACTGCGATGCGATGTGGCAGGTTCT 420  
Qy 421 GCGAGCCCCAAAGGGTCAAGATTTGTGTGAAAGCTATCCCTTAAATGCTCACTGTGAATG 480  
Db 421 GCGAGCCCCAAAGGGTCAAGATTTGTGTGAAAGCTATCCCTTAAATGCTCACTGTGAATG 480  
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[illegible]

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DEFINITION	Sequence 169 from Patent WO0168848.		
ACCESSION	AX376102		
VERSION	AX376102.1 GI:19170443		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0168848-A 169 20-SEP-2001; Genentech, Inc. (US)		
FEATURES	Location/Qualifiers		
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Query Match	100.0%; Score 2846; DB 6; Length 2846;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2846; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Qy	181	GTGCGTCTGCCCGGAAAGGAAGTCGTGGGTTATACCATCCCTTGGTCGAGGAATGA	240



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ACCESSION AX403343  
VERSION AX403343.1 GI:21436887  
KEYWORDS  
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REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,  
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,  
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,  
Paoni,N.F., Roy,M., Stewart,T.A., Tamas,D., Watanabe,C.K.,  
Williams,P., Wood,W.I. and Zhang,Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brugh,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
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Xie,M.H., Yanura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
JOURNAL 12975309  
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REFERENCE Clark,H.F.  
AUTHORS Direct Submission  
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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DEFINITION  
ACCESSION AL832391  
VERSION AL832391.1 GI:21732954  
KEYWORDS  
SOURCE Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Koshner, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.  
TITLE Direct Submission  
JOURNAL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFZp667H2312) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.  
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RESULT 7
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DEFINITION
Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD157134
VERSION     BD157134.1  GI:27862892
KEYWORDS   JP 2002191363-A/11977.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2784)
AUTHORS   Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
           Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE      Primer for synthesizing full-length cDNA and use thereof
JOURNAL   Patent: JP 2002191363-A 11977 09-JUL-2002;
           HELIX RESEARCH INSTITUTE
COMMENT    OS Homo sapiens (human)
           PN JP 2002191363-A/11977
           PD 09-JUL-2002
           PF 28-JUL-2000 JP 2000280990
           PI TOSHIO OTA, TAKAO ISOgai, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
           PI SAITO,
           PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
           PI KEIICHI NAGAI, TETSUJI OTSUKI
           PC
           C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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Qy      841 AAATC-----TCCT 849
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Qy      850 TGAAGAAAGAAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGG 909
Db      922 TGAAGAAAGAAACTGCTCAGACCCCTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGG 981
Qy      910 GGGCCCTGGCTTATCAACGAGCGCATGCTAAAAATGGCACCGCTGTGTCTTTCTTTTG 969
Db      982 GGGCCCTGGCTTATCAACGAGCGCATGCTAAAAATGGCACCGCTGTGTCTTTCTTTTG 1041
Qy      970 TAACAACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTCCAGCAGAGATGGAGAGTG 1029
Db      1042 TAACAACTCTTATGTTCTTAGTGGCAATGAGAAAGAACTTCCAGCAGAGATGGAGAGTG 1101
Qy      1030 GTTCAGGAAACAGCCCATCTGTCATAAAAGCCTGCCGAGAACCAAGAATTTTCAGACTGT 1089
Db      1102 GTTCAGGAAACAGCCCATCTGTCATAAAAGCCTGCCGAGAACCAAGAATTTTCAGACTGT 1161
Qy      1090 GAGAAGGAGAGTTCTTCCATGTCAGGTTCACTCAAGGGAGACACCATTAACACAGCTATA 1149
Db      1162 GAGAAGGAGAGTTCTTCCGATGTCAGTTTCAAGGGAGACACCATTAACACAGCTATA 1221
Qy      1150 CTCAGCGGCTTTCAGCAAGCAGAACTGCAGATGCCCTACCAAGAGCCAGCCCTTCC 1209
Db      1222 CTCAGCGGCTTTCAGCAAGCAGAAACTGCAGAGTCCCCCTACCAAGAGCCAGCCCTTCC 1281

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Query Match		92.6%;	Score 2636.8;	DB 6;	Length 2784;
Best Local Similarity		98.0%;	Pred. No. 0;		
Matches 2710;		Conservative	0;	Mismatches	2;
				Indels	52;
				Gaps	2;
Qy	1	CGCTGGGCAACGACCGCGGCAAGGATGAGCTGGGTTGCTGGACGACGTTGGGGCTCAC	60		
Db	22	CGCTGGGCAACGACCGCGGCAAGGATGAGCTGGGTTGCTGGACGACGTTGGGGCTCAC	81		
Qy	61	TTTTCTTACGCTCTTCTCATCTCGTCTTGTGCGGAGTGTGAGATGATGATGATGATGATG	120		
Db	82	TTTTCTTACGCTCTTCTCATCTCGTCTTGTGCGGAGTGTGAGATGATGATGATGATGATG	141		
Qy	121	CTGCCCCTGAGCAGAGTGAATATCATGTGTGCGGAGTGTGAGATGATGATGATGATGATG	180		
Db	142	CTGCCCCTGAGCAGAGTGAATATCATGTGTGCGGAGTGTGAGATGATGATGATGATGATG	201		
Qy	181	GTGCGTCTGCGCGGCAAGGAGGAGTGTGCGGTTATACATCCCTGTGTCAGGATGA	240		
Db	202	GTGCGTCTGCGCGGCAAGGAGGAGTGTGCGGTTATACATCCCTGTGTCAGGATGA	261		
Qy	241	GGAGATGATGTGACTCTGCTGCTGATCCACCCAGGTGTGACCATCTTTGAAATCTGCAA	300		
Db	262	GGAGATGATGTGACTCTGCTGCTGATCCACCCAGGTGTGACCATCTTTGAAATCTGCAA	321		
Qy	301	GAGCTGCCGAATGGCTCATGGGGGGTACCTTTGGATGACTTCTATGTGAAGGGGTTCTA	360		
Db	322	GAGCTGCCGAATGGCTCATGGGGGGTACCTTTGGATGACTTCTATGTGAAGGGGTTCTA	381		
Qy	361	CTGTGAGAGTGCAGAGCAGGTGTTACGAGAGAGCTGCATGCCGATGTGGCAGGTTCT	420		
Db	382	CTGTGAGAGTGCAGAGCAGGTGTTACGAGAGAGCTGCATGCCGATGTGGCAGGTTCT	441		
Qy	421	GGAGCCCCAAAGGGTCAAGATTTGTTGGAAGCTATCCCTAAATGCTCACTGTGAATG	480		
Db	442	GGAGCCCCAAAGGGTCAAGATTTGTTGGAAGCTATCCCTAAATGCTCACTGTGAATG	501		
Qy	481	GACATTTACGTCTAAACCTGGGTTGTCTATCCAACTAAGATTTGCTAGTCTGGA	540		
Db	502	GACATTTACGTCTAAACCTGGGTTGTCTATCCAACTAAGATTTGCTAGTCTGGA	561		
Qy	541	GTGTTGACATGTCAGTATGACTATGTGTGAGGTTGCTGATGGAGACAACCGGATGG	600		
Db	562	GTGTTGACATGTCAGTATGACTATGTGTGAGGTTGCTGATGGAGACAACCGGATGG	621		
Qy	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGCCAGCTCTATCCAGAGCATAGGATC	660		
Db	622	CCAGATCATCAAGCGTGTCTGTGGCAACGAGGGCCAGCTCTATCCAGAGCATAGGATC	681		
Qy	661	CTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTTCCATGCCAT	720		
Db	682	CTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAGAAATTTGACGGTTTCCATGCCAT	741		
Qy	721	TTATGAGGAGATCAGCATGTCTCTCATCCCTTGTGTTCCATGAGCGACGTCGTCTCT	780		
Db	742	TTATGAGGAGATCAGCATGTCTCTCATCCCTTGTGTTCCATGAGCGACGTCGTCTCT	801		
Qy	781	TGACAGGCTGGATCTTCAAGTGTGCTGCTGTGGCAGGCTATCTGGCAGCGCTGTCGA	840		
Db	802	TGACAGGCTGGATCTTCAAGTGTGCTGCTGTGGCAGGCTATCTGGCAGCGCTGTCGA	861		
Qy	841	AAATC-----TCCT	849		
Db	862	AAATCTTTGGAGGCTGGGAAGTCCAAGATCAAGCGTCCAGAGATTTCAATGCTGCTCT	921		
Qy	850	TGAAGAAAGAACTGCTCAGACCTTGGGGCCAGTCAATGGGTACCAAGAAATACAGG	909		
Db	922	TGAAGAAAGAACTGCTCAGACCTTGGGGCCAGTCAATGGGTACCAAGAAATACAGG	981		
Qy	910	GGGCTTGGGCTTATCAACGGAGCCATGCTAAATTTGCAACGGTGTCTTTCTTTG	969		
Db	982	GGGCTTGGGCTTATCAACGGAGCCATGCTAAATTTGCAACGGTGTCTTTCTTTG	1041		

Qy	970	TAAACAATCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTCCAGCAGAAATGGAGAGTG	1029
Db	1042	TAAACAATCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTCCAGCAGAAATGGAGAGTG	1101
Qy	1030	GTACGGGAAACAGCCCATCTGCATAAAAGCCTGCCAGAAACCAAGATTTTCAGACCTGGT	1089
Db	1102	GTACGGGAAACAGCCCATCTGCATAAAAGCCTGCCAGAAACCAAGATTTTCAGACCTGGT	1161
Qy	1090	GAGAAGGAGAGTTCTTTCGATGACAGTTTCAGTCAAGGGAGACACCAATTAACACAGCTATA	1149
Db	1162	GAGAAGGAGAGTTCTTTCGATGACAGTTTCAGTCAAGGGAGACACCAATTAACACAGCTATA	1221
Qy	1150	CTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGCCCTTACCAAGAACCGACCCCTTCC	1209
Db	1222	CTCAGCGGCTTTCAGCAAGCAGAACTGCAGAGTGCCCTTACCAAGAACCGACCCCTTCC	1281
Qy	1210	CTTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGTCCAGTATGAGTGCAT	1269
Db	1282	CTTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGTCCAGTATGAGTGCAT	1341
Qy	1270	CTCACCCCTTTACCCGCGCTTGGGAGCAGCAGAGGAGCAATGCTCTGAGGACTGGGAAGTG	1329
Db	1342	CTCACCCCTTTACCCGCGCTTGGGAGCAGCAGAGGAGCAATGCTCTGAGGACTGGGAAGTG	1401
Qy	1330	GAGTGGGCGGCAACCATCTGTCATCCCTATCTGCGGGGAAAATTTGAGAAATCATCTGCTCC	1389
Db	1402	GAGTGGGCGGCAACCATCTGTCATCCCTATCTGCGGGGAAAATTTGAGAAATCATCTGCTCC	1461
Qy	1390	AAAGACCCAAAGGTTGCGCTGGCGGAGCGTGGCTTCTAGTCTGCGAGCGTCCCTGCTGAA	1449
Db	1462	AAAGACCCAAAGGTTGCGCTGGCGGAGCGTGGCTTCTAGTCTGCGAGCGTCCCTGCTGAA	1521
Qy	1450	GCATGACCGGAGCCTTACCAAGGGAGCGTGGTTCCTAGTCTGCGAGCGTCCCTGCTGAA	1509
Db	1522	GCATGACCGGAGCCTTACCAAGGGAGCGTGGTTCCTAGTCTGCGAGCGTCCCTGCTGAA	1581
Qy	1510	TGAGCGCATGTGTGGTGGCTGGCCCATCTGTGTTACTGACTGCGGGGAGGTCACCATGAT	1569
Db	1582	TGAGCGCATGTGTGGTGGCTGGCCCATCTGTGTTACTGACTGCGGGGAGGTCACCATGAT	1641
Qy	1570	CAAGACAGCAGACCTGAAAGTTGTTTGGGAAAATTTCTACCGGGAATGACCGGATGA	1629
Db	1642	CAAGACAGCAGACCTGAAAGTTGTTTGGGAAAATTTCTACCGGGAATGACCGGATGA	1701
Qy	1630	GAAAGCCATCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCAATATGACCCCAT	1689
Db	1702	GAAAGCCATCAGAGCCTACAGATTTCTGCTATCATTTCTGCAATCCCAATATGACCCCAT	1761
Qy	1690	CCTGCTGATGTGACATCGCCCATCTGAAAGCTCTTAGAAGGCGCGTATCAGCAACCG	1749
Db	1762	CCTGCTGATGTGACATCGCCCATCTGAAAGCTCTTAGAAGGCGCGTATCAGCAACCG	1821
Qy	1750	AGTCAGGCCCATCTGCTGCTGCGAGTCCGAGTCTGAGCATCTCAGCATCTCCTCCAGGATCCCA	1809
Db	1822	AGTCAGGCCCATCTGCTGCTGCGAGTCCGAGTCTGAGCATCTCAGCATCTCCTCCAGGATCCCA	1881
Qy	1810	CATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGCTGAGGAGCCCTTGGCTTCAAGAACGA	1869
Db	1882	CATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGCTGAGGAGCCCTTGGCTTCAAGAACGA	1941
Qy	1870	CACACTGCGCTCTGGGGTGGTCACTGTGTGGTGGACTCGCTGTGTGTGAGGAGCAGCATGA	1929
Db	1942	CACACTGCGCTCTGGGGTGGTCACTGTGTGGTGGACTCGCTGTGTGTGAGGAGCAGCATGA	2001
Qy	1930	GGACCATGGCATCCAGTGAGTGTCACTGATTAACATGTTCTGTGCCAGCTGGGAAACCCAC	1989
Db	2002	GGACCATGGCATCCAGTGAGTGTCACTGATTAACATGTTCTGTGCCAGCTGGGAAACCCAC	2061
Qy	1990	TGCCCTTCTGTGATATCTGCACTGACAGACGAGGAGCATCGCGGCTGTGCTCTTCCCGGG	2049
Db	2062	TGCCCTTCTGTGATATCTGCACTGACAGACGAGGAGCATCGCGGCTGTGCTCTTCCCGGG	2121
Qy	2050	ACGAGCATCTCTGAGCCACGCTGGCATCTGTATGGAGCTGGGTGAGCTGATGATTA	2109

Db 2122 ACAGCATCTCTGAGCCACGCTGGCATCTGATGGAGCTGGTGCAGTGGAGCTATGATAA 2181  
Qy 2110 AACATGACGACAGGCTCTCACTGCTTACCAAGGTGCTGCTTTAAAGACTGGAT 2169  
Db 2182 AACATGACGACAGGCTCTCACTGCTTACCAAGGTGCTGCTTTAAAGACTGGAT 2241  
Qy 2170 TGAAGAATAATGAATGAACATGCTCATGCACTCTTGGAAAGTGTTCGTATATACC 2229  
Db 2242 TGAAGAATAATGAATGAACATGCTCATGCACTCTTGGAAAGTGTTCGTATATACC 2301  
Qy 2230 GTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGCCCTGAAGTGTGATTTGGCCCTGTGAA 2289  
Db 2302 GTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGCCCTGAAGTGTGATTTGGCCCTGTGAA 2361  
Qy 2290 CTTGGCTGTGCCAGGCTCTTGACCTTCAGGGAACAACTCAGTGAAGGTTGATGACCT 2349  
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Qy 2350 CCAATGCTGTAGGTGATGTCGGCTTCACTACTAGGACAGCAATTTGAAGATGCCAGG 2409  
Db 2422 CCAATGCTGTAGGTGATGTCGGCTTCACTACTAGGACAGCAATTTGAAGATGCCAGG 2481  
Qy 2410 GCTTGCACGAAGTAAAGTTCTTCAAGAGAACCATATACAAACCTCTCCACTCCACTGA 2469  
Db 2482 GCTTGCACGAAGTAAAGTTCTTCAAGAGAACCATATACAAACCTCTCCACTCCACTGA 2541  
Qy 2470 CTTGGTGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACAGGGAAGATC 2529  
Db 2542 CTTGGTGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGC-TGACCAAGGGAAGATC 2600  
Qy 2530 TGGGCTTCATAGAGCCCTTTTGAAGCTCTCAAGTCTAGAGAGCTGCTGTGGACAGC 2589  
Db 2601 TGGGCTTCATAGAGCCCTTTTGAAGCTCTCAAGTCTAGAGAGCTGCTGTGGACAGC 2660  
Qy 2590 CCAGGACGACAGCTGGGATGTGTGATGCTTTGTGTACATGCCACAGTACAGTCT 2649  
Db 2661 CCAGGACGACAGCTGGGATGTGTGATGCTTTGTGTACATGCCACAGTACAGTCT 2720  
Qy 2650 GGTCTCTTCTTCCCATCTCTGTACACATTTAAATAAGGTTGGCTTCTGAA 2709  
Db 2721 GGTCTCTTCTTCCCATCTCTGTACACATTTAAATAAGGTTGGCTTCTGAA 2780  
Qy 2710 CTAC 2713  
Db 2781 CTAC 2784

RESULT 9  
BD012234  
LOCUS  
DEFINITION A novel gene encoding a serine protease-like protein.  
ACCESSION BD012234  
VERSION BD012234.1 GI:22092423  
KEYWORDS WO 0109349-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2784)  
Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto.J.,  
Ishii.S., Sugiyama.T., Wakamatsu.A., Nagai.K., Otsuki.T., Yano.K.,  
Murakami.K., Kanazaki.K., Inoue.Y., Hashimoto.E. and Kashima.A.  
A novel gene encoding a serine protease-like protein  
Parent: WO 0109349-A 1 08-FEB-2001;  
HELIIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,  
KOJI HAYASHI, KAORU SAITO, JUNICHI YAMAMOTO, SHIZUKO ISHII, OMOYASU  
SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO,  
KOJI MURAKAMI, KOJI KANZAKI, YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO  
KASHIMA  
OS Homo sapiens (human)  
PN WO 0109349-A/1  
PD 08-FEB-2001

PF 28-JUL-2000 WO 2000JP005062  
PR 29-JUL-1999 JP 99P 248036.27-AUG-1999 JP 99P 300253 PR  
11-JAN-2000 JP 00P 118776.02-MAY-2000 JP 00P 183767 PR  
18-OCT-1999 US 60/159590,17-FEB-2000 US 60/183322 PI TOSHIO  
OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, PI KAORU SAITO,  
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
PI KEIICHI NAGAI, TETSUJI OTSUKI, KAZUHIRO YANO, KOJI MURAKAMI, PI  
KOJI KANZAKI,  
PI YOSHIHISA INOUE, EMI HASHIMOTO, AKIKO KASHIMA  
PC C12N15/57, C12N9/64, C12N15/63, C12N5/06, C07K16/40, C12Q1/68, PC  
G01N33/573,  
PC A61K38/48, A61K31/7052, A61K48/00//C12P21/08, (C12N9/64, C12R1:91)  
CC  
FH Key Location/Qualifiers  
FT CDS (47)..(2257).  
FEATURES  
source  
ORIGIN  
Query Match 92.6%; Score 2636.8; DB 6; Length 2784;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 2710; Conservative 0; Mismatches 2; Indels 52; Gaps 2;  
Qy 1 CGCTGGGACACAGCGCGCAAGGATGGAGCTGGGTTGCTGGACGCGAGTTGGGGCTCAC 60  
Db 22 CGCTGGGACACAGCGCGCGCAAGGATGGAGCTGGGTTGCTGGACGCGAGTTGGGGCTCAC 81  
Qy 61 TTTTCTTCAGCTCTCTCATCT 120  
Db 82 TTTTCTTCAGCTCTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 141  
Qy 121 CTGCTCTGGAGAGAGTGGAAATATCATGTGTCTGGAGTGTCTGTGAATATGATGATGATGA 180  
Db 142 CTGCTCTGGAGAGAGTGGAAATATCATGTGTCTGGAGTGTCTGTGAATATGATGATGATGA 201  
Qy 181 GTGGCTCTGCCCGGAAAGAGGAGTGTGGGTTTATACCATCCCTCTCTCGCAGCAATGA 240  
Db 202 GTGGCTCTGCCCGGAAAGAGGAGTGTGGGTTTATACCATCCCTCTCTCGCAGCAATGA 261  
Qy 241 GGAGAAATGAGTGTGACTCTCTCTCTGATCCACCCAGGTTGTACCATCTTTTGAAGAACTGCAA 300  
Db 262 GGAGAAATGAGTGTGACTCTCTCTGATCCACCCAGGTTGTACCATCTTTTGAAGAACTGCAA 321  
Qy 301 GAGCTGCCGAAATGGCTCATGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTA 360  
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Qy 361 CTGTGACAGTGGCGAGCAGGCTGTGTCGGAGGAGACTGCATGCGATGTGGCAGGTTCT 420  
Db 382 CTGTGACAGTGGCGAGCAGGCTGTGTCGGAGGAGACTGCATGCGATGTGGCAGGTTCT 441  
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Qy 481 GACCAATTCATGCTAAACCTGGGTTTGTTCATCCAACTAAGATTTGTGATGATGATGATGATG 540  
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Qy 541 GTTTGACTACATGTGCCAGTATGATGTTGAGGTTGCTGTATGAGACAAACCGGATGG 600  
Db 562 GTTTGACTACATGTGCCAGTATGATGTTGAGGTTGCTGTATGAGACAAACCGGATGG 621  
Qy 601 CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCGAGCTCCTATCCAGAGCATAGGATC 660  
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Qy 661 CTCACTCCAGCTCTCTTCCACTCGATGGCTCCAGAAATTTTGAAGGTTTCCATGCCAT 720  
Db 682 CTCACTCCAGCTCTCTTCCACTCGATGGCTCCAGAAATTTTGAAGGTTTCCATGCCAT 741

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Db 742 TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACCGCACGTGCGTCT 801  
QY 781 TGACAGGCTGGATCTTACAGTGTGCTGCTTGGCAGGCTATCTAGGCGAGCGCTGGA 840  
Db 802 TGACAGGCTGGACCTTACAGTGTGCTGCTTGGCAGGCTATCTAGGCGAGCGCTGGA 861  
QY 841 AAATC-----TCCT 849  
Db 862 AAATCTTCTGGAGGTGGAGTCCAAGATCAAGCGCTCAGAAGATTCAITGTCTGTCT 921  
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Db 922 TGAAGAAAGAAATGCTCTCAGACCTTGGGGGCCAGTCAATGGGTACCAAGAAATAACAGG 981  
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Db 982 GGGCCCTGGCTTATCAAGGACGCGCATCTTAAATTTGGCACCGTGGTCTTCTTTTGG 1041  
QY 970 TAAACATCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGCCAGCAGAAATGGAGAGTG 1029  
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QY 1030 CTCAGGGAAACAGCCCATCTGCATAAAAAGCCTGCCGAGAACCAAGATTTTTCAGACCTGGT 1089  
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QY 1090 GAGAAGGAGAGTTCTTCCGATGTCAGGTTTCAGTCAAGGAGAGACACCATTACACCGACTATA 1149  
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QY 1690 CCTGCTTATGCTGACATCGGCATCTCAAGCTCTTACAGAGGCGCGTATCAGACCCG 1749  
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QY 1750 AGTCAGGCCCATCTGCTCGCTGCGCATGCGGATCTCAGACATCTTCTTCCAGGAGTCCCA 1809  
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Db 1882 CATCACTGTGCTGCTGGAATGCTTGGCAGAGCTGAGGAGCCCTGCTTCAAGAACGA 1941  
QY 1870 CACATGCGCTCTGCGGGTGTGCTGCTGTGTGGAATCTCGCTGTGTGAGGAGCAGCATGA 1929  
Db 1942 CACATGCGCTCTGCGGGTGTGCTGCTGTGTGGAATCTCGCTGTGTGAGGAGCAGCATGA 2001  
QY 1930 GGAACATGGAATCCAGTGAAGTGTCACTGATPAAATGTTTCTGTCAGCTGGGAACCCAC 1989  
Db 2002 GGACCATGGCATCCAGTGAAGTGTCACTGATPAAATGTTTCTGTCAGCTGGGAACCCAC 2061  
QY 1990 TGCCCTTCTGATATCTGCACCTGCAGAGCAGGAGGATCCGCGTGTGCTTCCCGGG 2049  
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QY 2050 ACAGCATCTCTCTGAGCCACGCTGCGCATCTCATGGGACTGTGTGAGCTGGAGCTATGATAA 2109  
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QY 2110 AACATGAGCAGCAGGCTCTCAGCTGCTTCAACAGGTGCTGCTTTTAAAGACTGGAT 2169  
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QY 2350 CCATTTGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2409  
Db 2422 CCATTTGCTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2481  
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QY 2470 CTTGGTGTCTTCCCACTTTTCAAGTATATACGAATGCCATCAGCTTGACCGGGAAGATC 2529  
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QY 2650 GGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAGGTTGGCTTCTGAA 2709  
Db 2721 GGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAGGTTGGCTTCTGAA 2780  
QY 2710 CTAC 2713  
Db 2781 CTAC 2784

RESULT 10  
AK027841  
LOCUS  
DEFINITION Homo sapiens cDNA FLJ14935 fis, clone PLACB100992, weakly similar

2784 bp mRNA linear PRI 30-JAN-2004  
AK027841







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VERSION AX704692.1 GI:29561394
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Deleane, A.M., Gandhi, A.R., Hafalia, A.J., Lu, D.A., Patterson, C.,
Tribouley, C.M., Das, D., Kallik, D.A., Nguyen, D.B., Lee, E.A.,
Khan, F.A., Yue, H., Au-Yang, J., Griffin, J.A., Policky, J.L.,
Ramkumar, J., Yang, J., Thangavelu, K., Ding, L., Kearney, L.,
Baughn, M.R., Borowsky, M.L., Sanjanwalla, M.S., Yao, M.G., Burford, N.,
Walia, N.K., Lal, P., Lee, S., Todd, S., Lo, T.P., Tang, Y.T.,
Elliot, V.S., Azimzai, Y. and Lu, Y.
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JOURNAL Patent: WO 0208396-A 38 31-JAN-2002;
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/note="Incyte ID No: 7479181CBI"
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ACCESSION AR263926

VERSION AR263926.1 GI:28075930  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2886)  
AUTHORS Robison, K.E.  
TITLE Protease homologs  
JOURNAL Patent: US 6331427-A 104 18-DBC-2001;  
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BC038457

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Homo sapiens regeneration associated muscle protease, mRNA (CDNA  
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ACCESSION BC038457  
VERSION  
KEYWORDS BC038457.1 GI:23620401

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 2350)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Alschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Wotley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL PUBMED 12477932

2 (bases 1 to 2350)  
 Strausberg, R.

Direct Submission

Submitted (04-OCT-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisac.nih.gov/>

Contact: [nisc.mgc@nigri.nih.gov](mailto:nisc.mgc@nigri.nih.gov)

Akhter, N., Ayle, K., Beckstrom-Steenberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,  
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 McDowell, J., Pearson, R., Scantripop, S., Thomas, P.J., Touchman, J.W.,  
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 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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VERSION AX133839.1 GI:14139791  
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AUTHORS Shimkets, R.A., Fernandes, E., Herrmann, J.L., Liu, X., Yang, M. and Boldog, F.L.  
TITLE Secreted human proteins, polynucleotides encoding them and methods of using the same  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AW918019	EST349323
CN296855	170004250
BU253929	603747035
BE048236	tz48g03.y
BM254217	515580.MA
AI990243	w620c03.x
AI088620	qb14f05.x
AW028008	wv61b05.x
AA043793	zk59g10.x
BP312143	BP312143
AI823626	wi8e01.x
AU067539	AU067539
AI432522	th38b12.x
BP464936	BP464936
BM106593	510508.MA
BE231795	136621.MA
BF197805	7p92f09.x
BI346989	376376.MA
AA708420	2157a04.x
AI624892	t672f03.x
AA430705	zw52f06.x
BP216550	BP216550
CB712029	AMGNNUC.N
BS683792	183732.MA
AW206753	UI-H-B11-
AA812954	ai77a01.s
BY745962	BY745962
CK522160	mi01d03.y
BM929450	UI-E-EJ1-
BU742789	UI-E-EJ1-
BI526460	602925034
BU383403	603582549
AW484384	60496.MAR
AW511691	xu51b03.x
AI057206	oz11a09.x
BX515589	BX515589
AA444868	cr48b11.x
BM088773	ve75f07.x
CD707019	502313.MA
EST33546	EST33546
BE653376	UI-M-ALI-
CN334668	170005999

C 98	339.2	11.9	356	7	N94393	N94393 zb76e06.s1	171	186	6.5	188	6	C21546	C21546 HUMS001054
C 99	338	11.9	359	2	AW340199	AW340199 hc9ad04.x	C 172	185.8	6.5	731	9	AG511653	AG511653 Mus muscu
C 100	337.8	11.9	521	2	BE910833	BE910833 601661905	C 173	185	6.5	188	5	BO694586	BO694586 1000729 H
C 101	337	11.8	337	1	AA433935	AA433935 zw52f05.s	C 174	184.4	6.5	438	1	AI972676	AI972676 wr41b06.x
C 102	335.2	11.8	458	1	AI549757	AI549757 ve5f07.y	C 175	181.8	6.4	539	9	CG991118	CG991118 CH240_449
C 103	329.4	11.6	338	1	AA375185	AA375185 EST87423	C 176	181.8	6.4	633	5	BU252479	BU252479 603746867
C 104	329	11.6	373	1	AA126930	AA126930 z123a01.r	C 177	177	6.2	185	2	BF366351	BF366351 IL2-NT009
C 105	327.4	11.5	456	7	C0260289	C0260289 4131981.B	C 178	175.2	6.2	399	1	AJ696577	AJ696577 AJ696577
C 106	326.8	11.5	330	1	AI583699	AI583699 tt01h09.x	C 179	175.2	6.2	776	9	CC530365	CC530365 CH240_406
C 107	326.6	11.5	320	1	AI536361	AI536361 ma97e11.y	C 180	173.4	6.1	409	5	BY264071	BY264071 BY264071
C 108	325	11.4	325	1	AI420902	AI420902 tf03g11.x	C 181	172.4	6.1	270	6	CD371468	CD371468 UI-R-DX0-
C 109	319.8	11.2	410	5	BA473159	BA473159 DKF2p686f1	C 182	172	6.0	445	5	BY289536	BY289536 BY289536
C 110	319.8	11.2	419	4	BM484683	BM484683 538615.MA	C 183	171	6.0	611	5	BU477941	BU477941 603847283
C 111	316.4	11.1	422	2	AW3223842	AW3223842 uo77d04.y	C 184	170.6	6.0	389	4	BM876043	BM876043 if86h06.y
C 112	315	11.1	315	1	AI579963	AI579963 tq35905.x	C 185	168.6	5.9	714	7	CF525168	CF525168 AGENCOURT
C 113	314.8	11.1	378	2	AW426139	AW426139 59708.MAR	C 186	166.6	5.9	688	8	AZ794032	AZ794032 2M0047D11
C 114	314	11.0	817	7	CK775452	CK775452 966578.MA	C 187	163	5.7	163	7	CN334667	CN334667 170005319
C 115	312.4	11.0	411	7	CN296856	CN296856 170005326	C 188	162.6	5.7	752	5	EX879710	EX879710 BX067747
C 116	311	10.9	664	7	CN059249	CN059249 Salamande	C 189	161.4	5.7	902	1	AU067747	AU067747 AU067747
C 117	298.2	10.5	489	5	BY243636	BY243636	C 190	159.2	5.6	620	6	BY761773	BY761773 BY761773
C 118	290.8	10.2	310	7	CN122781	CN122781 TgESTzyl2	C 191	157.6	5.5	256	6	CD371132	CD371132 UI-R-DY0-
C 119	284.2	10.0	814	5	BM090462	BM090462 505887.MA	C 192	157	5.5	569	7	C0631899	C0631899 DG9-66k1
C 120	284	10.0	378	4	BM090462	BM090462 505887.MA	C 193	157	5.5	569	7	C0631899	C0631899 DG9-66k1
C 121	283.4	10.0	756	7	CN334669	CN334669 170006000	C 194	156.2	5.5	352	5	BY929055	BY929055 AGENCOURT
C 122	280.4	9.9	482	5	BY243643	BY243643	C 195	155.2	5.5	352	5	BY310228	BY310228 BY310228
C 123	275	9.7	482	4	BM105355	BM105355 508793.MA	C 196	152.4	5.4	241	5	BU788909	BU788909 il192e10.y
C 124	268.6	9.4	395	2	AW416537	AW416537 51984.MAR	C 197	151.4	5.3	949	5	BU938597	BU938597 AGENCOURT
C 125	268	9.4	385	5	BY275139	BY275139	C 198	151.2	5.3	489	2	AW528858	AW528858 UI-R-BT1-
C 126	267.6	9.4	504	7	CN061039	CN061039 Ag20_p42	C 199	151	5.3	975	6	C0517925	C0517925 AGENCOURT
C 127	267	9.4	504	1	AA199196	AA199196 mv43503.f	C 200	150.6	5.3	304	6	CB341161	CB341161 CA23E1011
C 128	265	9.3	435	6	CB793009	CB793009 AMGNNUC.N	C 201	150.6	5.3	995	5	BU559882	BU559882 AGENCOURT
C 129	264.4	9.3	343	2	AW307893	AW307893 1225.MARC	C 202	149.2	5.2	935	5	BU842252	BU842252 AGENCOURT
C 130	263.6	9.3	381	7	CR772910	CR772910 DKF2p468N	C 203	148.8	5.2	375	6	C0888705	C0888705 if04e03.b
C 131	259.6	9.1	465	5	BY244862	BY244862	C 204	148.8	5.2	412	7	CR765787	CR765787 DKF2p468I
C 132	258	9.1	959	1	AU051031	AU051031	C 205	148.8	5.2	615	7	CR958946	CR958946 4093793.B
C 133	257	9.0	274	1	AI824672	AI824672 wc48c08.x	C 206	148.8	5.2	1067	5	BU942149	BU942149 AGENCOURT
C 134	252.2	8.9	371	5	BY131558	BY131558	C 207	148.8	5.2	748	5	CF782696	CF782696 AGENCOURT
C 135	252	8.9	258	1	AL701986	AL701986 DKF2p686N	C 208	148.4	5.2	327	6	C0739971	C0739971 taa22h05.
C 136	250.4	8.8	662	5	BU218794	BU218794	C 209	148.2	5.2	901	5	BU531218	BU531218 AGENCOURT
C 137	249.6	8.8	421	5	BY295210	BY295210	C 210	148	5.2	345	4	BM534831	BM534831 fx71h06.y
C 138	247.4	8.7	325	2	AW957673	AW957673 EST369743	C 211	148	5.2	374	4	BM154585	BM154585 fv86h02.y
C 139	243.4	8.6	416	6	CB768218	CB768218 AMGNNUC.N	C 212	148	5.2	478	7	CO722515	CO722515 Mdf3017c
C 140	241	8.5	333	7	TS2085	TS2085 yb10g01.r1	C 213	148	5.2	886	5	BU555623	BU555623 AGENCOURT
C 141	240.8	8.5	410	2	BF920134	BF920134 MR1-NT017	C 214	147.8	5.2	642	9	AG144714	AG144714 Pan trogl
C 142	237.8	8.4	416	5	BY238364	BY238364	C 215	147.6	5.2	339	1	AL731319	AL731319 AGENCOURT
C 143	237	8.3	237	1	AA989716	AA989716 am65h09.s	C 216	147.6	5.2	857	5	BU534369	BU534369 AGENCOURT
C 144	234.6	8.2	425	5	BY266233	BY266233	C 217	147.4	5.2	354	4	BM154696	BM154696 fv86c03.y
C 145	234	8.2	494	2	BE374037	BE374037 601228074	C 218	147.4	5.2	356	4	BM155084	BM155084 fv93c11.y
C 146	232.2	8.2	907	5	BU358450	BU358450 603477265	C 219	147.2	5.2	305	6	CA391105	CA391105 cs11e08.y
C 147	232	8.2	651	5	BO205135	BO205135 UI-R-D21-	C 220	147.2	5.2	406	5	BO526114	BO526114 NISC no14
C 148	230.6	8.1	427	5	BY273129	BY273129	C 221	147.2	5.2	479	7	CN833789	CN833789 AGENCOURT
C 149	230.2	8.1	414	5	BY282746	BY282746	C 222	147	5.2	273	7	CO416891	CO416891 Mdf3011i
C 150	229.8	8.1	404	5	BY271161	BY271161	C 223	147	5.2	454	7	CF315576	CF315576 HD-04-12
C 151	228.8	8.0	708	7	CO039157	CO039157 UI-M-AL1-	C 224	147	5.2	829	6	CD357006	CD357006 AGENCOURT
C 152	226.4	8.0	643	8	BZ245624	BZ245624 CH230-314	C 225	147	5.2	5949	3	HSB804512	HSB804512 Homo sap1
C 153	224.6	7.9	506	1	AA266124	AA266124 mz49a06.r	C 226	146.8	5.2	257	5	BX476287	BX476287 DKF2p686F
C 154	221.8	7.8	348	7	R47049	R47049 Y436 Rat in	C 227	146.8	5.2	270	4	CB696724	CB696724 BJ696724
C 155	221.2	7.8	808	5	BU359706	BU359706 603478496	C 228	146.8	5.2	282	6	CD641456	CD641456 AGENCOURT
C 156	217.2	7.6	386	2	BF451877	BF451877 uz80g03.y	C 229	146.8	5.2	408	7	CR770942	CR770942 DKF2p469G
C 157	215.6	7.6	425	5	BY295062	BY295062	C 230	146.6	5.2	255	4	CB879342	CB879342 lb62905.y
C 158	214.4	7.5	791	5	BU316123	BU316123 603850187	C 231	146.6	5.2	447	6	CR723709	CR723709 UI-M-GK0-
C 159	213.6	7.5	369	1	AA833210	AA833210 ud03b01.r	C 232	146.4	5.2	509	6	CB080062	CB080062 hp80f10.b
C 160	212.8	7.5	410	5	BY287911	BY287911	C 233	146.4	5.1	340	1	A1436456	A1436456 ti09c12.x
C 161	211	7.4	297	2	AW483167	AW483167 52006.MAR	C 234	146.4	5.1	395	6	CB044960	CB044960 NISC gc07
C 162	205.6	7.2	327	2	AW353000	AW353000 35212.MAR	C 235	146.4	5.1	573	5	BQ395751	BQ395751 NISC_1916
C 163	204.4	7.2	262	2	AW431829	AW431829 73099.MAR	C 236	146.4	5.1	1130	4	BM480137	BM480137 AGENCOURT
C 164	198.2	7.0	427	5	BY265763	BY265763	C 237	146.2	5.1	302	5	BU760983	BU760983 sas61c10.
C 165	196	6.9	749	5	BU298865	BU298865 603736330	C 238	146.2	5.1	871	5	BU587772	BU587772 AGENCOURT
C 166	195.8	6.9	423	5	BY259943	BY259943	C 239	146.2	5.1	992	7	CK798269	CK798269 Drosophil
C 167	192	6.7	358	5	BY128083	BY128083	C 240	146.2	5.1	974	9	CNS001TT	CNS001TT
C 168	189.6	6.7	359	6	BY783505	BY783505	C 241	146	5.1	390	6	CA379181	CA379181 558209.NC
C 169	188.6	6.6	359	5	BY341239	BY341239	C 242	146	5.1	415	7	CF546043	CF546043 lad89c05-
C 170	186.8	6.6	357	5	BY339892	BY339892	C 243	146	5.1	1000	5	BQ721431	BQ721431

244	145.8	5.1	313	6	CB709542	CB709542	AMGNNUC.N	1066	4	BM802531	BM802531	AGENCOURT
245	145.8	5.1	393	5	BX507033	BX507033	DKF2p779B	1334	4	BM555708	BM555708	AGENCOURT
246	145.8	5.1	919	5	BX529432	BX529432	AGENCOURT	3028	3	HSM801560	HSM801560	Homo sapi
247	145.6	5.1	316	5	BQ523462	BQ523462	NISC n122	182	6	CB101650	CB101650	Y
248	145.6	5.1	320	1	AL706784	AL706784	DKF2p686F	222	1	AL696218	AL696218	Y
249	145.6	5.1	332	7	CO185234	CO185234	EC29979.5	272	5	BX507023	BX507023	DKF2p779A
250	145.6	5.1	386	6	CB044394	CB044394	NISC_9C04	283	5	BX644833	BX644833	DKF2p781M
251	145.6	5.1	450	7	CR763214	CR763214	DKF2p470M	340	5	BM155408	BM155408	fwa4e06.Y
252	145.6	5.1	409	6	CB094467	CB094467	h270d02.b	378	5	BU763909	BU763909	saa849f12.Y
253	145.6	5.1	694	5	BQ391639	BQ391639	NISC mg19	459	6	CA356573	CA356573	628793.NC
254	145.6	5.1	785	5	BU842680	BU842680	AGENCOURT	459	6	CB523798	CB523798	UI-M-GK0-
255	145.6	5.1	1200	5	BQ39624	BQ39624	AGENCOURT	462	6	CB410573	CB410573	NISC_ncl12
256	145.4	5.1	314	2	BE047863	BE047863	cz43c10.Y	497	5	BQ522457	BQ522457	NISC_ncl16
257	145.4	5.1	318	7	CF621703	CF621703	lae5a08.	569	5	BQ521934	BQ521934	NISC_nl13
258	145.4	5.1	387	5	BX552476	BX552476	Y	627	5	BQ522332	BQ522332	NISC_nl16
259	145.4	5.1	439	6	CB945953	CB945953	AGENCOURT	683	1	AV682672	AV682672	AV682672
260	145.4	5.1	487	6	CD238190	CD238190	FNPAXA08	693	6	CD640412	CD640412	AGENCOURT
261	145.4	5.1	503	6	CB350381	CB350381	ACHG165.H	718	7	CB839409	CB839409	AGENCOURT
262	145.2	5.1	252	7	CR771899	CR771899	DKF2p468C	806	7	CF783082	CF783082	AGENCOURT
263	145.2	5.1	275	7	CF612845	CF612845	lae11h04.	809	5	BU958264	BU958264	AGENCOURT
264	145.2	5.1	448	7	CF127350	CF127350	UI-HF-ES0	826	7	CV483860	CV483860	AGENCOURT
265	145.2	5.1	582	5	BP306922	BP306922	BP306922	861	5	BU851081	BU851081	AGENCOURT
266	145.2	5.1	770	7	CK399259	CK399259	AGENCOURT	866	5	BU962475	BU962475	AGENCOURT
267	145.2	5.1	957	5	BU563253	BU563253	AGENCOURT	870	8	BH157873	BH157873	ENTR411FR
268	145.2	5.1	1213	5	BQ718626	BQ718626	AGENCOURT	875	5	BU529558	BU529558	AGENCOURT
269	145	5.1	222	6	CA935086	CA935086	saue4b10.	888	5	BU955497	BU955497	AGENCOURT
270	145	5.1	668	6	CD772534	CD772534	AGENCOURT	892	7	CF289361	CF289361	AGENCOURT
271	145	5.1	895	5	BU852045	BU852045	AGENCOURT	931	5	BU960826	BU960826	AGENCOURT
272	145	5.1	965	5	BQ428205	BQ428205	AGENCOURT	1261	5	BQ427870	BQ427870	AGENCOURT
273	145	5.1	1025	3	BC027804	BC027804	Mus muscu	1492	4	BM555359	BM555359	AGENCOURT
274	144.8	5.1	259	1	AL697721	AL697721	DKF2p686E	283	6	CB288125	CB288125	CMD74_E02
275	144.8	5.1	381	6	CA736353	CA736353	wp11s.pK0	334	2	AW100809	AW100809	sd61e08.Y
276	144.8	5.1	442	1	AV681872	AV681872	Y	535	1	AV757455	AV757455	CA757455
277	144.8	5.1	591	7	CK426420	CK426420	rx15b10.Y	741	3	BC050975	BC050975	Mus muscu
278	144.8	5.1	637	7	CK005551	CK005551	AGENCOURT	832	5	BU540250	BU540250	AGENCOURT
279	144.8	5.1	661	1	AV710608	AV710608	Y	833	7	CK793654	CK793654	AGENCOURT
280	144.8	5.1	821	3	BC015144	BC015144	Homo sapi	840	5	BU567115	BU567115	AGENCOURT
281	144.6	5.1	215	7	CF207515	CF207515	CAB20001	845	5	BU935967	BU935967	AGENCOURT
282	144.6	5.1	280	7	CK975391	CK975391	4106215.B	906	5	BU943644	BU943644	AGENCOURT
283	144.6	5.1	397	1	AL723541	AL723541	Y	918	6	CA455250	CA455250	AGENCOURT
284	144.6	5.1	398	3	AF116644	AF116644	Homo sapi	956	5	BU563381	BU563381	AGENCOURT
285	144.6	5.1	415	7	CK193529	CK193529	Y	1073	5	BQ230841	BQ230841	AGENCOURT
286	144.6	5.1	421	1	AV682249	AV682249	Y	1235	4	BM470058	BM470058	AGENCOURT
287	144.6	5.1	791	1	AV755207	AV755207	Y	1379	6	CD049761	CD049761	AGENCOURT
288	144.6	5.1	871	5	BU589926	BU589926	AGENCOURT	261	4	BJ469921	BJ469921	BJ469921
289	144.6	5.1	891	4	BM449741	BM449741	AGENCOURT	310	4	BJ703028	BJ703028	BJ703028
290	144.6	5.1	965	5	BQ921874	BQ921874	AGENCOURT	328	5	BA476122	BA476122	DKF2p686H
291	144.4	5.1	305	5	EX479066	EX479066	DKF2p686L	425	7	CF279639	CF279639	14ETL--06
292	144.4	5.1	308	5	BX506616	BX506616	MDfE3001F	430	5	BQ395458	BQ395458	NISC ng15
293	144.4	5.1	437	7	CK384228	CK384228	lah06h09.	684	1	AV706164	AV706164	AV706164
294	144.4	5.1	510	7	CV057219	CV057219	BNEL25c9	713	7	CK655902	CK655902	AGENCOURT
295	144.4	5.1	656	7	CV064567	CV064567	WNE11284	714	7	CV064496	CV064496	WNE111F11
296	144.4	5.1	884	7	CK385218	CK385218	LE2TR03A0	842	5	BU563468	BU563468	AGENCOURT
297	144.4	5.1	891	5	BU531156	BU531156	AGENCOURT	856	5	BU940785	BU940785	AGENCOURT
298	144.4	5.1	1026	3	HSM803537	HSM803537	Homo sapi	865	5	BU555370	BU555370	AGENCOURT
299	144.2	5.1	230	4	BJ697384	BJ697384	Y	870	6	CB566939	CB566939	AGENCOURT
300	144.2	5.1	278	7	CF123167	CF123167	UI-HF-CH0	885	5	BU850517	BU850517	AGENCOURT
301	144.2	5.1	285	6	CD521457	CD521457	AGENCOURT	947	5	BQ921561	BQ921561	AGENCOURT
302	144.2	5.1	296	7	CK353572	CK353572	AGENCOURT	1057	6	CB561919	CB561919	AGENCOURT
303	144.2	5.1	314	7	CF123198	CF123198	UI-HF-CH0	239	6	CA802785	CA802785	saue42b04.
304	144.2	5.1	332	7	CV122318	CV122318	MD1v4003e	252	7	CO415260	CO415260	Mdfc3006k
305	144.2	5.1	371	7	CK377132	CK377132	lah98g02.	295	6	CD641171	CD641171	AGENCOURT
306	144.2	5.1	415	7	CO192413	CO192413	EC33671.5	302	7	CB831978	CB831978	AGENCOURT
307	144.2	5.1	421	5	BQ396582	BQ396582	NISC_ng21	353	6	CD639674	CD639674	AGENCOURT
308	144.2	5.1	424	1	AV682809	AV682809	Y	364	7	CK430797	CK430797	oj54a08.Y
309	144.2	5.1	485	6	CD721930	CD721930	oj03c10.Y	510	1	AV755613	AV755613	Y
310	144.2	5.1	488	7	CF755040	CF755040	lae51903.	559	5	BQ520502	BQ520502	NISC_nl05
311	144.2	5.1	536	6	CN194226	CN194226	rg91b06.Y	820	5	BU555053	BU555053	AGENCOURT
312	144.2	5.1	635	6	CD638395	CD638395	AGENCOURT	840	7	CF578759	CF578759	AGENCOURT
313	144.2	5.1	664	7	CO072107	CO072107	GR_Ea31B	930	6	CA977162	CA977162	AGENCOURT
314	144.2	5.1	1066	5	BU589860	BU589860	AGENCOURT	971	9	CL120194	CL120194	ISB1-78J1

390	143.4	5.0	1009	5	BU540024	AGENCOURT	463	142.6	5.0	506	7	CO394068	AGENCOURT
391	143.4	5.0	2007	3	HSMB07665	Hom o sapi	464	142.6	5.0	510	1	AV755290	AV755290
392	143.2	5.0	1978	7	CO38540	tah73a03.	465	142.6	5.0	808	5	BU530709	AGENCOURT
393	143.2	5.0	276	7	CK385496	lah40c02.	466	142.6	5.0	819	5	BU844250	AGENCOURT
394	143.2	5.0	286	7	CR765052	DKF2p470P	467	142.6	5.0	840	5	BU844250	AGENCOURT
395	143.2	5.0	283	1	AL589270	DKF2p451D	468	142.6	5.0	856	7	CO796836	AGENCOURT
396	143.2	5.0	361	7	CF370119	rg48d07.Y	469	142.6	5.0	961	8	AZ691838	ENTW156TF
397	143.2	5.0	404	7	CF358374	tm89g07.Y	470	142.6	5.0	1041	6	CD051043	AGENCOURT
398	143.2	5.0	494	7	CF544979	lad85g10.Y	471	142.6	5.0	1534	3	CR749559	Hom o sapi
399	143.2	5.0	590	6	BO533229	NISC_g113	472	142.6	5.0	8296	3	CR749511	Hom o sapi
400	143.2	5.0	603	5	BQ397550	NISC rg28	473	142.4	5.0	242	1	AL697724	DKF2p6861
401	143.2	5.0	806	5	BU851562	AGENCOURT	474	142.4	5.0	259	7	CO159753	FLDI_15.D
402	143.2	5.0	870	5	BU589706	AGENCOURT	C 475	142.4	5.0	265	5	BX480600	DKF2p686G
403	143.2	5.0	942	5	BU932709	AGENCOURT	C 476	142.4	5.0	325	6	CB079273	hp69a01.b
404	143.2	5.0	963	5	BU902691	AGENCOURT	C 477	142.4	5.0	367	5	BO525045	NISC no08
405	143.2	5.0	996	5	BU843390	AGENCOURT	C 478	142.4	5.0	376	5	BX486637	DKF2p686M
406	143	5.0	197	4	BG179993	602329538	479	142.4	5.0	398	5	AX499601	DKF2p779M
407	143	5.0	249	7	CK004667	ip21e07.g	480	142.4	5.0	398	7	CK375940	lah76h05.
408	143	5.0	255	6	CA802891	sau43g09.	481	142.4	5.0	402	6	CN161832	951158.MA
409	143	5.0	326	7	CK384989	lah57a09.	C 482	142.4	5.0	426	6	CD678845	hq01b11.x
410	143	5.0	347	4	BM534581	fx69b06.Y	483	142.4	5.0	443	7	CF743770	UI-M-G10-
411	143	5.0	384	7	CF321906	HD--13-F0	484	142.4	5.0	443	7	CK000623	AGENCOURT
412	143	5.0	408	7	CK004614	AGENCOURT	485	142.4	5.0	494	7	CK371886	lai20d05.
413	143	5.0	585	7	CO403863	AGENCOURT	C 486	142.4	5.0	519	7	CK431148	oJ58e08.Y
414	143	5.0	651	6	CD433621	EL01N0313	C 487	142.4	5.0	555	5	BQ397268	NISC rg26
415	143	5.0	667	6	CD770733	AGENCOURT	C 488	142.4	5.0	555	5	BX555180	BX555180
416	143	5.0	730	7	CV484196	AGENCOURT	C 489	142.4	5.0	556	7	CK791071	AGENCOURT
417	143	5.0	747	7	CV068710	f2_new_ch	490	142.4	5.0	624	7	CK468331	939713.MA
418	143	5.0	878	5	BU540331	AGENCOURT	491	142.4	5.0	678	6	CD639699	AGENCOURT
419	143	5.0	886	5	BU955707	AGENCOURT	492	142.4	5.0	770	1	AV756342	AV756342
420	143	5.0	1076	4	BM803989	AGENCOURT	493	142.4	5.0	806	5	BU842092	AGENCOURT
421	143	5.0	4807	3	CR749565	Hom o sapi	494	142.4	5.0	813	5	BU842692	AGENCOURT
422	142.8	5.0	178	6	CA334893	NISC_l102	495	142.4	5.0	865	5	BU601053	AGENCOURT
423	142.8	5.0	197	7	CF208356	CAB20003	496	142.4	5.0	882	3	BC022402	Hom o sapi
424	142.8	5.0	207	7	CK119802	210107.P1	497	142.4	5.0	891	7	CN384691	LE2TR01J2
425	142.8	5.0	219	6	CF214757	CGF100082	498	142.4	5.0	928	5	BU954720	AGENCOURT
426	142.8	5.0	225	7	CB970600	CAB10004	499	142.4	5.0	939	6	CB205499	AGENCOURT
427	142.8	5.0	245	5	BA476550	DKF2p686O	500	142.4	5.0	979	4	BM415625	OP20703.M
428	142.8	5.0	252	7	CF212181	CGF100066	C 501	142.4	5.0	994	5	BQ948873	AGENCOURT
429	142.8	5.0	326	5	BM504841	DKF2p686M	502	142.4	5.0	1047	5	BU908460	AGENCOURT
430	142.8	5.0	334	7	CR544048	DKF2p470J	C 503	142.4	5.0	1264	5	BU908460	AGENCOURT
431	142.8	5.0	362	5	BQ521590	NISC_n114	504	142.4	5.0	1794	3	HSMB04571	
432	142.8	5.0	380	2	BF449584	maa45b06.	505	142.4	5.0	2500	3	BC026293	Hom o sapi
433	142.8	5.0	385	6	CR702425	AMGNNUC.N	506	142.4	5.0	178	5	BM965687	ko15f05.Y
434	142.8	5.0	427	7	CK049668	V4_P2_G5	507	142.2	5.0	189	5	BQ909669	ku18e11.Y
435	142.8	5.0	430	1	AV682289	AV682289-	508	142.2	5.0	260	7	CK772316	DKF2p468L
436	142.8	5.0	463	7	CO866181	Mdfr3020m	509	142.2	5.0	261	7	CV280938	WS0138.LB2
437	142.8	5.0	513	1	AV757158	AV757158	510	142.2	5.0	298	5	BX953231	DKF2p781D
438	142.8	5.0	514	6	CB051745	NISC_g102	511	142.2	5.0	325	6	CD722153	oJ06b12.Y
439	142.8	5.0	569	5	BP306287	BP306287	512	142.2	5.0	307	6	CD722153	oJ06b12.Y
440	142.8	5.0	607	7	CV490737	AGENCOURT	513	142.2	5.0	346	7	CF380767	lac78d04.
441	142.8	5.0	747	2	B6202334	601483329	514	142.2	5.0	359	6	CA372266	652974.NC
442	142.8	5.0	778	7	CK161630	950941.MA	515	142.2	5.0	424	6	CA3796123	AMGNNUC:IS
443	142.8	5.0	795	5	BU963666	AGENCOURT	516	142.2	5.0	448	6	CA391870	cs19g10.x
444	142.8	5.0	820	5	BU803056	AGENCOURT	C 517	142.2	5.0	448	6	CA379465	658553.NC
445	142.8	5.0	821	5	BU960727	AGENCOURT	518	142.2	5.0	504	6	CA379465	658553.NC
446	142.8	5.0	841	5	BU861035	AGENCOURT	519	142.2	5.0	562	7	CN786219	4120178.B
447	142.8	5.0	853	5	BU927591	AGENCOURT	520	142.2	5.0	623	6	CD770235	AGENCOURT
448	142.8	5.0	871	5	BU529398	AGENCOURT	521	142.2	5.0	808	6	CD520988	AGENCOURT
449	142.8	5.0	944	5	BU904705	AGENCOURT	522	142.2	5.0	819	5	BU531148	AGENCOURT
450	142.8	5.0	967	6	CB204352	AGENCOURT	523	142.2	5.0	827	6	CB317350	AGENCOURT
451	142.8	5.0	1251	4	BM453439	AGENCOURT	C 524	142.2	5.0	845	7	CK193161	FGAS00157
452	142.6	5.0	216	6	CA935095	sau464d09.	525	142.2	5.0	857	5	BU843015	AGENCOURT
453	142.6	5.0	219	4	BI791181	ld05g09.Y	C 526	142.2	5.0	863	2	BE964633	601658560
454	142.6	5.0	293	2	BE023554	sm82a07.Y	527	142.2	5.0	864	5	BU534869	AGENCOURT
455	142.6	5.0	370	7	CK593922	tad29h07.	528	142.2	5.0	866	5	BU587173	AGENCOURT
456	142.6	5.0	407	2	BF022275	uy55c06.Y	529	142.2	5.0	876	6	CA988174	AGENCOURT
457	142.6	5.0	452	3	BC050981	Mus_muscu	530	142.2	5.0	885	5	BU957927	AGENCOURT
458	142.6	5.0	458	1	AV682521	AV682521	531	142.2	5.0	888	6	CB590474	AGENCOURT
459	142.6	5.0	464	1	AV708119	AV708119	C 532	142.2	5.0	891	9	CNS009JU	AL053767.Drosoph1
460	142.6	5.0	471	1	A1404883	GH24733.5	533	142.2	5.0	893	6	CD251249	AGENCOURT
461	142.6	5.0	471	7	CF307986	ABF--01-J	534	142.2	5.0	900	5	BU589675	AGENCOURT
462	142.6	5.0	482	7	CV122300	Md1v4003a	535	142.2	5.0	904	5	BU842136	AGENCOURT

536	142.2	5.0	913	5	BUS54763	AGENCOURT	609	141.8	5.0	613	7	CK787090	
537	142.2	5.0	932	4	BG033403	602301577	610	141.8	5.0	664	2	BF144889	
538	142.2	5.0	935	6	CB193258	AGENCOURT	611	141.8	5.0	721	7	CN845011	
539	142.2	5.0	1066	5	BUS40067	AGENCOURT	612	141.8	5.0	775	6	CB319351	
540	142.2	5.0	1297	5	BUS40145	AGENCOURT	613	141.8	5.0	784	7	CV487253	
541	142.2	5.0	1531	9	AG381853	Mus muscu	614	141.8	5.0	785	7	CK790726	
542	142	5.0	222	4	B1863321	r103d06.y	c	615	141.8	5.0	796	9	CNS0118D
543	142	5.0	240	4	BG156328	AGENCOURT	616	141.8	5.0	875	5	BUS28010	
544	142	5.0	286	7	CO067491	Mdfx3014e	617	141.8	5.0	902	3	AF116631	
545	142	5.0	294	2	AW101221	ed75f11.y	618	141.8	5.0	908	7	CK797283	
546	142	5.0	313	5	BQ523667	BQ523667	619	141.8	5.0	920	5	BUS29185	
547	142	5.0	319	5	BX489110	AGENCOURT	620	141.8	5.0	921	5	BQ960309	
548	142	5.0	331	4	BG155453	AGENCOURT	621	141.8	5.0	942	5	BQ960309	
549	142	5.0	341	5	BX953635	AGENCOURT	622	141.8	5.0	942	5	BQ960309	
550	142	5.0	374	7	CR549911	AGENCOURT	623	141.8	5.0	966	5	BUS34727	
551	142	5.0	397	6	CB570896	AGENCOURT	624	141.8	5.0	1005	9	CL077409	
552	142	5.0	403	1	AV682162	AGENCOURT	625	141.8	5.0	2157	3	BC050969	
553	142	5.0	405	4	BF970162	AGENCOURT	626	141.8	5.0	5940	3	CR627133	
554	142	5.0	429	1	AV681857	AGENCOURT	627	141.8	5.0	198	5	BQ667440	
555	142	5.0	431	6	CB044460	NISC gc04	628	141.6	5.0	201	6	CA802122	
556	142	5.0	433	5	BX565773	AGENCOURT	629	141.6	5.0	201	6	CA802122	
557	142	5.0	453	7	CK005374	AGENCOURT	630	141.6	5.0	201	6	CB045621	
558	142	5.0	462	6	CD363777	UI-M-GLO-	631	141.6	5.0	213	6	CA935478	
559	142	5.0	466	7	CF369737	AGENCOURT	632	141.6	5.0	233	7	CV525079	
560	142	5.0	476	5	BQ391140	NISC mq17	633	141.6	5.0	243	7	CO752945	
561	142	5.0	515	7	CN049660	V4_P2_G11	634	141.6	5.0	249	2	BE059724	
562	142	5.0	568	5	BQ396954	AGENCOURT	635	141.6	5.0	282	7	CR750600	
563	142	5.0	613	7	CV121985	Mdlv4002b	636	141.6	5.0	283	4	BI324331	
564	142	5.0	615	4	BG435835	AGENCOURT	637	141.6	5.0	287	5	BX503626	
565	142	5.0	687	6	CD639714	AGENCOURT	638	141.6	5.0	301	7	CF123294	
566	142	5.0	689	7	CN832074	AGENCOURT	639	141.6	5.0	302	2	AW100887	
567	142	5.0	824	5	BUS11157	AGENCOURT	640	141.6	5.0	314	1	AL715133	
568	142	5.0	830	5	BUS65577	AGENCOURT	641	141.6	5.0	314	1	AL715133	
569	142	5.0	833	6	CB945951	AGENCOURT	642	141.6	5.0	316	7	CF653832	
570	142	5.0	842	7	CN409658	AGENCOURT	643	141.6	5.0	331	5	BX501227	
571	142	5.0	849	2	BF792099	AGENCOURT	644	141.6	5.0	341	7	CF369462	
572	142	5.0	911	5	BUS55479	AGENCOURT	645	141.6	5.0	368	4	BM573701	
573	142	5.0	914	5	BUS11349	AGENCOURT	646	141.6	5.0	368	4	BM573701	
574	142	5.0	926	7	CK415124	AUF Ip8it	647	141.6	5.0	411	1	AL120854	
575	142	5.0	939	7	CK421563	AUF Ip8pn	648	141.6	5.0	418	7	CF370486	
576	142	5.0	939	7	CN310359	AGENCOURT	649	141.6	5.0	429	5	BQ454029	
577	142	5.0	941	6	CD050342	AGENCOURT	650	141.6	5.0	514	5	BQ389814	
578	142	5.0	944	5	BUI78666	AGENCOURT	651	141.6	5.0	574	7	CO092611	
579	142	5.0	979	5	BUI76137	AGENCOURT	652	141.6	5.0	613	7	CK005475	
580	142	5.0	984	6	CD513662	AGENCOURT	653	141.6	5.0	624	7	CO891923	
581	142	5.0	992	5	BUS15127	AGENCOURT	654	141.6	5.0	642	4	BI870677	
582	142	5.0	1018	5	BUS29315	AGENCOURT	655	141.6	5.0	745	7	CN175619	
583	142	5.0	1023	5	BUS29766	AGENCOURT	656	141.6	5.0	772	1	AV733397	
584	142	5.0	1034	2	BS964486	601658194	657	141.6	5.0	826	5	BUS30680	
585	142	5.0	1050	5	BUS02650	AGENCOURT	658	141.6	5.0	839	5	BUS34549	
586	142	5.0	1079	6	CD516973	AGENCOURT	659	141.6	5.0	847	5	BUS51147	
587	142	5.0	1646	4	BM550636	AGENCOURT	c	660	141.6	5.0	852	7	CK195112
588	142	5.0	2080	3	CR749502	AGENCOURT	661	141.6	5.0	856	5	BUS65327	
589	142	5.0	2735	3	HSN806723	AGENCOURT	662	141.6	5.0	864	5	BUS30880	
590	142	5.0	5058	3	BC054079	Mus muscu	663	141.6	5.0	871	5	BUS29359	
591	142	5.0	5527	3	CR627393	AGENCOURT	664	141.6	5.0	877	5	BUS55691	
592	142	5.0	5856	3	HSN803500	AGENCOURT	665	141.6	5.0	893	5	BUS29816	
593	142	5.0	6082	3	CR749803	AGENCOURT	c	666	141.6	5.0	896	7	CK197478
594	141.8	5.0	195	4	BM186912	AGENCOURT	667	141.6	5.0	957	4	BM472626	
595	141.8	5.0	206	7	CO938248	AGENCOURT	668	141.6	5.0	1009	5	BUS58877	
596	141.8	5.0	212	7	CO195530	AGENCOURT	669	141.6	5.0	1012	5	BQ954248	
597	141.8	5.0	234	6	CD722269	AGENCOURT	670	141.6	5.0	1027	6	CB205525	
598	141.8	5.0	245	5	BX951835	AGENCOURT	671	141.6	5.0	1034	5	BUS22201	
599	141.8	5.0	272	2	AW0711349	xaf5a08.x	672	141.6	5.0	1180	6	CD384928	
600	141.8	5.0	281	4	BM261286	dai46d01.	673	141.6	5.0	1214	5	BUI67807	
601	141.8	5.0	315	7	CV2800973	AGENCOURT	674	141.6	5.0	1241	3	BC050978	
602	141.8	5.0	360	7	CK430943	AGENCOURT	675	141.6	5.0	3775	3	CR627381	
603	141.8	5.0	408	4	BM154430	fv85a07.y	676	141.4	5.0	225	4	BM186096	
604	141.8	5.0	431	4	BG363877	dc71h01.y	677	141.4	5.0	226	4	BM533163	
605	141.8	5.0	465	6	CD237889	FNPARA08	678	141.4	5.0	234	1	BM154438	
606	141.8	5.0	478	5	BQ394696	AGENCOURT	679	141.4	5.0	235	1	AI443075	
607	141.8	5.0	507	1	AV755614	AV755614	680	141.4	5.0	239	7	CK376983	
608	141.8	5.0	589	5	BQ525311	NISC no10	681	141.4	5.0	245	2	AW100988	
										247	4	BM187242	

682 141.4 5.0 254 4 BI705355 fr57g11.y 755 141.2 5.0 1106 4 BM553776  
683 141.4 5.0 286 7 CF640321 D26\_A01.F 756 141.2 5.0 1141 5 BM905793 AGENCOURT  
684 141.4 5.0 296 7 CF640327 D25\_A01.F 757 141.2 5.0 1268 4 BM804120 AGENCOURT  
685 141.4 5.0 303 7 CO752990 MdfF302ze 758 141.2 5.0 1550 3 EC049704 Mus\_muscu  
686 141.4 5.0 341 6 CB523177 UI-W-GK0- 759 141 5.0 183 5 BX508387 DkfZp686e  
687 141.4 5.0 346 7 CV199646 km17g09.y 760 141 5.0 190 6 CA802078 sauJ9g04  
688 141.4 5.0 351 7 CO417094 MdfF3011p 761 141 5.0 216 2 BR048071 tz47f01.y  
689 141.4 5.0 368 7 CO4181059 EC13411.5 762 141 5.0 228 6 CA819677 sau74c10.y  
690 141.4 5.0 370 4 BG610096 324577.MA 763 141 5.0 231 2 AW733931 sk85c03.y  
691 141.4 5.0 398 5 BX503633 DkfZp686e1 764 141 5.0 237 7 CK616649 ou23d05.y  
692 141.4 5.0 402 1 AJ799457 AJ799457 765 141 5.0 240 7 CR774358 DkfZp459p  
693 141.4 5.0 410 6 CB079957 hp79c04.b 766 141 5.0 243 7 CO180411 EC01519.5  
694 141.4 5.0 405 7 CN048820 AGENCOURT 767 141 5.0 248 1 AL712394 DkfZp686M  
695 141.4 5.0 414 6 CA336104 NISC\_lu08 768 141 5.0 265 4 BI674494 sahs96g05.  
696 141.4 5.0 420 6 CB640131 AGENCOURT 769 141 5.0 280 4 BJ019482 BJ019482  
697 141.4 5.0 421 2 BE048319 tz49h10.y 770 141 5.0 310 7 CR752937 DkfZp468P  
698 141.4 5.0 432 6 CB638524 AGENCOURT 771 141 5.0 335 4 BM534829 fx71h04.y  
699 141.4 5.0 462 5 BQ393864 NISC ng05 772 141 5.0 340 2 BF021460 uy35c02.y  
700 141.4 5.0 486 7 CF369647 xg54d11.y 773 141 5.0 345 5 BQ085914 il11f11.y  
701 141.4 5.0 503 7 CO417413 MdfF30121 774 141 5.0 349 4 BM574077 fx58g05.y  
702 141.4 5.0 512 7 CN994160 MdfF30029 775 141 5.0 450 7 CO065850 MdfF3016a  
703 141.4 5.0 530 4 BM573742 fy03b10.y 776 141 5.0 473 6 CD251358 AGENCOURT  
704 141.4 5.0 664 1 AV705644 AV705644 777 141 5.0 482 4 BI858408 603383996  
705 141.4 5.0 728 5 BU803096 SJFARA03 778 141 5.0 525 6 CB409572 NISC nc02  
706 141.4 5.0 735 7 CV064887 WNEL16e12 779 141 5.0 529 7 CF520953 AGENCOURT  
707 141.4 5.0 806 7 CK790380 AGENCOURT 780 141 5.0 535 7 CK427445 wz68g06.x  
708 141.4 5.0 822 6 CB520787 AGENCOURT 781 141 5.0 623 1 AI969567 wz68g06.x  
709 141.4 5.0 834 5 BU534913 AGENCOURT 782 141 5.0 659 6 CB640691 AGENCOURT  
710 141.4 5.0 872 9 CL466757 SAIL\_1260 783 141 5.0 681 6 CD768296 AGENCOURT  
711 141.4 5.0 893 6 CD243740 AGENCOURT 784 141 5.0 687 6 CD772154 AGENCOURT  
712 141.4 5.0 979 5 BU531500 AGENCOURT 785 141 5.0 819 5 BU168192 AGENCOURT  
713 141.4 5.0 1010 6 CD389001 AGENCOURT 786 141 5.0 824 5 BU936038 AGENCOURT  
714 141.4 5.0 2105 3 HS803705 787 141 5.0 826 5 BU529199 AGENCOURT  
715 141.2 5.0 228 5 BM888956 kb03b11.y 788 141 5.0 829 5 BU843782 AGENCOURT  
716 141.2 5.0 219 7 CF216003 CAST0002 789 141 5.0 830 5 BU843607 AGENCOURT  
717 141.2 5.0 240 4 BM521849 sak76g12 790 141 5.0 836 5 BU927827 AGENCOURT  
718 141.2 5.0 258 7 CK429184 oJ33c07.y 791 141 5.0 846 5 BU927827 AGENCOURT  
719 141.2 5.0 256 7 CO195335 EC40072.5 792 141 5.0 853 5 BU588997 AGENCOURT  
720 141.2 5.0 302 7 CF253048 mdv004\_e0 793 141 5.0 864 5 BU851178 AGENCOURT  
721 141.2 5.0 302 7 CF546452 DkfZp470A 794 141 5.0 876 7 CK398238 AGENCOURT  
722 141.2 5.0 343 6 CB084676 hq19g11.b 795 141 5.0 885 5 BU554652 AGENCOURT  
723 141.2 5.0 353 4 BI744697 rk91c06.y 796 141 5.0 951 7 CK425505 AUF\_lpt68  
724 141.2 5.0 362 1 AI106593 GH06644.5 797 141 5.0 966 5 BU540401 AGENCOURT  
725 141.2 5.0 362 7 CK594208 lab42h11 798 141 5.0 960 5 BU860843 AGENCOURT  
726 141.2 5.0 371 7 CN269273 170005999 799 141 5.0 987 5 BQ430188 AGENCOURT  
727 141.2 5.0 376 6 CB094547 hz71d07.b 800 141 5.0 1059 9 CKN50022B  
728 141.2 5.0 389 4 BF970446 602272785 801 141 5.0 1073 5 BQ930284 AGENCOURT  
729 141.2 5.0 431 7 CO191531 EC31328.5 802 141 5.0 1309 4 BM463041 AGENCOURT  
730 141.2 5.0 439 1 AL727204 AL727204 803 141 5.0 1321 7 CF579295 AGENCOURT  
731 141.2 5.0 462 6 CA394496 Cs52b12.y 804 141 5.0 1679 3 BC017752 Homo sapi  
732 141.2 5.0 494 5 BQ391155 NISC\_mq17 805 141 5.0 1999 3 BC027914 Homo sapi  
733 141.2 5.0 495 6 CD236950 FNPAEG11 806 141 5.0 2700 3 BC036824 Homo sapi  
734 141.2 5.0 504 5 BQ524016 NISC\_no02 807 141 5.0 4793 3 CR749666 Homo sapi  
735 141.2 5.0 561 7 CV198844 km31g03.y 808 140.8 4.9 181 5 BM897277 Ph39b09.y  
736 141.2 5.0 578 2 AW733627 sk83a06.y 809 140.8 4.9 187 7 CO191674 EC31648.5  
737 141.2 5.0 604 1 AV756703 AV756703 810 140.8 4.9 198 5 BQ392333 NISC\_mq23  
738 141.2 5.0 640 6 CB522981 UI-W-GK0- 811 140.8 4.9 209 5 CO417475 MdfF30121  
739 141.2 5.0 644 7 CO9898186 MdfF3021c 812 140.8 4.9 229 5 BQ075610 fz06g08.y  
740 141.2 5.0 681 1 AV703695 AV703695 813 140.8 4.9 263 6 CF040070 QCH8409.y  
741 141.2 5.0 696 4 BF970731 602273732 814 140.8 4.9 267 5 BM880221 ed06g08.y  
742 141.2 5.0 752 8 AE2531014 ENTBD19Ff 815 140.8 4.9 270 2 AW101788 ad70609.y  
743 141.2 5.0 805 9 CKN5009F8 816 140.8 4.9 272 6 CD520705 AGENCOURT  
744 141.2 5.0 812 5 BU534591 AGENCOURT 817 140.8 4.9 273 7 CN266183 170004250  
745 141.2 5.0 858 5 BU953187 AGENCOURT 818 140.8 4.9 280 6 CA802930 sau44d08  
746 141.2 5.0 872 5 BU588646 AGENCOURT 819 140.8 4.9 281 5 BQ392472 NISC\_mq4  
747 141.2 5.0 909 5 BU587993 AGENCOURT 820 140.8 4.9 289 7 CK429678 OJ39g11.y  
748 141.2 5.0 927 7 CV069684 WPAEHux15 821 140.8 4.9 290 5 BX501576 DkfZp779M  
749 141.2 5.0 927 6 CA455489 AGENCOURT 822 140.8 4.9 340 7 CN836173 AGENCOURT  
750 141.2 5.0 929 5 BU588911 AGENCOURT 823 140.8 4.9 342 7 CV193374 SNEStb2  
751 141.2 5.0 947 5 BU504804 AGENCOURT 824 140.8 4.9 351 7 CK378884 lai27f04.  
752 141.2 5.0 953 5 BU159214 AGENCOURT 825 140.8 4.9 353 6 CB973642 CAB30003  
753 141.2 5.0 954 5 BQ220010 AGENCOURT 826 140.8 4.9 360 5 BQ400218 NISC\_mq08  
754 141.2 5.0 963 5 BQ221886 AGENCOURT 827 140.8 4.9 361 7 CK004628 AGENCOURT

BM553776 AGENCOURT  
BM905793 AGENCOURT  
BM804120 AGENCOURT  
BC049704 Mus\_muscu  
BX508387 DkfZp686e  
CA802078 sauJ9g04  
BE048071 tz47f01.y  
CA819677 sau74c10.y  
AW733931 sk85c03.y  
CK616649 ou23d05.y  
CR774358 DkfZp459p  
CO180411 EC01519.5  
AL712394 DkfZp686M  
BI674494 sahs96g05.  
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CR752937 DkfZp468P  
BM534829 fx71h04.y  
BF021460 uy35c02.y  
BQ085914 il11f11.y  
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CF520953 AGENCOURT  
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AI969567 wz68g06.x  
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CD772154 AGENCOURT  
BU168192 AGENCOURT  
BU936038 AGENCOURT  
BU529199 AGENCOURT  
BU843782 AGENCOURT  
BU843607 AGENCOURT  
CV077516 AGENCOURT  
BU927827 AGENCOURT  
BU588997 AGENCOURT  
BU851178 AGENCOURT  
CK398238 AGENCOURT  
BU554652 AGENCOURT  
CK425505 AUF\_lpt68  
BU540401 AGENCOURT  
BU860843 AGENCOURT  
BQ430188 AGENCOURT  
AQ97133 Drosophil  
BQ30284 AGENCOURT  
BM463041 AGENCOURT  
CF579295 AGENCOURT  
BC017752 Homo sapi  
BC027914 Homo sapi  
BC036824 Homo sapi  
CR749666 Homo sapi  
BM897277 Ph39b09.y  
CO191674 EC31648.5  
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BQ075610 fz06g08.y  
CF040070 QCH8409.y  
BM880221 ed06g08.y  
AW101788 ad70609.y  
CD520705 AGENCOURT  
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CA802930 sau44d08  
BQ392472 NISC\_mq4  
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BX501576 DkfZp779M  
CN836173 AGENCOURT  
CV193374 SNEStb2  
CK378884 lai27f04.  
CB973642 CAB30003  
BQ400218 NISC\_mq08  
CK004628 AGENCOURT

828	140.8	4.9	364	7	CV524008	CV524008 Mdlv2 401	901	140.6	4.9	848	6	CB236020	CB236020 AGENCOURT	
829	140.8	4.9	373	7	CK429577	CK429577 oJ38e03.Y	902	140.6	4.9	853	6	CA455655	CA455655 AGENCOURT	
830	140.8	4.9	412	6	CA386106	CA386106 667646 NC	903	140.6	4.9	867	5	BUS30924	BUS30924 AGENCOURT	
831	140.8	4.9	419	6	CB079306	CB079306 hp69d02.b	904	140.6	4.9	869	5	BUS63713	BUS63713 AGENCOURT	
832	140.8	4.9	435	7	CK373916	CK373916 lai65g04.	905	140.6	4.9	879	5	BUS51061	BUS51061 AGENCOURT	
833	140.8	4.9	440	5	BQ522645	BQ522645 NISC nl17	906	140.6	4.9	882	5	BUS60445	BUS60445 AGENCOURT	
834	140.8	4.9	445	7	CN838051	CN838051 AGENCOURT	907	140.6	4.9	885	5	BUS48031	BUS48031 AGENCOURT	
835	140.8	4.9	448	7	CV514719	CV514719 taj69g12.	908	140.6	4.9	893	5	BUS42336	BUS42336 AGENCOURT	
836	140.8	4.9	454	5	BX500915	BX500915 DKFp779D	909	140.6	4.9	905	5	BUS95672	BUS95672 AGENCOURT	
837	140.8	4.9	469	7	CK429230	CK429230 oJ33h02.Y	910	140.6	4.9	955	2	BE890041	BE890041 601512310	
838	140.8	4.9	478	6	CF030791	CF030791 QCD26e06.	911	140.6	4.9	960	7	CK421571	CK421571 AUF Ipsn	
839	140.8	4.9	503	5	BX561337	BX561337 BX561337	912	140.6	4.9	977	7	BUS58387	BUS58387 AGENCOURT	
840	140.8	4.9	561	5	BQ395163	BQ395163 NISC ng13	913	140.6	4.9	980	5	BUS44064	BUS44064 AGENCOURT	
841	140.8	4.9	639	1	AI969601	AI969601 wz69b11.x	c	914	140.6	4.9	1101	9	CNS00AYO	ALJ05506 Drosophila
842	140.8	4.9	674	7	CK462872	CK462872 933697 MA	915	140.6	4.9	1356	3	CR749814	CR749814 Homo sapi	
843	140.8	4.9	704	1	AV681630	AV681630 AV681630	916	140.6	4.9	1521	3	AF118070	AF118070 Homo sapi	
844	140.8	4.9	707	1	AV681647	AV681647 AV681647	917	140.6	4.9	169	5	BM898046	BM898046 ph46f05.Y	
845	140.8	4.9	709	7	CN835711	CN835711 AGENCOURT	918	140.4	4.9	189	4	BM178937	BM178937 saj61c09.	
846	140.8	4.9	724	6	CD339470	CD339470 AGENCOURT	919	140.4	4.9	202	4	BM154309	BM154309 f983e04.Y	
847	140.8	4.9	729	7	CV486640	CV486640 AGENCOURT	920	140.4	4.9	205	6	CD723715	CD723715 oJ25f03.Y	
848	140.8	4.9	835	5	BUS292221	BUS292221 AGENCOURT	921	140.4	4.9	254	2	BE057342	BE057342 en01h03.Y	
849	140.8	4.9	748	1	AV682252	AV682252 AGENCOURT	922	140.4	4.9	210	6	CA935503	CA935503 sa955a10.	
850	140.8	4.9	779	7	CV482560	CV482560 AGENCOURT	923	140.4	4.9	221	4	BM532327	BM532327 fy06e11.Y	
851	140.8	4.9	786	1	AV682266	AV682266 AGENCOURT	924	140.4	4.9	229	6	CA802763	CA802763 sau41506.	
852	140.8	4.9	824	5	BUS65362	BUS65362 AGENCOURT	925	140.4	4.9	244	4	BM154314	BM154314 f983e11.Y	
853	140.8	4.9	835	5	BUS292221	BUS292221 AGENCOURT	926	140.4	4.9	254	2	BE057342	BE057342 en01h03.Y	
854	140.8	4.9	835	5	BUS292221	BUS292221 AGENCOURT	927	140.4	4.9	254	2	BE057342	BE057342 en01h03.Y	
855	140.8	4.9	841	5	BUS555504	BUS555504 AGENCOURT	928	140.4	4.9	256	6	CB088964	CB088964 f08a08.b	
856	140.8	4.9	843	5	BUS532179	BUS532179 AGENCOURT	929	140.4	4.9	257	7	CO065740	CO065740 Mdf3015j	
857	140.8	4.9	854	5	BUS555510	BUS555510 AGENCOURT	930	140.4	4.9	274	5	BM897348	BM897348 ph40h12.Y	
858	140.8	4.9	868	5	BUS587825	BUS587825 AGENCOURT	c	930	140.4	4.9	277	4	BM644186	BM644186 170006873
859	140.8	4.9	874	7	CK426624	CK426624 AUF Iptes	931	140.4	4.9	290	5	BM476522	BM476522 DKF2p688K	
860	140.8	4.9	898	3	BC017007	BC017007 Homo sapi	932	140.4	4.9	294	6	CA802699	CA802699 sau40g02.	
861	140.8	4.9	913	5	BUS663702	BUS663702 AGENCOURT	933	140.4	4.9	297	4	BM531692	BM531692 fx90a12.Y	
862	140.8	4.9	920	8	AZ691914	AZ691914 ENTWU26TR	934	140.4	4.9	307	7	CV525614	CV525614 Mdlv40120	
863	140.8	4.9	1022	3	CD050966	CD050966 Mus muscu	935	140.4	4.9	309	5	BU761114	BU761114 sae63c06	
864	140.8	4.9	1027	6	CD389435	CD389435 AGENCOURT	936	140.4	4.9	314	2	AN101789	AN101789 bd70a10.Y	
865	140.8	4.9	1055	4	BM562625	BM562625 AGENCOURT	937	140.4	4.9	326	5	BQ128910	BQ128910 i124e02.Y	
866	140.8	4.9	1106	9	CL103937	CL103937 ISB1-42D1	938	140.4	4.9	328	7	CK377760	CK377760 lai08b12.	
867	140.8	4.9	1322	5	BC022318	BC022318 AGENCOURT	939	140.4	4.9	329	4	BM774043	BM774043 ra88g10.Y	
868	140.8	4.9	1322	5	BC022318	BC022318 AGENCOURT	940	140.4	4.9	342	6	CF566569	CF566569 AGENCOURT	
869	140.8	4.9	1869	3	BC032469	BC032469 Homo sapi	941	140.4	4.9	342	7	CF546441	CF546441 lae73f10.	
870	140.8	4.9	2090	3	AF130105	AF130105 Homo sapi	942	140.4	4.9	343	7	CV525143	CV525143 Mdlv4010m	
871	140.8	4.9	3226	3	CR627326	CR627326 Homo sapi	943	140.4	4.9	348	6	CB704554	CB704554 AGMNUC1S	
872	140.8	4.9	3611	3	CR627025	CR627025 Homo sapi	944	140.4	4.9	362	7	CK350334	CK350334 hggfha23D	
873	140.6	4.9	195	6	CB817512	CB817512 d3k12p2.f	945	140.4	4.9	373	7	CK431025	CK431025 oJ57a05.Y	
874	140.6	4.9	220	7	CF330411	CF330411 DKF2p469D	946	140.4	4.9	379	7	CF425735	CF425735 lad43e11.	
875	140.6	4.9	233	7	CF533625	CF533625 UI-M-GHO-	947	140.4	4.9	388	7	CV524829	CV524829 Mdlv2 402	
876	140.6	4.9	236	6	CB948288	CB948288 AGENCOURT	948	140.4	4.9	396	2	BE806949	BE806949 sa90a08.Y	
877	140.6	4.9	239	5	BX503636	BX503636 DKF2p686J	949	140.4	4.9	399	7	CF369492	CF369492 f960e02.Y	
878	140.6	4.9	246	1	AL696192	AL696192 DKF2p686B	950	140.4	4.9	410	6	CB567405	CB567405 AGENCOURT	
879	140.6	4.9	257	4	AJ768204	AJ768204 AJ768204	951	140.4	4.9	410	7	CF425879	CF425879 lad45f06.	
880	140.6	4.9	257	4	BM582842	BM582842 170006872	952	140.4	4.9	410	7	CK625494	CK625494 mj10a08.Y	
881	140.6	4.9	270	1	AV836739	AV836739 AV836739	953	140.4	4.9	418	4	BF981774	BF981774 602305439	
882	140.6	4.9	273	6	CB945895	CB945895 AGENCOURT	954	140.4	4.9	430	7	CO415525	CO415525 Mdf3007C	
883	140.6	4.9	314	1	AL598254	AL598254 DKF2p468K	955	140.4	4.9	431	1	AK582351	AK582351 AGENCOURT	
884	140.6	4.9	318	5	BX500893	BX500893 DKF2p779B	956	140.4	4.9	448	7	CK597630	CK597630 AGENCOURT	
885	140.6	4.9	346	6	CA337022	CA337022 NISC 1v08	957	140.4	4.9	476	6	CD802812	CD802812 UI-M-GVO-	
886	140.6	4.9	398	7	CO066729	CO066729 Mdf30059	958	140.4	4.9	477	6	CD677843	CD677843 ho23b03.Y	
887	140.6	4.9	424	7	CK233937	CK233937 ref1f12.Y	959	140.4	4.9	490	7	CK430328	CK430328 oJ48a08.Y	
888	140.6	4.9	445	7	CF969977	CF969977 lai94h07.	960	140.4	4.9	492	7	CK849950	CK849950 EST1992.Z	
889	140.6	4.9	450	5	BQ395409	BQ395409 NISC ng14	961	140.4	4.9	500	1	AV757598	AV757598 AV757598	
890	140.6	4.9	472	7	CF124560	CF124560 UI-HF-CHO	962	140.4	4.9	500	4	BG571546	BG571546 602592845	
891	140.6	4.9	487	1	AV755581	AV755581 AV755581	963	140.4	4.9	502	6	CA380461	CA380461 659741 NC	
892	140.6	4.9	507	7	CK431107	CK431107 oJ58a07.Y	964	140.4	4.9	503	6	CA376868	CA376868 655327 NC	
893	140.6	4.9	528	2	BE968552	BE968552 601649669	965	140.4	4.9	515	7	CK120087	CK120087 209f01.p1	
894	140.6	4.9	544	5	BQ398892	BQ398892 NISC mo12	966	140.4	4.9	523	5	BM473088	BM473088 DKF2p686K	
895	140.6	4.9	582	4	BG925169	BG925169 HNC39-1-G	967	140.4	4.9	567	6	CB977562	CB977562 CAB40004	
896	140.6	4.9	594	6	CB218991	CB218991 NISC nb11	968	140.4	4.9	596	4	BG575780	BG575780 602597276	
897	140.6	4.9	599	6	CB052505	CB052505 NISC gl08	969	140.4	4.9	616	7	CK452365	CK452365 907985 MA	
898	140.6	4.9	773	7	CV064559	CV064559 WNE1248	970	140.4	4.9	628	6	CD766420	CD766420 AGENCOURT	
899	140.6	4.9	812	5	BUS55199	BUS55199 AGENCOURT	971	140.4	4.9	679	7	C0735887	C0735887 SLLJ05b13	
900	140.6	4.9	843	5	BUS51629	BUS51629 AGENCOURT	972	140.4	4.9	698	2	BF792767	BF792767 602253310	
							973	140.4	4.9	710	2	AW349204	AW349204 GM210004A	



974	140.4	4.9	716	6	CD641621	AGENCOURT	1047	140.2	4.9	893	5	B0851134	AGENCOURT
975	140.4	4.9	766	5	B0534557	AGENCOURT	1048	140.2	4.9	901	5	B0181433	AGENCOURT
976	140.4	4.9	808	6	CD520111	AGENCOURT	1049	140.2	4.9	914	5	B0718907	AGENCOURT
977	140.4	4.9	843	5	B0533556	AGENCOURT	1050	140.2	4.9	921	5	BQ222825	AGENCOURT
978	140.4	4.9	855	5	B055022	AGENCOURT	1051	140.2	4.9	926	5	B0554921	AGENCOURT
979	140.4	4.9	864	5	B0842866	AGENCOURT	1052	140.2	4.9	927	5	BQ722633	AGENCOURT
980	140.4	4.9	872	5	B0529249	AGENCOURT	1053	140.2	4.9	942	5	B0908292	AGENCOURT
981	140.4	4.9	872	7	CK022958	AGENCOURT	1054	140.2	4.9	1002	6	CD389396	AGENCOURT
982	140.4	4.9	908	5	B0945120	AGENCOURT	1055	140.2	4.9	1040	5	B0944642	AGENCOURT
983	140.4	4.9	914	5	B0587541	AGENCOURT	1056	140.2	4.9	1109	5	B0530365	AGENCOURT
984	140.4	4.9	920	9	CNS0062R	AL061710 Drosophil	1057	140.2	4.9	1158	4	B0556158	AGENCOURT
c 985	140.4	4.9	927	7	CV068663 f2 new_ch	AGENCOURT	1058	140.2	4.9	1699	3	HS0801509	AGENCOURT
986	140.4	4.9	946	5	BQ037422	AGENCOURT	1059	140.2	4.9	1926	3	HS0802868	AGENCOURT
987	140.4	4.9	951	6	CA792153	AGENCOURT	1060	140	4.9	189	7	CO182475	AGENCOURT
988	140.4	4.9	954	5	BQ278347	AGENCOURT	1061	140	4.9	203	1	AA624239	AGENCOURT
989	140.4	4.9	956	9	CL495518	AGENCOURT	1062	140	4.9	205	5	BX504787	AGENCOURT
990	140.4	4.9	960	5	B0512150	AGENCOURT	1063	140	4.9	208	6	CA802715	AGENCOURT
c 991	140.4	4.9	966	4	BM415421	OP20495 M	1064	140	4.9	218	7	CK377805	AGENCOURT
992	140.4	4.9	991	6	CD050059	AGENCOURT	1065	140	4.9	233	2	BE030380	AGENCOURT
993	140.4	4.9	1005	5	B0529990	AGENCOURT	1066	140	4.9	238	7	CO184969	AGENCOURT
994	140.4	4.9	1036	9	CNS031MJ	AGENCOURT	1067	140	4.9	277	7	CO185085	AGENCOURT
995	140.4	4.9	1040	6	CD047873	AGENCOURT	1068	140	4.9	294	1	AL725181	AGENCOURT
996	140.4	4.9	1040	6	CD356857	AGENCOURT	1069	140	4.9	294	7	CF328198	AGENCOURT
c 997	140.4	4.9	1253	5	BQ230949	AGENCOURT	1070	140	4.9	302	5	BQ740768	AGENCOURT
998	140.4	4.9	1258	4	BM476721	AGENCOURT	1071	140	4.9	333	4	CK378960	AGENCOURT
999	140.4	4.9	2596	3	BC053452	Mus muscu	1072	140	4.9	340	4	BG736364	AGENCOURT
1000	140.4	4.9	2623	3	HS0808057	AGENCOURT	1073	140	4.9	346	6	CA380966	AGENCOURT
1001	140.4	4.9	5201	3	BC063852	AGENCOURT	1074	140	4.9	350	6	CB045394	AGENCOURT
1002	140.2	4.9	175	4	BM187396	AGENCOURT	c1075	140	4.9	371	7	CO736053	AGENCOURT
1003	140.2	4.9	193	5	BX955696	AGENCOURT	c1076	140	4.9	381	8	CA802337	AGENCOURT
1004	140.2	4.9	196	6	CA819430	AGENCOURT	1077	140	4.9	391	6	BH924432	AGENCOURT
1005	140.2	4.9	217	4	BJ251664	AGENCOURT	c1078	140	4.9	411	7	CO193835	AGENCOURT
1006	140.2	4.9	222	4	B0475503	AGENCOURT	1079	140	4.9	418	4	B1323943	AGENCOURT
1007	140.2	4.9	229	5	BQ085944	AGENCOURT	1080	140	4.9	418	5	BX569452	AGENCOURT
1008	140.2	4.9	229	5	BQ087771	AGENCOURT	c1081	140	4.9	442	6	CD679816	AGENCOURT
1009	140.2	4.9	264	6	CB570894	AGENCOURT	1082	140	4.9	467	6	CB722109	AGENCOURT
1010	140.2	4.9	282	7	CO417188	AGENCOURT	1083	140	4.9	512	5	BQ266641	AGENCOURT
1011	140.2	4.9	298	7	CO184759	AGENCOURT	c1084	140	4.9	554	7	CK384476	AGENCOURT
1012	140.2	4.9	332	7	CO194028	AGENCOURT	1085	140	4.9	627	1	AV723953	AGENCOURT
1013	140.2	4.9	333	6	CA422505	AGENCOURT	1086	140	4.9	629	1	AV723953	AGENCOURT
c1014	140.2	4.9	339	7	CF512490	AGENCOURT	1087	140	4.9	640	6	CD766813	AGENCOURT
1015	140.2	4.9	361	7	CK005157	AGENCOURT	1088	140	4.9	680	7	CO074617	AGENCOURT
1016	140.2	4.9	369	6	CD638357	AGENCOURT	1089	140	4.9	688	7	CO074646	AGENCOURT
1017	140.2	4.9	375	7	CK371897	AGENCOURT	1090	140	4.9	693	6	CD641480	AGENCOURT
1018	140.2	4.9	378	1	AV762488	AGENCOURT	1091	140	4.9	699	6	CD641614	AGENCOURT
1019	140.2	4.9	405	1	A0790913	AGENCOURT	1092	140	4.9	722	6	CD237110	AGENCOURT
1020	140.2	4.9	433	1	AV681987	AGENCOURT	1093	140	4.9	738	6	CD641072	AGENCOURT
c1021	140.2	4.9	457	5	BQ527792	NISC no24	1094	140	4.9	776	5	B0554919	AGENCOURT
1022	140.2	4.9	490	7	CK400599	AGENCOURT	1095	140	4.9	799	5	B0564423	AGENCOURT
1023	140.2	4.9	491	1	AV757797	AGENCOURT	1096	140	4.9	814	5	B0564423	AGENCOURT
1024	140.2	4.9	495	7	CO752765	AGENCOURT	1097	140	4.9	828	5	B056151	AGENCOURT
1025	140.2	4.9	498	7	CK428252	AGENCOURT	1098	140	4.9	833	5	B056151	AGENCOURT
c1026	140.2	4.9	516	1	AV757012	AGENCOURT	1099	140	4.9	840	5	BM985977	AGENCOURT
1027	140.2	4.9	519	5	B0523357	AGENCOURT	1100	140	4.9	842	9	CNS010QN	AGENCOURT
1028	140.2	4.9	545	7	CV223275	taj59h05	1101	140	4.9	849	5	B0955415	AGENCOURT
1029	140.2	4.9	558	4	BG110283	AGENCOURT	1102	140	4.9	889	5	B056131	AGENCOURT
1030	140.2	4.9	583	5	BP209684	AGENCOURT	1103	140	4.9	895	7	CF595897	AGENCOURT
1031	140.2	4.9	583	5	BP341772	AGENCOURT	1104	140	4.9	904	7	CF580123	AGENCOURT
c1032	140.2	4.9	583	5	BQ525020	NISC no08	1105	140	4.9	905	5	B0946070	AGENCOURT
c1033	140.2	4.9	608	1	AI731270	ENLGH1903	1106	140	4.9	940	5	B0170642	AGENCOURT
1034	140.2	4.9	661	6	CD640938	AGENCOURT	1107	140	4.9	970	5	B0587989	AGENCOURT
1035	140.2	4.9	663	7	CV481556	AGENCOURT	1108	140	4.9	983	5	CK419790	AGENCOURT
1036	140.2	4.9	686	1	AV682222	AGENCOURT	1109	140	4.9	998	5	B0536971	AGENCOURT
1037	140.2	4.9	802	7	CF153371	AGENCOURT	1110	140	4.9	1001	5	B0172943	AGENCOURT
1038	140.2	4.9	803	5	B0530984	AGENCOURT	c1111	140	4.9	1006	5	CK425508	AGENCOURT
1039	140.2	4.9	820	7	CO403732	AGENCOURT	1112	140	4.9	1068	5	B0908068	AGENCOURT
1040	140.2	4.9	843	5	B0555489	AGENCOURT	1113	140	4.9				
1041	140.2	4.9	849	7	CK791811	AGENCOURT	1114	140	4.9				
1042	140.2	4.9	850	6	CA465239	AGENCOURT	1115	140	4.9				
c1043	140.2	4.9	852	7	CK196873	AGENCOURT	1116	140	4.9				
c1044	140.2	4.9	854	7	CK200376	FGAS00889	1117	140	4.9				
1045	140.2	4.9	858	5	B0959480	AGENCOURT	1118	140	4.9				
1046	140.2	4.9	870	5	B0958052	AGENCOURT	c1119	140	4.9				

1120	140	4.9	1222	5	BUS959505	BUS959505	AGENCOURT	1193	139.8	4.9	801	7	CV482505	CV482505	AGENCOURT
1121	140	4.9	2260	3	AFI16602	Homo sapi		1194	139.8	4.9	804	5	BUS953549	BUS953549	AGENCOURT
1122	140	4.9	2417	3	BC021396	Mus muscu		1195	139.8	4.9	806	5	BUS66414	BUS66414	AGENCOURT
1123	140	4.9	4347	3	CR749550	Homo sapi		1196	139.8	4.9	830	5	BUS35906	BUS35906	AGENCOURT
1124	140	4.9	5168	3	CR749408	Homo sapi		1197	139.8	4.9	832	5	BUS65229	BUS65229	AGENCOURT
1125	139.8	4.9	184	6	CA935285	saui5f03		1198	139.8	4.9	833	5	BUS43391	BUS43391	AGENCOURT
1126	139.8	4.9	200	5	BQ667387	pb60g04.y		1199	139.8	4.9	833	5	CNS007X3	CNS007X3	AGENCOURT
c1127	139.8	4.9	203	5	BQ399198	NISC mp02		1200	139.8	4.9	853	5	BUS941622	BUS941622	AGENCOURT
c1128	139.8	4.9	205	7	CO473086	QO0411.B		1201	139.8	4.9	856	5	BUS66974	BUS66974	AGENCOURT
1129	139.8	4.9	217	4	BG731047	daeo9h01		c1202	139.8	4.9	856	8	BH163251	BH163251	ENTSY51FR
1130	139.8	4.9	-217	7	CR545913	KDF2p470D		1203	139.8	4.9	893	5	BUS34614	BUS34614	AGENCOURT
1131	139.8	4.9	222	4	BM186176	fv98h07.y		1204	139.8	4.9	906	5	BUS43325	BUS43325	AGENCOURT
1132	139.8	4.9	223	1	AL697974	KDF2p686J		1205	139.8	4.9	919	6	CA979732	CA979732	AGENCOURT
1133	139.8	4.9	225	4	BM154392	BM154392		1206	139.8	4.9	921	6	CB844970	CB844970	M2PN-0536
1134	139.8	4.9	225	4	BM155365	fw03e12.y		1207	139.8	4.9	923	5	BUS29873	BUS29873	AGENCOURT
1135	139.8	4.9	225	4	BM811854	fx11c08.y		1208	139.8	4.9	962	6	CD388825	CD388825	AGENCOURT
1136	139.8	4.9	229	4	BM186136	fv98d05.y		1209	139.8	4.9	966	5	BUS34245	BUS34245	AGENCOURT
1137	139.8	4.9	229	4	BM532465	fy08e01.y		1210	139.8	4.9	1024	5	BUS907570	BUS907570	AGENCOURT
1138	139.8	4.9	229	5	BQ075932	BQ075932		1211	139.8	4.9	1060	6	CB203437	CB203437	AGENCOURT
1139	139.8	4.9	231	4	BM529684	fy14h03.y		1212	139.8	4.9	1063	4	BM469499	BM469499	AGENCOURT
1140	139.8	4.9	232	4	BM155357	fw03c02.y		1213	139.8	4.9	1091	9	CL078619	CL078619	CH216-151
1141	139.8	4.9	241	7	CR823371	ij29d11.y		1214	139.8	4.9	1511	3	BC030320	Mus muscu	
1142	139.8	4.9	244	4	BM573234	fy01d08.y		1215	139.8	4.9	2330	3	BC020201	Homo sapi	
1143	139.8	4.9	245	4	BI840174	fv07d09.y		1216	139.8	4.9	174	5	BM896563	ph52h07.y	
1144	139.8	4.9	245	4	BM342819	BM342819		1217	139.8	4.9	182	1	AL697655	AL697655	DKF2p686A
1145	139.8	4.9	246	6	CA802566	saui38d12.y		1218	139.8	4.9	182	4	BM155169	BM155169	fw09g10.y
1146	139.8	4.9	246	6	CR559419	KDF2p468I		1219	139.8	4.9	186	2	BF343172	BF343172	602015819
1147	139.8	4.9	248	4	BM154574	fv85g03.y		1220	139.8	4.9	187	4	BI749319	BI749319	ro76f11.y
1148	139.8	4.9	248	5	BX507072	KDF2p779G		1221	139.8	4.9	199	4	BJ699239	BJ699239	BJ699239
1149	139.8	4.9	248	6	CA935253	CA935253		1222	139.8	4.9	208	4	BI901084	BI901084	ib84g08.y
1150	139.8	4.9	249	4	BM187301	BM187301		1223	139.8	4.9	209	6	CA819818	CA819818	saui76e11.y
1151	139.8	4.9	251	4	BM573771	fy03e10.y		1224	139.8	4.9	216	7	CR753195	CR753195	DKF2p468G
1152	139.8	4.9	252	7	CR384699	CR384699		c1225	139.8	4.9	221	7	CN290189	CN290189	170006000
1153	139.8	4.9	261	4	BM154485	fv85g02.y		1226	139.8	4.9	221	7	CO168252	CO168252	Mdf33013
1154	139.8	4.9	265	2	AW185173	se87h05.y		1227	139.8	4.9	230	9	AG043664	Pan trogl	
1155	139.8	4.9	266	4	BM154640	BM154640		1228	139.8	4.9	231	9	AG043664	Pan trogl	
1156	139.8	4.9	268	4	BM154858	BM154858		1229	139.8	4.9	233	7	CF572716	CF572716	MCSA05380
1157	139.8	4.9	268	5	BM889222	BM889222		1230	139.8	4.9	233	7	CF124181	CF124181	UI-HP-CH0
1158	139.8	4.9	272	7	CR655115	CR655115		1231	139.8	4.9	240	6	CD520495	CD520495	AGENCOURT
1159	139.8	4.9	273	7	CF635575	CF635575		1232	139.8	4.9	244	1	AA624252	AA624252	vm98f10.r
1160	139.8	4.9	279	4	BI671444	fs48d07.y		1233	139.8	4.9	245	7	CF212786	CF212786	IPCGJx13
1161	139.8	4.9	280	4	BM532335	BM532335		c1234	139.8	4.9	246	5	BQ394140	BQ394140	NISC ng07
1162	139.8	4.9	283	6	CB100809	k162a09.y		1235	139.8	4.9	265	6	CB345713	CB345713	CA48EN000
1163	139.8	4.9	290	6	CD640448	CD640448		1236	139.8	4.9	273	2	AW164794	AW164794	se77h06.y
1164	139.8	4.9	316	6	CD639207	CD639207		c1237	139.8	4.9	274	5	BQ385858	BQ385858	NISC mm14
1165	139.8	4.9	320	2	AW509353	AW509353		1238	139.8	4.9	304	4	BJ686940	BJ686940	BJ686940
1166	139.8	4.9	343	6	CB693202	CB693202		c1239	139.8	4.9	312	5	BX479900	BX479900	KDF2p686D
1167	139.8	4.9	348	4	BJ696950	BJ696950		1240	139.8	4.9	312	7	CO191506	CO191506	EC31225.5
1168	139.8	4.9	364	2	BF054789	BF054789		1241	139.8	4.9	317	2	AW827203	AW827203	xn09c12.y
1169	139.8	4.9	386	6	CB939082	CB939082		1242	139.8	4.9	333	7	CO184639	CO184639	EC28357.5
1170	139.8	4.9	387	7	CF426295	CF426295		c1243	139.8	4.9	350	1	AL709448	AL709448	KDF2p686C
1171	139.8	4.9	390	6	CA935536	CA935536		1244	139.8	4.9	358	5	BX505899	BX505899	KDF2p686P
1172	139.8	4.9	406	6	CB807444	CB807444		1245	139.8	4.9	361	7	CF780317	CF780317	ta06e09
1173	139.8	4.9	432	7	CO193025	CO193025		1246	139.8	4.9	367	7	CO183483	CO183483	EC25802.5
1174	139.8	4.9	441	7	CK428352	CK428352		1247	139.8	4.9	369	2	BE018711	BE018711	bb83h12.y
1175	139.8	4.9	452	7	CK427279	CK427279		1248	139.8	4.9	379	7	CK937918	CK937918	CBK7100448
1176	139.8	4.9	456	7	CK428499	CK428499		1249	139.8	4.9	385	6	CB986763	CB986763	AGENCOURT
1177	139.8	4.9	478	7	CK984157	CK984157		1250	139.8	4.9	385	6	CD641149	CD641149	AGENCOURT
1178	139.8	4.9	494	6	CB451987	CB451987		1251	139.8	4.9	399	1	A1226246	A1226246	ue88h04.y
1179	139.8	4.9	514	5	BQ521704	BQ521704		1252	139.8	4.9	418	7	CF370429	CF370429	rg65b01.y
c1180	139.8	4.9	525	2	BF284124	BF284124		1253	139.8	4.9	478	6	CB094707	CB094707	hz74b01.b
1181	139.8	4.9	528	7	CV223252	CV223252		c1254	139.8	4.9	493	5	BQ521529	BQ521529	NISC nl11
1182	139.8	4.9	559	7	CV199777	CV199777		1255	139.8	4.9	501	5	BQ396639	BQ396639	NISC ng22
1183	139.8	4.9	560	4	BG928605	BG928605		1256	139.8	4.9	507	6	CB347782	CB347782	CAB35G000
1184	139.8	4.9	596	7	CO087667	CO087667		1257	139.8	4.9	512	6	CA744558	CA744558	wr11a.pk0
1185	139.8	4.9	615	7	CK793480	CK793480		1258	139.8	4.9	515	7	CN975324	CN975324	25047.125
1186	139.8	4.9	635	6	CD773201	CD773201		1259	139.8	4.9	516	7	CN975322	CN975322	25045.125
1187	139.8	4.9	666	7	CN156992	CN156992		1260	139.8	4.9	527	7	CN975127	CN975127	24831.125
1188	139.8	4.9	728	1	AV756770	AV756770		c1261	139.8	4.9	528	6	CF006965	CF006965	QBI24d05
1189	139.8	4.9	759	7	CV200528	CV200528		1262	139.8	4.9	530	1	AV727776	AV727776	AV727776
1190	139.8	4.9	770	5	BUS37695	BUS37695		c1263	139.8	4.9	536	5	BQ521883	BQ521883	NISC nl13
1191	139.8	4.9	789	5	BUS67045	BUS67045		c1264	139.8	4.9	538	5	BQ397543	BQ397543	NISC ng28
1192	139.8	4.9	797	5	BUS37719	BUS37719		1265	139.8	4.9	566	6	CB079925	CB079925	hp78h06.b

1266	139.6	4.9	571	3	BC049598	Mus muscu	1339	139.4	4.9	426	7	CF545613	CF545613
1267	139.6	4.9	582	3	BC061127	Mus muscu	1340	139.4	4.9	440	7	CF301049	CF301049
1268	139.6	4.9	590	6	CB937830	IpocGjX13_	1341	139.4	4.9	454	5	BX500114	BX500114
1269	139.6	4.9	594	6	CV199728	kml19b10.y	1342	139.4	4.9	461	1	AV681668	AV681668
1270	139.6	4.9	607	1	AA522011	vh78c09.r	1343	139.4	4.9	473	1	AU791816	AU791816
1271	139.6	4.9	661	6	CD641297	AGENCOURT	1344	139.4	4.9	475	7	CN843209	CN843209
1272	139.6	4.9	667	6	CD638527	AGENCOURT	1345	139.4	4.9	486	4	BI743903	BI743903
1273	139.6	4.9	697	4	BC925969	HNC22-1-F	1346	139.4	4.9	550	7	CN164657	CN164657
1274	139.6	4.9	702	7	CV065824	WNEI27b1	1347	139.4	4.9	589	1	AI207510	AI207510
1275	139.6	4.9	729	4	BF982046	602305336	1348	139.4	4.9	601	7	CF369687	CF369687
1276	139.6	4.9	730	2	BE613622	601504411	1349	139.4	4.9	608	6	CD766630	CD766630
1277	139.6	4.9	730	6	CD638709	AGENCOURT	1350	139.4	4.9	619	7	CF357352	CF357352
1278	139.6	4.9	796	9	CNS011GK	Drosophil	1351	139.4	4.9	623	7	CN051788	CN051788
1279	139.6	4.9	821	5	BU960356	AGENCOURT	1352	139.4	4.9	734	5	BU535289	BU535289
1280	139.6	4.9	823	5	BU844017	AGENCOURT	1353	139.4	4.9	739	1	AV706777	AV706777
1281	139.6	4.9	833	8	BA2667852	ENTWN74TR	1354	139.4	4.9	779	7	CV482931	CV482931
1282	139.6	4.9	868	7	CO797683	AGENCOURT	1355	139.4	4.9	792	7	CV162353	CV162353
1283	139.6	4.9	873	5	BU852003	AGENCOURT	1356	139.4	4.9	796	7	CV489012	CV489012
1284	139.6	4.9	878	5	BU844333	AGENCOURT	1357	139.4	4.9	803	5	BU536633	BU536633
1285	139.6	4.9	905	5	BU589645	AGENCOURT	1358	139.4	4.9	805	5	BU957844	BU957844
1286	139.6	4.9	906	5	BU531084	AGENCOURT	1359	139.4	4.9	811	3	BC050987	BC050987
1287	139.6	4.9	913	6	CB588741	AGENCOURT	1360	139.4	4.9	813	7	CV487986	CV487986
1288	139.6	4.9	923	5	BU943690	AGENCOURT	1361	139.4	4.9	815	7	CK396579	CK396579
1289	139.6	4.9	925	4	BM416279	OP21369 M	1362	139.4	4.9	822	5	BU534594	BU534594
1290	139.6	4.9	929	5	BU590108	AGENCOURT	1363	139.4	4.9	840	5	BU843224	BU843224
1291	139.6	4.9	930	7	CV068616	f2_new_ch	1364	139.4	4.9	848	5	BU529378	BU529378
1292	139.6	4.9	959	6	CD050373	AGENCOURT	1365	139.4	4.9	848	5	BU958202	BU958202
1293	139.6	4.9	977	2	BE777769	601463009	1366	139.4	4.9	853	5	BU847233	BU847233
1294	139.6	4.9	1011	6	BQ928127	AGENCOURT	1367	139.4	4.9	857	7	CO913882	CO913882
1295	139.6	4.9	1116	6	CA475599	AGENCOURT	1368	139.4	4.9	858	5	BU530595	BU530595
1296	139.6	4.9	1126	6	CD505160	CDA72-B09	1369	139.4	4.9	859	7	CO808031	CO808031
1297	139.6	4.9	1842	3	BC036564	Mus muscu	1370	139.4	4.9	867	5	BU959812	BU959812
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1300	139.6	4.9	160	5	BM896912	ph49f06.y	1373	139.4	4.9	878	5	BU958840	BU958840
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1309	139.4	4.9	221	7	CO415408	Mdf+3006j	1382	139.4	4.9	1012	5	BU904623	BU904623
1310	139.4	4.9	224	6	CA935085	sau44b08.	1383	139.4	4.9	1020	5	BQ218454	BQ218454
1311	139.4	4.9	236	4	CB199266	BU679266	1384	139.4	4.9	1052	5	BU560001	BU560001
1312	139.4	4.9	257	6	CB191298	SILL05b13	1385	139.4	4.9	1069	6	CD387126	CD387126
1313	139.4	4.9	258	7	CO735938	AGENCOURT	1386	139.4	4.9	1074	6	CD051138	CD051138
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1316	139.4	4.9	276	4	BM341177	fw52f11.y	1389	139.4	4.9	3645	3	HS8807326	HS8807326
1317	139.4	4.9	278	7	CO192919	EC34778.5	1390	139.2	4.9	191	1	AL696149	AL696149
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## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Homo sapiens mRNA; cDNA DKFZp686N24154 (from clone DKFZp686N24154).  
ACCESSION BX640676  
VERSION  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
CONSTRM The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the  
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA  
sequencing consortium of the German Genome Project. This clone  
(DKFZp686N24154) is available at the RZPD Deutsches  
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686N24154  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

## FEATURES

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LOCUS  
DEFINITION Homo sapiens HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,  
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ACCESSION AY406074  
VERSION AY406074.1 GI:39762048

2214 bp DNA linear GSS 12-DEC-2003



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KEYWORDS      GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS        1 (bases 1 to 2214)
                Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE          Inferring nonneutral evolution from human-chimp-mouse orthologous
                gene trios
JOURNAL        Science 302 (5652), 1960-1963 (2003)
PUBMED         14671302
REFERENCE      2 (bases 1 to 2214)
AUTHORS        Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE          Direct Submission
JOURNAL        Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
COMMENT        This sequence was made by sequencing genomic exons and ordering
                them based on alignment.
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RESULT 4
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DEFINITION   AK088017 2746 bp mRNA linear HTC 03-APR-2004
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ACCESSION   AK088017
VERSION     AK088017.1 GI:26352935
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SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
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REFERENCE
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE     High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED    10349636
REFERENCE
AUTHORS   Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20493374
PUBMED    11042159
REFERENCE
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2746)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,N., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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Qy 1939 CATCCAGTGTGAGTGTCACTGTATTAACATGTTCTGTGCCAGCTGGGAACCACTGCCCTTC 1998

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Qy 2359 GTAGGCTGATGCGGCTCCACTACTAGGACAGCAATTTGAAGATGCGAGGCTTTGCAAG 2418

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Qy 2419 AAGTAAGTTTCTTAAAGAGACCA-----TATACAAAACCTCTCCACTCCAGTACCT 2472

Db 2457 AACTGGATTTCTTCAAGAGACCATGTGACTAGAGAGGAGAACCTCTTGTCTCTTCTCA 2516

Qy 2473 GGTGTCTTCCCACTTTTCAAGTATACGAATGCCATCAGCTTGAACAGGAGAGATCTGG 2532

Db 2517 CTCAGAGTGTGACTGTCAATCAGTTTGGGTTGAAAAGTTGATTTGGGAGGCGCTGG 2576

Qy 2533 GCTTCATGAGGCGCTTTTGAAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGAGACAGCCCA 2592

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Qy 2593 GGGCAGCAGAGCTGGGATGTGTGATGCTTTTGTGTATACATGGCCACACAGTACAGTCTGT 2652

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DEFINITION Mus musculus HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,  
AY406076 genomic survey sequence.  
ACCESSION AY406076  
VERSION AY406076.1 GI:39762050  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 2214)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 2214)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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QY 1955 ACTGATAACATGTTCTGTGCCAGCTGGGAAACCCACTGCCCCCTTCTGATATCTGCATGCA 2014
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DEFINITION genomic survey sequence.
ACCESSION AY406075
VERSION AY406075.1 GI:39762049
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2214)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2214)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5757.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?&CS0D1086AH1NPI&c=5757.r.  
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primer. Five prime end enriched, double-strand cDNA was  
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Query Match 33.1%; Score 942; DB 5; Length 1008;  
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Db 126 CTCGAAGTTCTAGAGAGCTGCTGTGGGACAGCCGCCAGGCGCAGAGCTGGGATGTGTGC 67  
QY 2618 ATGCTTTGTGTATAGTGGCCACAGTACAGTCTGGTCTCTTTTCTTCCCATCTCTTGTAC 2677  
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QY 2678 ACATTTT 2684  
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RESULT 9  
BX434191/c  
LOCUS BX434191 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YD01  
DEFINITION 3-PRIME, mRNA sequence.  
ACCESSION BX434191  
VERSION BX434191.2 GI:47003442  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 897)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 15, 2003 this sequence version replaced gi.30775248.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 5757.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?&CS0BAK025BH09NM1&c=5757.r.  
Location/Qualifiers  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoR V sites of the pCMVSPORT 6 vector.  
Library was not normalized."

FEATURES

source  
Query Match 31.1%; Score 885.8; DB 5; Length 897;  
Best Local Similarity 99.2%; Pred. No. 3.8e-164;  
Matches 890; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1809 ACATCACTGTGGCTGGGAATGTCTTGGCAGACGTGAGGAGCCCTTGCATCAAGAACG 1868



QY 614 CGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTC 673  
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 QY 674 CTCCTCCACTCCGATGGGTCCAAAGATTTTGACGGTTTCCATGCCATTTATGAGGAGATC 733  
 Db 661 CTCCTCCACTCCGATGGGTCCAAAGATTTTGACGGTTTCCATGCCATTTATGAGGAGATC 720  
 QY 734 ACAGCATGCTCTCATCCCTTGTTCATGACGAGCATGGCTCCTTGACAAAGCTGGA 793  
 Db 721 ACAGCATGCTCTCATCCCTTGTTCATGACGAGCA-STGGTCTCTTGACAAAGCTGGA 779  
 QY 794 TCTTCAAGTGTGCTGCTTGGCAGCTATATCGGCAGCGCTGTGAAAATCTCTCTTCAA 853  
 Db 780 TCTTCAAGTGTGCTGCTTGGCAGCTATATCGGCAGCGCTGTGAAAATCTCTCTGGRG 839  
 QY 854 GAAAGAACTGC 865  
 Db 840 GCTGGGAAGTCC 851

RESULT 11  
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 LOCUS BX439313 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YD01  
 DEFINITION 5-PRIME, mRNA sequence.  
 ACCESSION BX439313  
 VERSION BX439313.2 GI:47007084  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 952)  
 Li.W.B., Gruber.C., Jessee.J. and Polayes.D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 15, 2003 this sequence version replaced gi:30779754.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
 was not normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 This sequence belongs to sequence cluster 5757.r  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdnaf8=CS0DE009CB01QPl6c=5757.r.  
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 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."

FEATURES  
 source

ORIGIN  
 Query Match 28.6%; Score 815.2; DB 5; Length 952;  
 Best Local Similarity 98.3%; Pred.No. 3.2e-150;  
 Matches 834; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
 QY 14 GCCGCGGCAAGATGAGCTGGGTCTCTGGACGACAGTGGGGCTCACTTTCTTCAGCTC 73  
 Db 1 GCCGCGGCAAGATGAGCTGGGTCTCTGGACGCA-TTGGGGCTCACTTTCTTCAGCTC 59

QY 74 CTTCTCATCTCGTCTCTGCGCAAGAGATACACAGTCAATTAATGAAGCCTGCCCTCGAGCA 133  
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 QY 134 GAGTGGAAATATCATGTGTGCGGAGTGTGTGAATATGATCAGATTGAGTGTGCGTCTGCCCC 193  
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 QY 254 GACTCTCTGCTGATCCACCCAGAGTTGTATACCATCTTTGAAAACTGCAAGAGCTGCCGAAAT 313  
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 QY 314 GGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTATCTGTCAGAGTGC 373  
 Db 300 GGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTATCTGTCAGAGTGC 359  
 QY 374 CGAGCAGGCTGGTACGGAGGAGACTGTCATGCGATGTGGCCAGAGTTCTCGAGCCCCAAG 433  
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 QY 434 GGTTCAGATTTTGTGAAAAAGCTATCCCTTAAATGCTCACTGTGAATGGACCATTCATGCT 493  
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 QY 494 AAACCTGGGTTTGTTCATCCAACTAAGATTTGTTCATGTTGAGTCTCGAGTTTGACTACATG 553  
 Db 480 AAACCTGGGTTTGTTCATCCAACTAAGATTTGTTCATGTTGAGTCTCGAGTTTGACTACATG 539  
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 Db 540 TCCAGTATGACTATGTTGAGTTTCTGATCGAGACAACCGCATGGCCAGATCATCAAG 599  
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 Db 780 TCTTCAAGTGTGCTGCTTGGCAGGCTATATCTGGCAGCGCTGTGAAAATCTGATTA 839  
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 Db 840 GATACGAA 847

RESULT 12  
 CD514783 879 bp mRNA linear EST 06-JUN-2003  
 LOCUS AGENCOURT 14376424 NIH.MGC 181 Homo sapiens cDNA clone  
 DEFINITION IMAGE:30396311 5', mRNA sequence.  
 ACCESSION CD514783  
 VERSION CD514783.1 GI:31446501  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 879)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM477 row: m column: 24  
High quality sequence stop: 613.

## FEATURES

source

Location/Qualifiers  
1. 879  
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/lab\_host="DH10B-Ton A (T1 and T5 phage resistances)"  
/clone\_lib="NIH\_MGC\_181"  
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV  
(destroyed); Library is oligo-dT primed and directionally  
cloned (EcoRV site is destroyed upon cloning). Average  
insert size 1.42 kb. Library was constructed by  
(Invitrogen). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 28.5%; Score 809.8; DB 6; Length 879;  
Best Local Similarity 99.2%; Pred. No. 3.7e-149;  
Matches 844; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

Qy 952 CGTGTGCTCTTTTGTAACTCTCTATGTTCTTAGTGCAATGAGAAAGAACTTG 1011  
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Qy 1012 CCAGCAGATGGAGTGGTCAGGAAACAGCCCATCTGCATTAAGCCTGCCGAGACC 1071  
Db 61 CCAGCAGATGGAGTGGTCAGGAAACAGCCCATCTGCATTAAGCCTGCCGAGACC 120

Qy 1072 AAAGATTTTCCAGCTGTGAGAGGAGAGTCTTCCGATGTCAGGTTTCACTCAAGGGAGAC 1131  
Db 121 AAAGATTTTCCAGCTGTGAGAGGAGAGTCTTCCGATGTCAGGTTTCACTCAAGGGAGAC 180

Qy 1132 ACCATTACACAGCTATATCTAGCGGCTTTCAGCAAGCAGAAACTGCGAGAGTGCCTTAC 1191  
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Qy 1192 CAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGATACCAACTCTGCATACCCA 1251  
Db 241 CAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGATACCAACTCTGCATACCCA 300

Qy 1252 GCTCCAGTATGAGTCATCTCACCTCTTACCGCGCTTGGGCGAGCAGGAGGACATG 1311  
Db 301 GCTCCAGTATGAGTCATCTCACCTCTTACCGCGCTTGGGCGAGCAGGAGGACATG 360

Qy 1312 TCTGAGGACTGGGAAGTGGAGTGGCGGCGACCATCTTCGATCTCTATCTGCGGGAAT 1371  
Db 361 TCTGAGGACTGGGAAGTGGAGTGGCGGCGACCATCTTCGATCTCTATCTGCGGGAAT 420

Qy 1372 TGAGACATCTCTCCAAAGACCAAGGGTGGCTGGCGTGGCAGGAGCCATCTA 1431  
Db 421 TGAGACATCTCTCTCCAAAGACCAAGGGTGGCTGGCGTGGCAGGAGCCATCTA 480

Qy 1432 CAGGAGGACCAAGCGGGTGCATGAGCGAGCTTACCAAGGAGGCGTGGTCTCTAGTCTG 1491  
Db 481 CAGGAGGACCAAGCGGGTGCATGAGCGAGCTTACCAAGGAGGCGTGGTCTCTAGTCTG 540

Qy 1492 CAGCGGTGCTGGTGAATGAGCGCACTGTGGTGGCTGCCCACTGTGTTACTGACCT 1551

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Qy 1552 GGGGAAGGTCCACCATGATCAAGACAGCAGACCTGAAAGTGTGTTGGGGAATTTCTACCG 1611  
Db 601 GNGGAGGTCCACCATGATCAAGACAGCAGACCTGAAAGTGTGTTGGGGAATTTCTACCG 660  
Qy 1612 GGATGATCAGCGGGATGAGAAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTGCA 1671  
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Qy 1789 CACTTCCTTCC 1799  
Db 841 CACTTCCTTCC 851

RESULT 13  
BX337781 886 bp mRNA linear EST 07-APR-2004  
LOCUS BX337781 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0DI051YA20 5-PRIME, mRNA sequence.  
ACCESSION BX337781  
VERSION BX337781.2 GI:46268407  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 886)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 2, 2003 this sequence version replaced gi:30333640.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5757.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?e=CS0DI051BA10QPl&c=5757.r.  
Location/Qualifiers  
1. 886  
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digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
source

Query Match 28.4%; Score 809.4; DB 5; Length 886;  
Best Local Similarity 98.6%; Pred. No. 4.5e-149;  
Matches 835; Conservative 2; Mismatches 8; Indels 2; Gaps 2;

Qy 1 CGCTCGGCGACAGCCGCGGCAAGATGGAGCTGGTGTGTCGACGCGAGTTGGGGCTCAC 60

Db 38 CGCTGGGACACAGCGCGGCAAGGATGGAGTCTGGGTTGCTGGACGCGAGTTGGGGCTCAC 97  
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Db 98 TTTTCTTCAGCTCTTCTCATCTCGTCTTGTGCAAGAGAGTACACAGTCATTATGAAGC 157  
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Db 218 GTGGCTCTGCCCCGAAAGAGGAAAGTCTGTGGGTTTATACCATCCCTTCTGCAGGAATGA 277  
Qy 241 GGAGATGAGTGTGACTCTGCTGCTGATCCAGCCAGGTTGTACCATCTTTGAAACTGCAA 300  
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Qy 301 GAGCTGCGGAATAGGCTCATGCGGGGGTACCTTTGGATGACTTCTATGTGAAGGGTCTCTA 360  
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Qy 361 CTGTGACAGATGCCAGCAGGCTGTGTACGGAGGAGACTGCATGCGATGTGCCAGGTTCT 420  
Db 398 CTGTGACAGATGCCAGCAGGCTGTGTACGGAGGAGACTGCATGCGATGTGCCAGGTTCT 457  
Qy 421 GCGAGCCCCAAGGGTCAAGTTTGTGGAAGGCTATCCCTAAATGCTCCTCATCTGTAATG 480  
Db 458 GCGAGCCCCAAGGGTCAAGTTTGTGGAAGGCTATCCCTAAATGCTCCTCATCTGTAATG 517  
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Qy 600 GCCAGATCATCAGCGTGTCTGTGCAAGAGGCGGCGAGTCTCTATCCAGAGCATAGAT 659  
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Qy 660 CTTCACTCCAGTCTCTTCCACTCCGATGGTCCCAAGAAATTTTCACGGTTTCCATGCCA 719  
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Qy 840 AAAATCT 846  
Db 877 AATCTCY 883

## RESULT 14

AK031254  
LOCUS AK031254 2184 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930437L24 product:hypothetical BGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine proteases, trypsin family domain containing protein, full insert sequence.  
ACCESSION AK031254  
VERSION AK031254.1 GI:26082224  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2184)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
1. 2184  
/organism="Mus musculus"  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
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ORIGIN
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Best Local Similarity 86.1%; Pred. No. 1e-146;
Matches 895; Conservative 0; Mismatches 144; Indels 1; Gaps 1;

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CD655367 795 bp mRNA linear EST 18-JUN-2003
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CD655367.1 GI:31895529
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS Contact: Daniela S. Gerhard, Ph.D.
JOURNAL Office of Cancer Genomics
COMMENT National Cancer Institute / NIH
Biolog. 31 Rm10A07 Bethesda, MD 20892
Email: csapbs-remail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
cDNA Library Preparation: Yulan Piao and Minoru Ko
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC c lone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM512 row: g column: 24
High quality sequence stop: 676.
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/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MEK feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with Trizol Reagent
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from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199] Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACATGCTTAGATCGGAGCGGCCCTTTTCTTTTCTTTT-3'] from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

Search completed: May 6, 2005, 15:01:47  
Job time : 6113 secs

## ORIGIN

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QY 877	GGGCCCCAGTCAATGGGTACCGAATAATACAGGGGGGCTTGGGCTTATCAAGGACGCCA	936		
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Db				
723	TATCTGGGGAAAATTGAG-ACATCACTGCTCCAAAGACCAAGGTT	768		



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 12:57:47 ; Search time 332 Seconds  
(without alignments)  
14026.637 Million cell updates/sec

Title: US-10-063-692-37

Perfect score: 2846  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents NA.\*

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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108	109.4	3.8	1771	4	US-09-905-381A-158	Sequence 158, App	c 181	98	3.4	3438	4	US-10-164-595-29	Sequence 29, Appl
109	109.4	3.8	1771	4	US-09-906-618-158	Sequence 158, App	182	97.2	3.4	272	4	US-09-270-767-11902	Sequence 11902, A
110	109.4	3.8	1771	4	US-09-906-618-158	Sequence 158, App	182	97.2	3.4	272	4	US-09-270-767-11902	Sequence 11902, A
111	109.2	3.8	359	4	US-09-621-976-16008	Sequence 16008, A	183	97.2	3.4	347	4	US-09-621-976-16026	Sequence 16026, A
112	109.2	3.8	359	4	US-09-621-976-16019	Sequence 16019, A	184	97	3.4	97	4	US-09-621-976-12430	Sequence 12430, A
113	109.2	3.8	362	4	US-09-621-976-16010	Sequence 16010, A	185	97	3.4	1098	3	US-09-248-335-35	Sequence 35, Appl
114	109	3.8	365	4	US-09-621-976-16042	Sequence 16042, A	186	96.8	3.4	1342	4	US-09-489-847-89	Sequence 89, Appl
115	109	3.8	111	3	US-09-297-535-23	Sequence 23, Appl	187	96.8	3.4	2665	3	US-08-971-089-5	Sequence 5, Appli
116	109	3.8	121	3	US-09-297-535-20	Sequence 20, Appl	188	96.6	3.4	1445	3	US-08-971-089-5	Sequence 5, Appli
117	108.6	3.8	371	4	US-09-621-976-16048	Sequence 16048, A	c 189	96.4	3.4	260	2	US-08-520-767A-29	Sequence 29, Appl
118	108.6	3.8	949	4	US-09-489-847-35	Sequence 35, Appl	c 190	96.4	3.4	260	3	US-08-897-126-29	Sequence 29, Appl
119	108.6	3.8	1493	1	US-08-340-820-24	Sequence 24, Appl	c 191	96.4	3.4	268	4	US-09-621-976-73	Sequence 73, Appl
120	108	3.8	2327	1	US-08-593-535-24	Sequence 24, Appl	c 192	96.4	3.4	582	4	US-09-787-292-3	Sequence 3, Appli
121	108	3.8	2434	4	US-10-066-130-20	Sequence 20, Appl	c 193	96.4	3.4	2852	3	US-09-027-137-2	Sequence 2, Appli
122	108	3.8	2674	4	US-10-066-130-19	Sequence 19, Appl	c 194	96.2	3.4	2852	3	US-09-344-441-2	Sequence 2, Appli
123	108	3.8	2771	4	US-10-066-130-18	Sequence 18, Appl	195	96.2	3.4	194	4	US-09-621-976-801	Sequence 801, App
124	108	3.8	5860	4	US-10-066-130-17	Sequence 17, Appl	196	96.2	3.4	3116	4	US-09-311-021-187	Sequence 187, App
c 125	108	3.8	9589	1	US-07-925-695-1	Sequence 1, Appli	197	96.2	3.4	4086	4	US-09-702-705-1801	Sequence 1801, Ap
c 126	108	3.8	9589	1	US-07-925-695-2	Sequence 2, Appli	198	96.2	3.4	4086	4	US-09-736-457-1801	Sequence 1801, Ap
c 127	108	3.8	12980	3	US-08-811-566-5	Sequence 5, Appli	199	96.2	3.4	4086	4	US-09-671-325-1801	Sequence 4, Appli
c 128	108	3.8	12980	3	US-09-034-756-5	Sequence 5, Appli	c 200	96	3.4	537	4	US-09-720-201A-4	Sequence 6, Appli
129	107.8	3.8	357	4	US-09-621-976-16058	Sequence 16058, A	c 201	96	3.4	644	4	US-09-720-201A-6	Sequence 24, Appl
130	107.8	3.8	1872	3	US-09-801-052-1	Sequence 1, Appli	202	96	3.4	2323	3	US-09-149-476-24	Sequence 24, Appl
131	107.8	3.8	1872	3	US-10-020-121-1	Sequence 1, Appli	203	95.4	3.4	1406	4	US-10-000-489-81	Sequence 81, Appl
132	107.6	3.8	1141	4	US-09-800-729-78	Sequence 78, Appl	204	95.4	3.4	3334	4	US-09-668-119-2	Sequence 2, Appli
133	107.6	3.8	2184	3	US-08-955-948C-1	Sequence 1, Appli	205	95.2	3.3	105	4	US-09-621-976-13820	Sequence 1, Appli
134	107.6	3.8	2184	3	US-08-697-766A-1	Sequence 1, Appli	206	95.2	3.3	351	4	US-09-559-023-1	Sequence 1, Appli
c 135	107	3.8	356	2	US-08-520-678A-22	Sequence 22, Appl	207	95	3.3	333	3	US-09-621-976-15134	Sequence 19, Appl
c 136	107	3.8	356	3	US-08-897-126-22	Sequence 22, Appl	208	95	3.3	1277	4	US-09-720-317A-19	Sequence 19, Appl
c 137	107	3.8	9646	3	US-08-811-566-1	Sequence 1, Appli	209	94.8	3.3	3556	4	US-09-270-767-25838	Sequence 25838, A
c 138	107	3.8	9646	3	US-09-034-756-1	Sequence 1, Appli	210	94.6	3.3	2216	4	US-09-426-783-5	Sequence 5, Appli
139	106.6	3.7	1641	1	US-08-300-903A-8	Sequence 8, Appli	c 211	94.6	3.3	2621	2	US-08-553-619B-8	Sequence 8, Appli
140	106.6	3.7	1641	4	US-08-988-197-8	Sequence 8, Appli	212	94.6	3.3	3715	4	US-09-234-245-1	Sequence 1, Appli
141	106.6	3.7	1641	4	US-10-385-072-8	Sequence 8, Appli	213	94.4	3.3	333	3	US-09-018-584A-27	Sequence 27, Appl
142	106	3.7	1454	3	US-09-372-422A-19	Sequence 19, Appl	214	94.4	3.3	1091	4	US-09-328-965-1	Sequence 1, Appli
143	105.6	3.7	1882	3	US-09-370-253-1	Sequence 1, Appli	215	94.4	3.3	333	3	US-09-784-423-27	Sequence 27, Appl
144	105.4	3.7	240	4	US-09-621-976-1324	Sequence 1324, Ap	216	94.4	3.3	2625	4	US-09-270-767-10080	Sequence 1, Appli
145	105.4	3.7	1273	4	US-09-270-767-14731	Sequence 14731, A	217	94.2	3.3	2239	3	US-09-196-390-1	Sequence 1, Appli
146	104	3.7	177	4	US-09-621-976-1047	Sequence 1047, Ap	218	94.2	3.3	2239	3	US-09-952-677-1	Sequence 1, Appli
147	103.6	3.6	2806	3	US-09-653-839-9	Sequence 9, Appli	219	94.2	3.3	601	4	US-09-949-016-195763	Sequence 195763, A
148	103.6	3.6	2806	4	US-10-203-619-9	Sequence 9, Appli	220	93.8	3.3	997	4	US-09-907-794A-376	Sequence 376, App
149	103.6	3.6	41736	4	US-09-949-016-17091	Sequence 17091, A	221	93.8	3.3	997	4	US-09-905-125A-376	Sequence 376, App
150	103.4	3.6	147	4	US-09-621-976-10254	Sequence 10254, A	222	93.8	3.3	997	4	US-09-905-125A-376	Sequence 376, App
151	102.6	3.6	147	4	US-09-621-976-10254	Sequence 10254, A	223	93.8	3.3	997	4	US-09-902-775A-376	Sequence 376, App
152	102.2	3.6	1052	4	US-09-244-805-29	Sequence 29, Appl	224	93.8	3.3	997	4	US-09-906-700-376	Sequence 376, App
153	102.2	3.6	2527	4	US-09-489-847-23	Sequence 23, Appl	225	93.8	3.3	997	4	US-09-903-603A-376	Sequence 376, App
154	102	3.6	102	4	US-09-621-976-14804	Sequence 14804, A	226	93.8	3.3	997	4	US-09-904-920A-376	Sequence 376, App
155	101.8	3.6	558	4	US-09-043-861-3	Sequence 3, Appli	227	93.8	3.3	997	4	US-09-909-064-376	Sequence 376, App
156	100.4	3.5	123	4	US-09-621-976-12330	Sequence 12330, A	228	93.8	3.3	997	4	US-09-905-381A-376	Sequence 376, App
c 157	100.4	3.5	251672	4	US-09-949-016-17296	Sequence 17296, A	229	93.8	3.3	1895	3	US-09-444-336-7	Sequence 7, Appli
c 158	100.4	3.5	251682	4	US-09-949-016-17296	Sequence 17296, A	230	93.6	3.3	903	5	PCT-US95-06406A-21	Sequence 21, Appl
159	100.2	3.5	1308	4	US-10-151-832-1	Sequence 1, Appli	231	93.6	3.3	1248	4	US-09-489-847-101	Sequence 101, App
160	100.2	3.5	1582	3	US-08-545-196B-10	Sequence 10, Appl	232	93.4	3.3	2223	1	US-08-257-073-4	Sequence 4, Appli
161	100.2	3.5	1582	3	US-08-545-196B-12	Sequence 12, Appl	233	93.2	3.3	1069	3	US-09-372-422A-7	Sequence 7, Appli
c 162	100.2	3.5	4419	4	US-09-620-312D-187	Sequence 187, App	234	93	3.3	1172	1	US-07-945-288-9	Sequence 9, Appli
163	100	3.5	2671	6	5168051-9	Sequence 187, App	235	93	3.3	1172	1	US-08-462-831-9	Sequence 9, Appli
164	100	3.5	2671	6	5168051-9	Patent No. 5168051	236	93	3.3	1172	1	US-08-461-809-9	Sequence 9, Appli
165	99.4	3.5	550	4	US-09-010-147B-5	Sequence 5, Appli	237	93	3.3	1172	1	US-08-461-809-9	Sequence 9, Appli
166	99	3.5	1411	3	US-08-964-127-5	Sequence 5, Appli	238	93	3.3	1172	5	PCT-US93-08518-9	Sequence 9, Appli
167	99	3.5	1411	3	US-09-496-692-5	Sequence 5, Appli	239	92.8	3.3	179	4	US-09-621-976-9575	Sequence 9575, Ap
168	99	3.5	1411	4	US-10-000-273-5	Sequence 5, Appli	240	92.4	3.2	1114	3	US-09-152-060-41	Sequence 41, Appl
169	99	3.5	1414	4	US-09-501-115-5	Sequence 5, Appli	241	92.4	3.2	1249	4	US-09-461-325-128	Sequence 128, App
170	98.8	3.5	193	4	US-09-621-976-10543	Sequence 10543, A	242	92.4	3.2	1249	4	US-10-012-542-128	Sequence 128, App
171	98.8	3.5	790	3	US-09-363-970-4	Sequence 4, Appli	243	92.4	3.2	1249	4	US-10-115-123-128	Sequence 128, App
c 172	98.4	3.5	270	2	US-08-520-678A-30	Sequence 30, Appl	c 244	92.4	3.2	1260	4	US-09-461-325-93	Sequence 93, Appl
c 173	98.4	3.5	270	3	US-08-897-126-30	Sequence 30, Appl	c 245	92.4	3.2	1260	4	US-10-012-542-93	Sequence 93, Appl

C 247	92.4	3.2	1260	4	US-10-115-123-93	Sequence 93, Appl	320	89	3.1	3410	4	US-09-651-236-110	Sequence 110, App
248	92.2	3.2	244	4	US-09-621-976-484	Sequence 484, App	321	88.8	3.1	1190	4	US-09-390-207-1	Sequence 1, Appl
249	92.2	3.2	271	4	US-09-621-976-10380	Sequence 10380, A	322	88.8	3.1	1508	3	US-09-039-046-1	Sequence 1, Appl
250	92.2	3.2	1193	3	US-09-372-422A-23	Sequence 23, Appl	323	88.6	3.1	1636	4	US-09-578-194-6	Sequence 6, Appl
251	92.2	3.2	1662	4	US-09-668-097A-13	Sequence 13, Appl	324	88.6	3.1	331	4	US-09-621-976-16100	Sequence 16100, A
252	92.2	3.2	2406	4	US-09-594-506-37	Sequence 37, Appl	325	88.6	3.1	339	4	US-09-621-976-16015	Sequence 16015, A
253	92	3.2	92	4	US-09-621-976-14689	Sequence 14689, A	326	88.6	3.1	601	4	US-09-949-016-40844	Sequence 40844, A
254	92	3.2	242	4	US-09-621-976-16324	Sequence 16324, A	327	88.6	3.1	601	4	US-09-949-016-40845	Sequence 40845, A
255	92	3.2	19124	2	US-08-487-826B-13	Sequence 13, Appl	328	88.6	3.1	601	4	US-09-949-016-40846	Sequence 40846, A
C 256	91.8	3.2	367	4	US-09-270-767-14713	Sequence 14713, A	C 329	88.6	3.1	462589	4	US-09-949-016-12900	Sequence 12900, A
257	91.8	3.2	601	4	US-09-949-016-160412	Sequence 160412, A	C 330	88.6	3.1	476044	4	US-09-949-016-12412	Sequence 12412, A
258	91.8	3.2	601	4	US-09-949-016-160413	Sequence 160413, A	331	88.4	3.1	146	4	US-09-621-976-8550	Sequence 8550, App
259	91.6	3.2	195	4	US-09-621-976-18062	Sequence 18062, A	332	88.4	3.1	160	4	US-09-621-976-10335	Sequence 10335, A
260	91.6	3.2	1878	3	US-09-465-558-39	Sequence 39, Appl	333	88.4	3.1	334	4	US-09-621-976-16044	Sequence 16044, A
261	91.6	3.2	2311	4	US-09-800-729-66	Sequence 66, Appl	C 334	88.4	3.1	601	4	US-09-949-016-150083	Sequence 150083, A
262	91.4	3.2	176	4	US-09-621-976-13903	Sequence 13903, A	335	88.4	3.1	2445	4	US-09-949-016-781	Sequence 781, App
263	91	3.2	92	4	US-09-621-976-13620	Sequence 13620, A	336	88.4	3.1	2539	4	US-10-144-198-21	Sequence 21, Appl
264	91	3.2	242	4	US-09-621-976-13620	Sequence 13620, A	C 337	88.4	3.1	26115	4	US-09-949-016-15959	Sequence 15959, A
265	91	3.2	246	4	US-09-621-976-13617	Sequence 13617, A	C 338	88	3.1	184	4	US-09-270-767-30942	Sequence 30942, A
266	90.8	3.2	601	4	US-09-949-016-182221	Sequence 182221, A	C 339	88	3.1	196	4	US-09-644-460-40	Sequence 40, Appl
C 267	90.8	3.2	133358	4	US-09-949-016-16964	Sequence 16964, A	340	88	3.1	332	4	US-09-621-976-16050	Sequence 16050, A
C 268	90.8	3.2	133360	4	US-09-949-016-12651	Sequence 12651, A	341	88	3.1	333	4	US-09-621-976-16032	Sequence 16032, A
269	90.6	3.2	163	4	US-09-621-976-9608	Sequence 9608, App	342	88	3.1	333	4	US-09-621-976-16045	Sequence 16045, A
270	90.6	3.2	454	2	US-08-623-908A-6	Sequence 6, Appl	C 343	88	3.1	2149	4	US-09-949-016-456	Sequence 456, App
271	90.6	3.2	1198	3	US-09-248-335-27	Sequence 27, Appl	344	88	3.1	3124	3	US-09-734-030-1	Sequence 1, Appl
C 272	90.6	3.2	7218	1	US-08-232-463-14	Sequence 14, Appl	345	88	3.1	3124	4	US-10-153-921-1	Sequence 1, Appl
C 273	90.6	3.2	57139	4	US-09-949-016-11771	Sequence 11771, A	346	88	3.1	3124	4	US-10-669-689-1	Sequence 1, Appl
C 274	90.6	3.2	57150	4	US-09-949-016-16233	Sequence 16233, A	347	87.8	3.1	336	4	US-09-621-976-16051	Sequence 16051, A
275	90.4	3.2	990	4	US-09-800-729-79	Sequence 79, Appl	348	87.8	3.1	376	2	US-08-623-908A-18	Sequence 18, Appl
276	90.4	3.2	1297	4	US-09-800-729-80	Sequence 80, Appl	349	87.8	3.1	1008	4	US-09-780-641-1	Sequence 1, Appl
277	90.4	3.2	1361	4	US-09-489-847-64	Sequence 64, Appl	350	87.8	3.1	1736	3	US-09-182-816-22	Sequence 22, Appl
278	90.4	3.2	1683	3	US-09-347-803-11	Sequence 11, Appl	C 351	87.8	3.1	1736	3	US-09-182-816-24	Sequence 24, Appl
279	90.4	3.2	2280	3	US-08-813-150-1	Sequence 1, Appl	352	87.8	3.1	1736	3	US-09-471-528-22	Sequence 22, Appl
280	90.4	3.2	2280	4	US-09-546-553-1	Sequence 1, Appl	C 353	87.8	3.1	1736	3	US-09-471-528-24	Sequence 24, Appl
281	90.2	3.2	1746	4	US-09-485-529-57	Sequence 57, Appl	354	87.8	3.1	1736	3	US-09-634-530-22	Sequence 22, Appl
282	90.2	3.2	1768	4	US-09-485-529-13	Sequence 13, Appl	C 355	87.8	3.1	1736	3	US-09-634-530-24	Sequence 24, Appl
C 283	90	3.2	601	4	US-09-949-016-150084	Sequence 150084, A	356	87.4	3.1	332	4	US-09-621-976-16053	Sequence 16053, A
284	89.8	3.2	1492	1	US-09-369-247-23	Sequence 23, Appl	357	87.4	3.1	639	4	US-09-482-273-49	Sequence 49, Appl
285	89.8	3.2	1817	1	US-08-473-981A-5	Sequence 5, Appl	358	87.4	3.1	1602	1	US-08-530-950-3	Sequence 3, Appl
286	89.8	3.2	1817	2	US-08-474-087-5	Sequence 5, Appl	359	87.4	3.1	1602	3	US-08-888-429A-3	Sequence 3, Appl
C 287	89.6	3.1	601	4	US-09-949-016-150085	Sequence 150085, A	360	87.4	3.1	1602	3	US-09-149-879-3	Sequence 3, Appl
288	89.6	3.1	711	4	US-09-621-976-17854	Sequence 17854, A	361	87.4	3.1	1602	4	US-09-057-009-3	Sequence 3, Appl
289	89.6	3.1	795	4	US-09-270-767-14068	Sequence 14068, A	362	87.4	3.1	1602	4	US-09-593-653-3	Sequence 3, Appl
290	89.6	3.1	1134	3	US-09-248-335-29	Sequence 29, Appl	C 363	87.4	3.1	131332	4	US-09-949-016-15535	Sequence 15535, A
291	89.6	3.1	1700	2	US-08-897-340-4	Sequence 4, Appl	C 364	87.4	3.1	360470	4	US-09-949-016-13173	Sequence 13173, A
292	89.6	3.1	1700	3	US-09-252-329-4	Sequence 4, Appl	365	87.2	3.1	812	3	US-09-091-097-7	Sequence 7, Appl
293	89.4	3.1	335	4	US-09-621-976-16061	Sequence 16061, A	366	87.2	3.1	1512	2	US-08-909-965C-8	Sequence 8, Appl
294	89.4	3.1	336	4	US-09-621-976-16013	Sequence 16013, A	C 367	86.8	3.0	593	3	US-09-385-982-282	Sequence 282, App
295	89.4	3.1	338	4	US-09-621-976-16041	Sequence 16041, A	368	86.8	3.0	601	4	US-09-949-016-29142	Sequence 29142, A
296	89.4	3.1	2628	1	US-08-143-219-1	Sequence 1, Appl	369	86.8	3.0	601	4	US-09-949-016-29143	Sequence 29143, A
297	89.2	3.1	1037	4	US-09-489-847-112	Sequence 112, App	370	86.8	3.0	601	4	US-09-949-016-29144	Sequence 29144, A
298	89.2	3.1	2010	1	US-07-864-475A-4	Sequence 4, Appl	371	86.8	3.0	601	4	US-09-949-016-41097	Sequence 41097, A
299	89.2	3.1	2010	2	US-08-468-249A-4	Sequence 4, Appl	372	86.8	3.0	601	4	US-09-949-016-41098	Sequence 41098, A
300	89	3.1	89	4	US-09-621-976-17479	Sequence 17479, A	373	86.8	3.0	601	4	US-09-949-016-41099	Sequence 41099, A
301	89	3.1	89	4	US-09-621-976-14974	Sequence 14974, A	374	86.8	3.0	1921	2	US-08-557-128-11	Sequence 11, Appl
302	89	3.1	147	4	US-09-621-976-8551	Sequence 8551, App	375	86.8	3.0	2202	3	US-09-465-558-59	Sequence 59, Appl
303	89	3.1	318	4	US-09-621-976-10247	Sequence 10247, A	C 376	86.8	3.0	16073	4	US-09-949-016-12312	Sequence 12312, A
304	89	3.1	554	4	US-09-696-169A-14	Sequence 14, Appl	C 377	86.8	3.0	16073	4	US-09-949-016-12905	Sequence 12905, A
305	89	3.1	688	6	5498694-3	Patent No. 5498694	378	86.6	3.0	1781	4	US-09-818-512-1	Sequence 1, Appl
306	89	3.1	688	6	5498694-3	Patent No. 5498694	379	86.4	3.0	332	4	US-09-621-976-16031	Sequence 16031, A
307	89	3.1	3410	3	US-09-020-956-110	Sequence 110, App	C 380	86.4	3.0	658	3	US-08-998-416-595	Sequence 595, App
308	89	3.1	3410	3	US-09-030-607-110	Sequence 110, App	381	86.4	3.0	2218	4	US-09-016-434-1157	Sequence 1157, App
309	89	3.1	3410	3	US-09-439-313-110	Sequence 110, App	382	86.4	3.0	2218	4	US-10-329-668-7	Sequence 7, Appl
310	89	3.1	3410	3	US-09-352-616A-110	Sequence 110, App	383	86.4	3.0	2233	1	US-08-496-631-1	Sequence 1, Appl
311	89	3.1	3410	3	US-09-602-877A-100	Sequence 100, App	384	86.2	3.0	329	4	US-09-621-976-16012	Sequence 16012, A
312	89	3.1	3410	3	US-09-232-149A-110	Sequence 110, App	385	86.2	3.0	443	4	US-09-621-976-17631	Sequence 17631, A
313	89	3.1	3410	4	US-09-159-812-110	Sequence 110, App	C 386	86.2	3.0	602	1	US-08-764-100-8	Sequence 8, Appl
314	89	3.1	3410	4	US-09-636-215-110	Sequence 110, App	387	86.2	3.0	642	1	US-08-764-100-13	Sequence 13, Appl
315	89	3.1	3410	4	US-09-685-166A-110	Sequence 110, App	C 388	86.2	3.0	643	1	US-08-764-100-7	Sequence 7, Appl
316	89	3.1	3410	4	US-09-115-453-110	Sequence 110, App	C 389	86.2	3.0	2993	1	US-08-764-100-2	Sequence 2, Appl
317	89	3.1	3410	4	US-09-688-489-110	Sequence 110, App	C 390	86.2	3.0	2993	1	US-08-764-100-10	Sequence 10, Appl
318	89	3.1	3410	4	US-09-679-426-110	Sequence 110, App	391	86.2	3.0	3000	1	US-08-764-100-9	Sequence 9, Appl
319	89	3.1	3410	4	US-09-759-143-110	Sequence 110, App	C 392	86.2	3.0	3001	1	US-08-764-100-1	Sequence 1, Appl

393	86.2	3.0	161124	4	US-09-949-016-11760	Sequence 11760, A	466	83.4	2.9	2230	3	US-08-378-313-24	Sequence 24, Appl
394	86	3.0	630	1	US-08-185-414E-1	Sequence 1, Appl	467	83.4	2.9	2550	6	5258287-23	Patent No. 5258287
C 395	86	3.0	276687	4	US-09-949-016-13840	Sequence 13840, A	468	83.4	2.9	2550	6	5258287-23	Patent No. 5258287
396	85.8	3.0	326	4	US-09-621-976-16024	Sequence 16024, A	469	83.4	2.9	2989	6	5378464-1	Patent No. 5378464
397	85.8	3.0	601	4	US-09-949-016-175160	Sequence 175160, A	470	83.4	2.9	2989	6	5378464-1	Patent No. 5378464
398	85.8	3.0	1835	3	US-09-485-549-1	Sequence 1, Appl	471	83.4	2.9	168174	4	US-10-071-411A-63	Sequence 63, Appl
399	85.8	3.0	2320	3	US-09-202-904A-13	Sequence 13, Appl	472	83.4	2.9	168273	4	US-10-071-411A-2	Sequence 2, Appl
C 400	85.8	3.0	8638	4	US-10-029-907-6	Sequence 6, Appl	C 473	83.4	2.9	250958	4	US-09-949-016-16061	Sequence 16061, A
C 401	85.8	3.0	19601	4	US-09-949-016-15629	Sequence 15629, A	474	83.2	2.9	300	4	US-09-621-976-16227	Sequence 16227, A
402	85.8	3.0	31111	4	US-09-949-016-15628	Sequence 15628, A	C 475	83.2	2.9	844	4	US-09-690-942-3	Sequence 3, Appl
403	85.6	3.0	273	4	US-09-809-545A-31	Sequence 31, Appl	476	83	2.9	83	4	US-09-621-976-14751	Sequence 14751, A
404	85.6	3.0	73519	4	US-09-949-016-16344	Sequence 16344, A	477	83	2.9	188	4	US-09-621-976-14959	Sequence 14959, A
405	85.6	3.0	105919	4	US-09-949-016-11769	Sequence 11769, A	478	83	2.9	188	4	US-09-621-976-10364	Sequence 10364, A
406	85.4	3.0	1325	1	US-08-306-691B-51	Sequence 51, Appl	C 479	83	2.9	253	2	US-08-520-678A-25	Sequence 25, Appl
407	85.4	3.0	1378	3	US-09-149-476-208	Sequence 208, App	C 480	83	2.9	253	2	US-08-897-126-25	Sequence 25, Appl
408	85.4	3.0	2276	4	US-09-205-258-183	Sequence 183, App	C 481	83	2.9	601	4	US-09-949-016-193621	Sequence 193621, A
409	85.2	3.0	323	4	US-09-621-976-10374	Sequence 10374, A	482	83	2.9	1192	4	US-09-439-554-23	Sequence 23, Appl
C 410	85.2	3.0	349	4	US-09-270-767-6612	Sequence 6612, Ap	C 483	83	2.9	54033	4	US-09-949-016-12091	Sequence 12091, A
C 411	85.2	3.0	349	4	US-09-270-767-21894	Sequence 21894, A	C 484	83	2.9	54033	4	US-09-949-016-14325	Sequence 14325, A
412	85.2	3.0	601	4	US-09-949-016-29145	Sequence 29145, A	485	82.8	2.9	190	4	US-09-621-976-16784	Sequence 16784, A
413	85.2	3.0	601	4	US-09-949-016-41100	Sequence 41100, A	486	82.8	2.9	293	4	US-09-621-976-16965	Sequence 16965, A
C 414	85.2	3.0	601	4	US-09-949-016-80104	Sequence 80104, A	487	82.8	2.9	1212	3	US-09-182-145-34	Sequence 34, Appl
C 415	85.2	3.0	175265	4	US-09-949-016-16089	Sequence 16089, A	C 488	82.8	2.9	1212	3	US-09-182-145-35	Sequence 35, Appl
C 416	85.2	3.0	312470	4	US-09-949-016-14043	Sequence 14043, A	489	82.8	2.9	1307	2	US-08-960-022-17	Sequence 17, Appl
C 417	85.2	3.0	336024	4	US-09-949-016-12373	Sequence 12373, A	490	82.8	2.9	5021	4	US-09-949-016-786	Sequence 786, App
418	85	3.0	85	4	US-09-621-976-13395	Sequence 13395, A	491	82.8	2.9	152070	4	US-09-949-016-15402	Sequence 15402, A
419	85	3.0	85	4	US-09-621-976-14949	Sequence 14949, A	C 492	82.6	2.9	124	6	5185243-1	Patent No. 5185243
420	85	3.0	299	4	US-09-621-976-16226	Sequence 16226, A	C 493	82.6	2.9	124	6	5185243-1	Patent No. 5185243
421	85	3.0	635	1	US-08-455-633A-35	Sequence 35, Appl	494	82.6	2.9	291	1	US-07-922-723A-7	Sequence 7, Appl
422	85	3.0	635	1	US-08-416-336-5	Sequence 5, Appl	495	82.6	2.9	291	1	US-07-799-828C-7	Sequence 7, Appl
423	85	3.0	635	2	US-08-456-460C-35	Sequence 35, Appl	496	82.6	2.9	291	1	US-08-074-275-7	Sequence 7, Appl
424	85	3.0	635	5	PCT-US94-05354-35	Sequence 35, Appl	497	82.6	2.9	291	1	US-08-480-366-7	Sequence 7, Appl
C 425	85	3.0	9636	1	US-08-323-170B-1	Sequence 1, Appl	498	82.6	2.9	291	2	US-07-952-277A-7	Sequence 7, Appl
C 426	85	3.0	9636	3	US-08-954-441-1	Sequence 1, Appl	499	82.6	2.9	3448	1	US-08-296-014A-3	Sequence 3, Appl
C 427	85	3.0	55841	4	US-09-949-016-16602	Sequence 16602, A	500	82.6	2.9	3448	2	US-08-596-405-3	Sequence 3, Appl
428	84.8	3.0	601	4	US-09-621-976-16038	Sequence 16038, A	501	82.6	2.9	3448	2	US-08-877-620-3	Sequence 3, Appl
429	84.8	3.0	1074	3	US-09-248-335-67	Sequence 67, Appl	502	82.6	2.9	3448	4	US-09-287-368-3	Sequence 3, Appl
430	84.8	3.0	1210	3	US-09-443-041A-29	Sequence 29, Appl	503	82.6	2.9	3448	4	US-09-626-795-3	Sequence 3, Appl
C 431	84.8	3.0	1709	4	US-09-426-783-6	Sequence 6, Appl	504	82.6	2.9	4182	1	US-08-296-014A-1	Sequence 1, Appl
C 432	84.8	3.0	1925	4	US-09-148-545-128	Sequence 128, App	505	82.6	2.9	4182	2	US-08-596-405-1	Sequence 1, Appl
C 433	84.8	3.0	2028	4	US-09-426-783-9	Sequence 9, Appl	506	82.6	2.9	4182	2	US-08-877-620-1	Sequence 1, Appl
C 434	84.8	3.0	2797	4	US-09-949-016-376	Sequence 376, App	507	82.6	2.9	4182	4	US-09-287-368-1	Sequence 1, Appl
C 435	84.6	3.0	145928	4	US-09-949-016-15444	Sequence 15444, A	508	82.6	2.9	4182	4	US-09-626-795-1	Sequence 1, Appl
436	84.6	3.0	1725	4	US-09-668-097A-21	Sequence 21, Appl	509	82.6	2.9	786431	4	US-09-751-389-3	Sequence 3, Appl
437	84.4	3.0	2271	4	US-09-205-258-243	Sequence 243, App	510	82.4	2.9	84	4	US-09-621-976-14571	Sequence 14571, A
C 438	84.4	3.0	3049	4	US-09-426-783-14	Sequence 14, Appl	511	82.2	2.9	169	4	US-09-621-976-11249	Sequence 11249, A
C 439	84.4	3.0	3080	3	US-09-099-041A-25	Sequence 25, Appl	512	82.2	2.9	1133	4	US-09-916-204-1	Sequence 1, Appl
440	84.4	3.0	3080	3	US-09-245-281-25	Sequence 25, Appl	513	82.2	2.9	1133	4	US-10-282-048-1	Sequence 1, Appl
441	84.4	3.0	3080	3	US-09-245-281-25	Sequence 25, Appl	514	82.2	2.9	1441	3	US-08-821-994-63	Sequence 63, Appl
442	84.4	3.0	3080	3	US-09-340-620A-25	Sequence 25, Appl	515	82	2.9	179	4	US-09-621-976-18054	Sequence 18054, A
443	84.4	3.0	3080	4	US-09-865-364-25	Sequence 25, Appl	516	82	2.9	329	4	US-09-621-976-16052	Sequence 16052, A
444	84.4	3.0	3080	4	US-09-865-364-25	Sequence 25, Appl	C 517	82	2.9	601	4	US-09-949-016-80450	Sequence 80450, A
C 445	84.4	3.0	250352	4	US-09-949-016-14724	Sequence 14724, A	518	82	2.9	1013	4	US-09-322-409-6	Sequence 6, Appl
C 446	84.2	3.0	324	4	US-09-621-976-16027	Sequence 16027, A	C 519	82	2.9	1013	4	US-09-322-409-8	Sequence 8, Appl
447	84.2	3.0	1927	3	US-09-336-536-66	Sequence 66, Appl	520	82	2.9	1013	4	US-09-451-527-6	Sequence 6, Appl
C 448	84.2	3.0	15722	4	US-09-949-016-16709	Sequence 16709, A	C 521	82	2.9	1013	4	US-09-451-527-8	Sequence 8, Appl
C 449	84.2	3.0	237510	4	US-09-949-016-14273	Sequence 14273, A	C 522	82	2.9	1461	3	US-08-722-126A-4	Sequence 4, Appl
450	84	3.0	127	4	US-09-621-976-13933	Sequence 13933, A	523	82	2.9	1461	5	PCT-US95-04258-4	Sequence 4, Appl
451	84	3.0	215	4	US-09-621-976-15321	Sequence 15321, A	C 524	82	2.9	90541	4	US-09-759-359A-3	Sequence 3, Appl
C 452	84	3.0	601	4	US-09-949-016-187282	Sequence 187282, A	C 525	82	2.9	90541	4	US-10-207-973-3	Sequence 3, Appl
453	84	3.0	1507	3	US-09-453-323-1	Sequence 1, Appl	C 526	82	2.9	113701	4	US-09-949-016-13214	Sequence 13214, A
454	84	3.0	7724	4	US-08-486-049-1	Sequence 1, Appl	C 527	82	2.9	154605	4	US-09-949-016-11894	Sequence 11894, A
C 455	84	3.0	12603	4	US-09-949-016-17096	Sequence 17096, A	C 528	82	2.9	670689	4	US-09-949-016-12505	Sequence 12505, A
456	83.8	2.9	327	4	US-09-621-976-16018	Sequence 16018, A	C 529	82	2.9	670690	4	US-09-949-016-14207	Sequence 14207, A
457	83.8	2.9	1325	2	US-08-464-517-1	Sequence 1, Appl	530	81.8	2.9	316	4	US-09-513-999C-838	Sequence 838, App
458	83.8	2.9	1325	2	US-08-246-361A-1	Sequence 1, Appl	C 531	81.8	2.9	2147	4	US-09-949-016-5245	Sequence 5245, App
459	83.8	2.9	1325	3	US-08-463-772-1	Sequence 1, Appl	C 532	81.8	2.9	19818	4	US-09-949-016-12198	Sequence 12198, A
460	83.8	2.9	1325	5	PCT-US93-05000-1	Sequence 1, Appl	C 533	81.8	2.9	19819	4	US-09-949-016-16987	Sequence 16987, A
461	83.8	2.9	94877	4	US-09-949-016-16114	Sequence 16114, A	534	81.6	2.9	189	4	US-09-621-976-14761	Sequence 14761, A
462	83.8	2.9	118143	4	US-09-949-016-17196	Sequence 17196, A	535	81.6	2.9	89689	4	US-09-949-016-13089	Sequence 13089, A
463	83.6	2.9	84	4	US-09-621-976-14577	Sequence 14577, A	C 536	81.4	2.9	601	4	US-09-949-016-13622	Sequence 13622, A
464	83.6	2.9	5852	1	US-07-867-106-2	Sequence 2, Appl	C 537	81.4	2.9	601	4	US-09-949-016-193623	Sequence 193623, A
C 465	83.6	2.9	12703	4	US-09-949-016-16685	Sequence 16685, A	C 538	81.4	2.9	601	4	US-09-949-016-193624	Sequence 193624, A

539	81.4	2.9	730	4	US-09-270-767-14600	Sequence 14600, A	612	80.4	2.8	10442	4	US-09-595-526C-1	Sequence 1, Appli
540	81.4	2.9	3527	2	US-08-909-965C-7	Sequence 7, Appli	613	80.4	2.8	10474	4	US-09-596-141C-7	Sequence 7, Appli
541	81.4	2.9	26849	4	US-09-949-016-17244	Sequence 17244, A	614	80.4	2.8	10474	4	US-09-596-141C-9	Sequence 9, Appli
542	81.2	2.9	604	4	US-09-334-819A-8	Sequence 8, Appli	615	80.4	2.8	10474	4	US-09-595-526C-7	Sequence 7, Appli
543	81.2	2.9	8643	4	US-10-029-907-4	Sequence 4, Appli	616	80.4	2.8	10474	4	US-09-595-526C-9	Sequence 9, Appli
544	81.2	2.9	39433	4	US-09-949-016-12014	Sequence 12014, A	617	80.4	2.8	42348	4	US-09-949-016-17157	Sequence 17157, A
545	81.2	2.9	68283	4	US-09-949-016-12261	Sequence 12261, A	618	80.4	2.8	49401	4	US-09-949-016-17080	Sequence 17080, A
546	81.2	2.9	156651	4	US-09-949-016-12611	Sequence 12611, A	619	80.4	2.8	113701	4	US-09-949-016-13214	Sequence 13214, A
547	81.2	2.9	254366	4	US-09-822-871-3	Sequence 3, Appli	620	80.4	2.8	275110	4	US-09-949-016-12706	Sequence 12706, A
548	81	2.8	81	4	US-09-621-976-13152	Sequence 13152, A	621	80.4	2.8	275110	4	US-09-949-016-16070	Sequence 16070, A
549	81	2.8	224	2	US-08-731-272A-26	Sequence 26, Appli	622	80.4	2.8	421491	4	US-09-949-016-12805	Sequence 12805, A
550	81	2.8	336	4	US-09-248-796A-13866	Sequence 13866, A	623	80.4	2.8	421494	4	US-09-949-016-14060	Sequence 14060, A
551	81	2.8	389	4	US-09-513-999C-420	Sequence 420, App	624	80.2	2.8	601	4	US-09-949-016-186943	Sequence 186943, A
552	81	2.8	601	4	US-09-949-016-155436	Sequence 155436, A	625	80.2	2.8	2407	3	US-09-370-807-7	Sequence 7, Appli
553	81	2.8	601	4	US-09-949-016-204599	Sequence 204599, A	626	80.2	2.8	2407	3	US-09-921-259-7	Sequence 7, Appli
554	81	2.8	601	4	US-09-949-016-204600	Sequence 204600, A	627	80.2	2.8	2407	3	US-09-949-016-13026	Sequence 13026, A
555	81	2.8	601	4	US-09-949-016-204601	Sequence 204601, A	628	80.2	2.8	10451	4	US-09-949-016-12192	Sequence 12192, A
556	81	2.8	601	4	US-09-949-016-204602	Sequence 204602, A	629	80	2.8	601	4	US-09-949-016-80449	Sequence 80449, A
557	81	2.8	601	4	US-09-949-016-204603	Sequence 204603, A	630	80	2.8	1332	2	US-09-057-762-1	Sequence 1, Appli
558	81	2.8	601	4	US-09-949-016-204604	Sequence 204604, A	631	80	2.8	1332	3	US-08-326-119A-1	Sequence 1, Appli
559	81	2.8	601	4	US-09-949-016-204605	Sequence 204605, A	632	80	2.8	258775	4	US-09-949-016-16435	Sequence 16435, A
560	81	2.8	601	4	US-09-949-016-204606	Sequence 204606, A	633	79.8	2.8	164	4	US-09-621-976-16692	Sequence 16692, A
561	81	2.8	601	4	US-09-949-016-204607	Sequence 204607, A	634	79.8	2.8	601	4	US-09-949-016-19137	Sequence 19137, A
562	81	2.8	700	3	US-09-152-060-26	Sequence 26, Appli	635	79.8	2.8	601	4	US-09-949-016-19138	Sequence 19138, A
563	81	2.8	29321	4	US-09-949-016-14257	Sequence 14257, A	636	79.8	2.8	601	4	US-09-949-016-19139	Sequence 19139, A
564	81	2.8	29321	4	US-09-949-016-14258	Sequence 14258, A	637	79.8	2.8	601	4	US-09-949-016-122876	Sequence 122876, A
565	81	2.8	55298	4	US-09-491-356C-1	Sequence 1, Appli	638	79.8	2.8	601	4	US-09-949-016-122877	Sequence 122877, A
566	81	2.8	87734	4	US-09-949-016-17521	Sequence 17521, A	639	79.8	2.8	601	4	US-09-949-016-122878	Sequence 122878, A
567	81	2.8	100877	4	US-09-949-016-13276	Sequence 13276, A	640	79.8	2.8	601	4	US-09-949-016-203158	Sequence 203158, A
568	81	2.8	132438	4	US-09-949-016-14349	Sequence 14349, A	641	79.8	2.8	601	4	US-09-949-016-203159	Sequence 203159, A
569	81	2.8	132438	4	US-09-949-016-14350	Sequence 14350, A	642	79.8	2.8	601	4	US-09-949-016-203160	Sequence 203160, A
570	81	2.8	151089	4	US-09-949-016-14348	Sequence 14348, A	643	79.8	2.8	601	4	US-09-949-016-203200	Sequence 203200, A
571	81	2.8	524032	4	US-09-949-016-16928	Sequence 16928, A	644	79.8	2.8	601	4	US-09-949-016-203201	Sequence 203201, A
572	81	2.8	524032	4	US-09-949-016-16929	Sequence 16929, A	645	79.8	2.8	601	4	US-09-949-016-203202	Sequence 203202, A
573	81	2.8	524032	4	US-09-949-016-16930	Sequence 16930, A	646	79.8	2.8	6920	4	US-09-949-016-15211	Sequence 15211, A
574	81	2.8	529885	4	US-09-949-016-16931	Sequence 16931, A	647	79.8	2.8	29927	4	US-09-949-016-11814	Sequence 11814, A
575	81	2.8	529885	4	US-09-949-016-14340	Sequence 14340, A	648	79.8	2.8	29927	4	US-09-949-016-17474	Sequence 17474, A
576	81	2.8	529885	4	US-09-949-016-14341	Sequence 14341, A	649	79.8	2.8	29927	4	US-09-949-016-17475	Sequence 17475, A
577	81	2.8	529885	4	US-09-949-016-14342	Sequence 14342, A	650	79.8	2.8	37802	4	US-09-949-016-12639	Sequence 12639, A
578	81	2.8	529885	4	US-09-949-016-14343	Sequence 14343, A	651	79.8	2.8	38566	4	US-09-949-016-15271	Sequence 15271, A
579	81	2.8	529885	4	US-09-949-016-14344	Sequence 14344, A	652	79.8	2.8	38566	4	US-09-949-016-15272	Sequence 15272, A
580	81	2.8	529885	4	US-09-949-016-14345	Sequence 14345, A	653	79.8	2.8	11067	4	US-09-497-855A-32	Sequence 32, Appli
581	81	2.8	529885	4	US-09-949-016-14346	Sequence 14346, A	654	79.6	2.8	173	4	US-09-621-976-9851	Sequence 9851, Ap
582	81	2.8	529885	4	US-09-949-016-14347	Sequence 14347, A	655	79.6	2.8	473	1	US-08-764-100-16	Sequence 16, Appli
583	80.8	2.8	333	4	US-09-248-796A-11241	Sequence 11241, A	656	79.6	2.8	601	4	US-09-949-016-45911	Sequence 45911, A
584	80.8	2.8	2744	3	US-09-071-101-1	Sequence 1, Appli	657	79.6	2.8	601	4	US-09-949-016-69770	Sequence 69770, A
585	80.8	2.8	2744	3	US-09-369-618-1	Sequence 1, Appli	658	79.6	2.8	601	4	US-09-949-016-69771	Sequence 69771, A
586	80.8	2.8	2744	3	US-09-369-617-1	Sequence 1, Appli	659	79.6	2.8	601	4	US-09-949-016-69771	Sequence 69771, A
587	80.8	2.8	5096	4	US-09-949-016-15105	Sequence 15105, A	660	79.6	2.8	601	4	US-09-949-016-162332	Sequence 162332, A
588	80.8	2.8	5173	1	US-08-242-677-1	Sequence 1, Appli	661	79.6	2.8	601	4	US-09-949-016-162333	Sequence 162333, A
589	80.8	2.8	23193	4	US-09-949-016-17215	Sequence 17215, A	662	79.6	2.8	601	4	US-09-949-016-162335	Sequence 162335, A
590	80.6	2.8	318	4	US-09-621-976-16040	Sequence 16040, A	663	79.6	2.8	601	4	US-09-949-016-162335	Sequence 162335, A
591	80.6	2.8	601	4	US-09-949-016-88560	Sequence 88560, A	664	79.6	2.8	601	4	US-09-949-016-204598	Sequence 204598, A
592	80.6	2.8	601	4	US-09-949-016-88565	Sequence 88565, A	665	79.6	2.8	1023	1	US-08-252-966B-16	Sequence 16, Appli
593	80.6	2.8	741	4	US-09-949-016-89215	Sequence 89215, A	666	79.6	2.8	1606	4	US-09-820-004-1	Sequence 1, Appli
594	80.6	2.8	763	4	US-09-621-976-1894	Sequence 1894, A	667	79.6	2.8	4970	1	US-08-764-100-14	Sequence 14, Appli
595	80.6	2.8	887	4	US-09-743-207-3	Sequence 3, Appli	668	79.6	2.8	11890	4	US-09-949-016-13794	Sequence 13794, A
596	80.6	2.8	887	4	US-09-270-767-9818	Sequence 9818, Ap	669	79.6	2.8	3000	4	US-10-007-010-10	Sequence 10, Appli
597	80.6	2.8	1129	3	US-09-227-357-40	Sequence 40, Appli	670	79.6	2.8	39433	4	US-09-949-016-12014	Sequence 12014, A
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600	80.6	2.8	3243	4	US-09-464-535-43	Sequence 43, Appli	673	79.6	2.8	113876	4	US-09-949-016-14829	Sequence 14829, A
601	80.6	2.8	72604	3	US-09-949-016-12186	Sequence 12186, A	674	79.6	2.8	115508	4	US-09-949-016-11800	Sequence 11800, A
602	80.6	2.8	72604	3	US-09-268-992-7	Sequence 7, Appli	675	79.6	2.8	115508	4	US-09-949-016-14826	Sequence 14826, A
603	80.6	2.8	260247	4	US-09-657-474-7	Sequence 7, Appli	676	79.6	2.8	115508	4	US-09-949-016-14827	Sequence 14827, A
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605	80.4	2.8	601	4	US-09-621-976-16317	Sequence 16317, A	678	79.4	2.8	601	4	US-09-949-016-155437	Sequence 155437, A
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609	80.4	2.8	3366	4	US-09-596-141C-6	Sequence 6, Appli	682	79.4	2.8	601	4	US-09-949-016-155442	Sequence 155442, A
610	80.4	2.8	3366	4	US-09-595-526C-6	Sequence 6, Appli	683	79.4	2.8	601	4	US-09-949-016-155445	Sequence 155445, A
611	80.4	2.8	10442	4	US-09-596-141C-1	Sequence 1, Appli	684	79.4	2.8	601	4	US-09-949-016-204750	Sequence 204750, A

c 685	79.4	2.8	13047	2	US-09-022-461-1	Sequence 1, Appli	c 758	78	2.7	65744	4	US-09-949-016-12591	Sequence 12591, A
c 686	79.4	2.8	12047	3	US-09-033-556-3	Sequence 3, Appli	c 759	78	2.7	65745	4	US-09-949-016-15871	Sequence 15871, A
c 687	79.4	2.8	12047	4	US-09-474-699-11	Sequence 11, Appli	c 760	78	2.7	106746	4	US-09-326-402C-1	Sequence 1, Appli
c 688	79.4	2.8	12047	4	US-09-151-376-3	Sequence 3, Appli	c 761	78	2.7	106746	4	US-09-326-402C-12	Sequence 12, Appli
c 689	79.4	2.8	12047	4	US-09-814-351-11	Sequence 11, Appli	c 762	78	2.7	118868	4	US-09-949-016-15746	Sequence 15746, A
c 690	79.4	2.8	53769	4	US-09-949-016-17527	Sequence 17527, A	c 763	78	2.7	128175	4	US-09-949-016-16268	Sequence 16268, A
c 691	79.4	2.8	58407	4	US-08-916-421B-2	Sequence 2, Appli	c 764	77.8	2.7	212	4	US-09-621-976-1325	Sequence 1325, Ap
c 692	79.4	2.8	58407	4	US-09-692-570-2	Sequence 2, Appli	c 765	77.8	2.7	601	4	US-09-949-016-155440	Sequence 155440, A
c 693	79.4	2.8	93398	4	US-09-949-016-14167	Sequence 14167, A	c 766	77.8	2.7	601	4	US-09-949-016-155443	Sequence 155443, A
c 694	79.4	2.8	97376	4	US-09-949-016-16093	Sequence 16093, A	c 767	77.8	2.7	601	4	US-09-949-016-182153	Sequence 182153, A
c 695	79.4	2.8	254405	4	US-09-949-016-14381	Sequence 14381, A	c 768	77.8	2.7	601	4	US-09-949-016-182154	Sequence 182154, A
c 696	79.4	2.8	389504	4	US-09-949-016-11774	Sequence 11774, A	c 769	77.8	2.7	1509	3	US-09-149-476-179	Sequence 179, App
c 697	79.2	2.8	196	4	US-09-270-767-29394	Sequence 29394, A	c 770	77.6	2.7	166	4	US-09-621-976-18390	Sequence 18390, A
c 698	79.2	2.8	601	4	US-09-949-016-179690	Sequence 179690, A	c 771	77.6	2.7	185	4	US-09-621-976-16779	Sequence 16779, A
c 699	79.2	2.8	624	4	US-09-270-767-13424	Sequence 13424, A	c 772	77.6	2.7	394	2	US-08-623-906A-7	Sequence 7, Appli
c 700	79.2	2.8	1027	3	US-09-465-558-57	Sequence 57, Appli	c 773	77.6	2.7	601	4	US-09-949-016-76961	Sequence 76961, A
c 701	79.2	2.8	1738	2	US-08-378-482A-2	Sequence 2, Appli	c 774	77.6	2.7	601	4	US-09-949-016-76962	Sequence 76962, A
c 702	79.2	2.8	3975	4	US-09-270-767-3	Sequence 3, Appli	c 775	77.6	2.7	601	4	US-09-949-016-76963	Sequence 76963, A
c 703	79.2	2.8	142783	4	US-09-949-016-15127	Sequence 15127, A	c 776	77.6	2.7	601	4	US-09-949-016-76964	Sequence 76964, A
c 704	79.2	2.8	202001	4	US-09-734-674-3	Sequence 3, Appli	c 777	77.6	2.7	601	4	US-09-949-016-179688	Sequence 179688, A
c 705	79	2.8	361	3	US-09-018-584A-9	Sequence 9, Appli	c 778	77.6	2.7	601	4	Sequence 179692,	Sequence 179692, A
c 706	79	2.8	601	4	US-09-784-423-9	Sequence 9, Appli	c 779	77.6	2.7	1798	2	US-08-557-128-12	Sequence 12, Appli
c 707	79	2.8	601	4	US-09-949-016-155444	Sequence 155444, A	c 780	77.6	2.7	25175	4	US-09-949-016-16247	Sequence 16247, A
c 708	79	2.8	958	2	US-08-757-046A-5	Sequence 5, Appli	c 781	77.6	2.7	25175	4	US-09-949-016-16248	Sequence 16248, A
c 709	79	2.8	958	3	US-09-447-208-5	Sequence 5, Appli	c 782	77.6	2.7	25175	4	US-09-949-016-16273	Sequence 16273, A
c 710	79	2.8	958	3	US-09-135-988-5	Sequence 5, Appli	c 783	77.6	2.7	38772	4	US-09-949-016-12382	Sequence 12382, A
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c 712	79	2.8	958	3	US-08-597-274A-5	Sequence 5, Appli	c 785	77.6	2.7	44453	3	US-09-146-053-5	Sequence 5, Appli
c 713	79	2.8	958	3	US-08-908-909-5	Sequence 5, Appli	c 786	77.6	2.7	236341	4	US-09-949-016-13978	Sequence 13978, A
c 714	79	2.8	958	3	US-09-609-161B-5	Sequence 5, Appli	c 787	77.6	2.7	390416	4	US-09-949-016-16923	Sequence 16923, A
c 715	79	2.8	958	3	US-08-990-103-5	Sequence 5, Appli	c 788	77.4	2.7	593	4	US-09-904-615-59	Sequence 59, Appli
c 716	79	2.8	958	3	US-09-746-485A-5	Sequence 5, Appli	c 789	77.4	2.7	601	4	US-09-949-016-161983	Sequence 161983, A
c 717	79	2.8	958	4	US-10-126-139-5	Sequence 5, Appli	c 790	77.4	2.7	25431	4	US-09-949-016-13234	Sequence 13234, A
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c 719	79	2.8	958	4	US-10-126-777-5	Sequence 5, Appli	c 792	77.4	2.7	144158	4	US-09-949-016-12936	Sequence 12936, A
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c 721	79	2.8	45469	4	US-09-949-016-113398	Sequence 113398, A	c 794	77.4	2.7	239815	4	US-09-949-016-16274	Sequence 16274, A
c 722	78.8	2.8	319	4	US-09-621-976-18055	Sequence 16055, A	c 795	77.2	2.7	443	4	US-09-936-885A-1	Sequence 1, Appli
c 723	78.8	2.8	601	4	US-09-949-016-179687	Sequence 179687, A	c 796	77.2	2.7	601	4	US-09-949-016-19140	Sequence 19140, A
c 724	78.8	2.8	664	4	US-09-904-615-66	Sequence 66, Appli	c 797	77.2	2.7	601	4	US-09-949-016-31458	Sequence 31458, A
c 725	78.8	2.8	2500	4	US-09-579-383-5	Sequence 5, Appli	c 798	77.2	2.7	601	4	US-09-949-016-31459	Sequence 31459, A
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c 727	78.8	2.8	36731	4	US-09-949-016-13770	Sequence 13770, A	c 800	77.2	2.7	601	4	US-09-949-016-127124	Sequence 127124, A
c 728	78.6	2.8	79	4	US-09-621-976-15090	Sequence 15090, A	c 801	77.2	2.7	601	4	US-09-949-016-127125	Sequence 127125, A
c 729	78.6	2.8	601	4	US-09-949-016-17919	Sequence 17919, A	c 802	77.2	2.7	601	4	US-09-949-016-127891	Sequence 127891, A
c 730	78.6	2.8	601	4	US-09-949-016-17920	Sequence 17920, A	c 803	77.2	2.7	601	4	US-09-949-016-128228	Sequence 128228, A
c 731	78.6	2.8	601	4	US-09-949-016-17920	Sequence 17920, A	c 804	77.2	2.7	601	4	US-09-949-016-203161	Sequence 203161, A
c 732	78.6	2.8	601	4	US-09-949-016-41809	Sequence 41809, A	c 805	77.2	2.7	601	4	US-09-949-016-203203	Sequence 203203, A
c 733	78.6	2.8	62908	4	US-09-949-016-17554	Sequence 17554, A	c 806	77.2	2.7	1100	3	US-07-861-458C-4	Sequence 4, Appli
c 734	78.6	2.8	93894	4	US-09-949-016-17554	Sequence 17554, A	c 807	77.2	2.7	17132	4	US-09-949-016-15361	Sequence 15361, A
c 735	78.6	2.8	137394	4	US-09-949-016-13629	Sequence 13629, A	c 808	77.2	2.7	24150	4	US-09-949-016-12438	Sequence 12438, A
c 736	78.6	2.8	137743	4	US-09-949-016-12178	Sequence 12178, A	c 809	77.2	2.7	300598	4	US-09-949-016-11868	Sequence 11868, A
c 737	78.4	2.8	601	4	US-09-949-016-127893	Sequence 127893, A	c 810	77.2	2.7	302604	4	US-09-949-016-14588	Sequence 14588, A
c 738	78.4	2.8	601	4	US-09-949-016-127894	Sequence 127894, A	c 811	77.2	2.7	302604	4	US-09-949-016-14589	Sequence 14589, A
c 739	78.4	2.8	601	4	US-09-949-016-128230	Sequence 128230, A	c 812	77.2	2.7	304533	4	US-09-949-016-15371	Sequence 15371, A
c 740	78.4	2.8	601	4	US-09-949-016-128231	Sequence 128231, A	c 813	77.2	2.7	304533	4	US-09-949-016-15372	Sequence 15372, A
c 741	78.4	2.8	731	1	US-08-451-405A-2	Sequence 2, Appli	c 814	77.2	2.7	308362	4	US-09-949-016-17119	Sequence 17119, A
c 742	78.4	2.8	960	3	US-09-248-335-57	Sequence 57, Appli	c 815	77	2.7	77	4	US-08-956-171E-2883	Sequence 2883, Ap
c 743	78.4	2.8	1147	1	US-08-665-716-1	Sequence 1, Appli	c 816	77	2.7	552	4	US-08-781-966A-2883	Sequence 2883, Ap
c 744	78.4	2.8	2463	4	US-09-270-767-12063	Sequence 12063, A	c 817	77	2.7	552	4	US-09-461-325-111	Sequence 111, App
c 745	78.4	2.8	34534	4	US-09-949-016-15141	Sequence 15141, A	c 818	77	2.7	552	4	US-10-012-542-111	Sequence 111, App
c 746	78.2	2.7	1292	4	US-09-270-767-12238	Sequence 12238, A	c 819	77	2.7	552	4	US-10-115-123-111	Sequence 111, App
c 747	78.2	2.7	1740	4	US-09-709-103-45	Sequence 45, Appli	c 820	77	2.7	572	3	US-09-342-653-5	Sequence 5, Appli
c 748	78.2	2.7	1740	4	US-09-439-410A-45	Sequence 45, Appli	c 821	77	2.7	601	4	US-09-949-016-17921	Sequence 17921, A
c 749	78.2	2.7	1801	4	US-09-709-103-3	Sequence 3, Appli	c 822	77	2.7	601	4	US-09-949-016-41811	Sequence 41811, A
c 750	78.2	2.7	1801	4	US-09-439-410A-3	Sequence 3, Appli	c 823	77	2.7	1296	4	US-09-461-325-29	Sequence 29, Appli
c 751	78.2	2.7	2445	6	5215909-9	Patent No. 5215909	c 824	77	2.7	1296	4	US-10-012-542-29	Sequence 29, Appli
c 752	78.2	2.7	2445	6	5215909-9	Patent No. 5215909	c 825	77	2.7	1296	4	US-10-115-123-29	Sequence 29, Appli
c 753	78	2.7	78	4	US-09-621-976-14824	Sequence 14824, A	c 826	77	2.7	1872	3	US-09-291-923-27	Sequence 27, Appli
c 754	78	2.7	78	4	US-09-621-976-15092	Sequence 15092, A	c 827	77	2.7	3581	2	US-08-738-349-1	Sequence 2, Appli
c 755	78	2.7	601	4	US-09-949-016-45912	Sequence 45912, A	c 828	77	2.7	8642	4	US-10-023-907-2	Sequence 2, Appli
c 756	78	2.7	601	4	US-09-949-016-45913	Sequence 45913, A	c 829	77	2.7	74177	4	US-09-949-016-11988	Sequence 11988, A
c 757	78	2.7	30337	4	US-09-949-016-13053	Sequence 13053, A	c 830	77	2.7	74177	4	US-09-949-016-17388	Sequence 17388, A



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c 832	76.8	2.7	601	4	US-09-949-016-127892	Sequence 127892, A	905	75.8	2.7	320	4	US-09-621-976-16056	Sequence 16056, A
c 833	76.8	2.7	601	4	US-09-949-016-128229	Sequence 128229, A	c 906	75.8	2.7	601	4	US-09-949-016-32559	Sequence 32559, A
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835	76.8	2.7	4949	3	US-09-138-024-22	Sequence 22, Appl	c 908	75.8	2.7	601	4	US-09-949-016-155362	Sequence 155362, A
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c 838	76.8	2.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl	911	75.8	2.7	7286	3	US-09-331-581-3	Sequence 31, Appl
c 839	76.8	2.7	1664976	4	US-09-692-570-1	Sequence 1, Appl	912	75.8	2.7	7938	3	US-09-331-581-14	Sequence 14, Appl
840	76.6	2.7	232	4	US-09-621-976-17701	Sequence 17701, A	913	75.8	2.7	53337	4	US-09-949-016-12500	Sequence 12500, A
841	76.6	2.7	451	4	US-09-270-767-2429	Sequence 2429, Ap	914	75.8	2.7	53337	4	US-09-949-016-16092	Sequence 16092, A
842	76.6	2.7	451	4	US-09-270-767-17711	Sequence 17711, A	915	75.8	2.7	113100	4	US-09-949-016-12245	Sequence 12245, A
843	76.6	2.7	588	4	US-09-205-258-64	Sequence 64, Appl	916	75.8	2.7	462589	4	US-09-949-016-12900	Sequence 12900, A
844	76.6	2.7	601	4	US-09-949-016-20852	Sequence 20852, A	917	75.8	2.7	476044	4	US-09-949-016-12412	Sequence 12412, A
845	76.6	2.7	601	4	US-09-949-016-110199	Sequence 110199, A	918	75.6	2.7	100	4	US-09-621-976-13474	Sequence 12774, A
846	76.6	2.7	675	4	US-09-621-976-2461	Sequence 2461, Ap	c 919	75.6	2.7	601	4	US-09-949-016-21578	Sequence 21578, A
847	76.6	2.7	1279	3	US-09-248-335-25	Sequence 25, Appl	c 920	75.6	2.7	601	4	US-09-949-016-21579	Sequence 21579, A
c 848	76.6	2.7	1467	4	US-09-949-016-2761	Sequence 2761, Ap	c 921	75.6	2.7	601	4	US-09-949-016-130330	Sequence 130330, A
849	76.6	2.7	1558	1	US-08-467-607-2	Sequence 2, Appl	c 922	75.6	2.7	601	4	US-09-949-016-130331	Sequence 130331, A
850	76.6	2.7	1558	2	US-08-469-362-2	Sequence 2, Appl	c 923	75.6	2.7	601	4	US-09-949-016-15055	Sequence 15055, A
851	76.6	2.7	1558	2	US-08-850-392-2	Sequence 2, Appl	924	75.6	2.7	601	4	US-09-949-016-161729	Sequence 161729, A
c 852	76.6	2.7	17331	4	US-09-949-016-14503	Sequence 14503, A	925	75.6	2.7	2908	4	US-09-904-615-35	Sequence 35, Appl
c 853	76.6	2.7	24040	4	US-09-949-016-12118	Sequence 12118, A	926	75.6	2.7	3848	3	US-09-112-096-28	Sequence 28, Appl
c 854	76.6	2.7	253345	4	US-09-949-016-13656	Sequence 12656, A	927	75.6	2.7	4285	3	US-09-410-464-1	Sequence 1, Appl
c 855	76.6	2.7	253364	4	US-09-949-016-13639	Sequence 13639, A	c 928	75.6	2.7	4600	4	US-09-702-705-1797	Sequence 1797, Ap
856	76.4	2.7	84	1	US-08-664-596B-3	Sequence 3, Appl	c 929	75.6	2.7	4600	4	US-09-736-457-1797	Sequence 1797, Ap
857	76.4	2.7	84	1	US-08-738-367-3	Sequence 3, Appl	c 930	75.6	2.7	4600	4	US-09-671-325-1797	Sequence 1797, Ap
858	76.4	2.7	159	4	US-09-621-976-17448	Sequence 17448, A	931	75.6	2.7	5668	4	US-09-112-096-14	Sequence 14, Appl
859	76.4	2.7	1046	1	US-08-361-467B-4	Sequence 4, Appl	932	75.6	2.7	5668	4	US-09-636-215-777	Sequence 777, App
860	76.4	2.7	1046	1	US-08-484-332C-4	Sequence 4, Appl	933	75.6	2.7	5668	4	US-09-685-166A-777	Sequence 777, App
861	76.4	2.7	1544	4	US-09-187-999-14	Sequence 14, Appl	934	75.6	2.7	5668	4	US-09-679-426-777	Sequence 777, App
862	76.4	2.7	1546	4	US-09-901-151-1	Sequence 1, Appl	935	75.6	2.7	5668	4	US-09-759-143-777	Sequence 777, App
863	76.2	2.7	348	4	US-09-621-976-16137	Sequence 16137, A	936	75.6	2.7	5668	4	US-09-651-236-777	Sequence 777, App
864	76.2	2.7	601	4	US-09-949-016-102626	Sequence 102626, A	937	75.6	2.7	87617	4	US-09-949-016-16551	Sequence 16551, A
865	76.2	2.7	601	4	US-09-949-016-102738	Sequence 102738, A	c 938	75.6	2.7	92327	4	US-09-949-016-11929	Sequence 11929, A
866	76.2	2.7	601	4	US-09-949-016-193088	Sequence 193088, A	c 939	75.6	2.7	92327	4	US-09-949-016-13521	Sequence 13521, A
867	76.2	2.7	601	4	US-09-949-016-193088	Sequence 193088, A	c 940	75.6	2.7	124110	4	US-09-949-016-13753	Sequence 13753, A
868	76.2	2.7	601	4	US-09-949-016-193180	Sequence 193180, A	c 941	75.6	2.7	130724	4	US-09-949-016-13753	Sequence 13753, A
869	76.2	2.7	601	4	US-09-949-016-193181	Sequence 193181, A	c 942	75.6	2.7	144922	4	US-09-949-016-15890	Sequence 15890, A
870	76.2	2.7	601	4	US-09-949-016-193273	Sequence 193273, A	c 943	75.6	2.7	152331	3	US-09-128-155-16	Sequence 16, Appl
871	76.2	2.7	601	4	US-09-949-016-193274	Sequence 193274, A	c 944	75.6	2.7	176373	3	US-09-128-155-17	Sequence 17, Appl
872	76.2	2.7	601	4	US-09-949-016-193366	Sequence 193366, A	945	75.4	2.6	98	4	US-09-621-976-11744	Sequence 11744, A
873	76.2	2.7	601	4	US-09-949-016-193367	Sequence 193367, A	c 946	75.4	2.6	257	2	US-08-520-678A-24	Sequence 24, Appl
874	76.2	2.7	1476	4	US-09-248-796A-5437	Sequence 5437, Ap	c 947	75.4	2.6	257	3	US-08-897-126-24	Sequence 24, Appl
875	76.2	2.7	86213	4	US-09-949-016-17240	Sequence 17240, A	c 948	75.4	2.6	25458	4	US-09-949-016-13986	Sequence 13986, A
876	76.2	2.7	86213	4	US-09-949-016-17241	Sequence 17241, A	c 949	75.4	2.6	41863	4	US-09-949-016-14948	Sequence 14948, A
877	76.2	2.7	86213	4	US-09-949-016-17242	Sequence 17242, A	c 950	75.4	2.6	129415	4	US-09-949-016-16997	Sequence 16997, A
878	76.2	2.7	86213	4	US-09-949-016-17243	Sequence 17243, A	c 951	75.4	2.6	312474	4	US-09-949-016-17434	Sequence 17434, A
c 879	76.2	2.7	133559	4	US-09-949-016-17243	Sequence 17243, A	952	75.2	2.6	8220	2	US-08-568-459A-11	Sequence 11, Appl
880	76.2	2.7	174029	4	US-09-949-016-13610	Sequence 12610, A	953	75.2	2.6	8220	3	US-09-210-288-11	Sequence 11, Appl
c 881	76.2	2.7	191433	4	US-09-949-016-13680	Sequence 13680, A	954	75.2	2.6	8220	3	US-09-210-288-11	Sequence 11, Appl
c 882	76.2	2.7	76	4	US-09-621-976-14931	Sequence 14931, A	955	75	2.6	77	4	US-09-621-976-14892	Sequence 14892, A
c 883	76.2	2.7	76	4	US-09-621-976-14931	Sequence 14931, A	956	75	2.6	601	4	US-09-949-016-20851	Sequence 20851, A
c 884	76.2	2.7	678533	4	US-09-949-016-14578	Sequence 14578, A	957	75	2.6	601	4	US-09-949-016-20853	Sequence 20853, A
885	76	2.7	76	4	US-09-949-016-14578	Sequence 14578, A	958	75	2.6	601	4	US-09-949-016-20854	Sequence 20854, A
886	76	2.7	76	4	US-09-621-976-14931	Sequence 14931, A	959	75	2.6	601	4	US-09-949-016-20855	Sequence 20855, A
887	76	2.7	109	4	US-09-621-976-14592	Sequence 14592, A	960	75	2.6	601	4	US-09-949-016-20856	Sequence 20856, A
888	76	2.7	415	3	US-09-018-584A-18	Sequence 18, Appl	961	75	2.6	601	4	US-09-949-016-20856	Sequence 20856, A
889	76	2.7	415	4	US-09-784-421-18	Sequence 18, Appl	962	75	2.6	601	4	US-09-949-016-65454	Sequence 65454, A
c 890	76	2.7	601	4	US-09-949-016-179689	Sequence 179689, A	963	75	2.6	601	4	US-09-949-016-110198	Sequence 110198, A
c 891	76	2.7	601	4	US-09-949-016-179691	Sequence 179691, A	964	75	2.6	601	4	US-09-949-016-110200	Sequence 110200, A
c 892	76	2.7	1298	3	US-08-971-089-1	Sequence 1, Appl	965	75	2.6	601	4	US-09-949-016-110201	Sequence 110201, A
c 893	76	2.7	2239	4	US-10-380-105-7	Sequence 7, Appl	966	75	2.6	601	4	US-09-949-016-110202	Sequence 110202, A
894	76	2.7	13184	4	US-09-949-016-16573	Sequence 16573, A	967	75	2.6	601	4	US-09-949-016-110203	Sequence 110203, A
c 895	76	2.7	23222	4	US-09-949-016-15949	Sequence 15949, A	c 968	75	2.6	601	4	US-09-949-016-149960	Sequence 149960, A
c 896	76	2.7	25922	4	US-09-949-016-11874	Sequence 11874, A	969	75	2.6	746	3	US-09-013-810-1	Sequence 1, Appl
c 897	76	2.7	35064	4	US-09-949-016-13778	Sequence 12778, A	970	75	2.6	3200	1	US-08-444-405-1	Sequence 1, Appl
c 898	76	2.7	35065	4	US-09-949-016-13196	Sequence 13196, A	971	75	2.6	3200	1	US-08-384-805-1	Sequence 1, Appl
c 899	76	2.7	40408	4	US-09-949-016-16331	Sequence 16331, A	972	75	2.6	14087	4	US-09-949-016-11898	Sequence 11898, A
900	75.8	2.7	62072	4	US-09-949-016-16076	Sequence 16076, A	973	75	2.6	14082	4	US-09-949-016-14783	Sequence 14783, A
901	75.8	2.7	165	4	US-09-621-976-8127	Sequence 8127, Ap	c 974	75	2.6	85675	4	US-09-949-016-12333	Sequence 12333, A
902	75.8	2.7	208	1	US-08-686-878A-37	Sequence 37, Appl	c 975	75	2.6	85675	4	US-09-949-016-15956	Sequence 15956, A
903	75.8	2.7	208	3	US-09-175-928-37	Sequence 37, Appl	c 976	75	2.6	87648	4	US-09-949-016-13655	Sequence 13655, A



977	74.8	2.6	351	4	US-09-621-976-16140	Sequence 16140, A	1050	73.8	2.6	1419	4	US-09-270-767-13127	Sequence 13127, A
c 978	74.8	2.6	80411	4	US-09-949-016-15777	Sequence 15777, A	1051	73.8	2.6	284328	4	US-09-820-790B-3	Sequence 3, Appli
c 979	74.8	2.6	100836	4	US-09-949-016-12871	Sequence 12871, A	1052	73.8	2.6	96327	4	US-09-949-016-16541	Sequence 16541, A
c 980	74.8	2.6	100837	4	US-09-949-016-17063	Sequence 17063, A	1053	73.8	2.6	194937	4	US-09-949-016-17032	Sequence 17032, A
c 981	74.8	2.6	225127	4	US-09-949-016-16480	Sequence 16480, A	1054	73.8	2.6	194937	4	US-09-949-016-17033	Sequence 17033, A
c 982	74.6	2.6	258	4	US-09-621-976-15353	Sequence 15353, A	1055	73.6	2.6	132	4	US-09-621-976-13468	Sequence 13468, A
c 983	74.6	2.6	318	3	US-09-134-001C-2112	Sequence 2112, Ap	1056	73.6	2.6	299	4	US-09-621-976-10211	Sequence 10211, A
c 984	74.6	2.6	601	4	US-09-949-016-47327	Sequence 47327, A	1057	73.6	2.6	334	2	US-08-623-906A-9	Sequence 9, Appli
c 985	74.6	2.6	760	4	US-09-205-258-232	Sequence 232, App	1058	73.6	2.6	601	4	US-09-949-016-79787	Sequence 79787, A
c 986	74.6	2.6	986	4	US-09-328-475C-141	Sequence 141, App	1059	73.6	2.6	601	4	US-09-949-016-126414	Sequence 126414, A
c 987	74.6	2.6	2163	4	US-09-710-279-2057	Sequence 2057, Ap	c1060	73.6	2.6	1486	4	US-09-461-325-73	Sequence 73, Appl
c 988	74.6	2.6	2187	3	US-09-134-001C-2131	Sequence 2131, Ap	1061	73.6	2.6	1486	4	US-10-012-542-73	Sequence 73, Appl
c 989	74.6	2.6	2218	4	US-09-205-258-103	Sequence 103, App	1062	73.6	2.6	1486	4	US-10-115-123-73	Sequence 73, Appl
c 990	74.6	2.6	3792	4	US-09-710-279-3396	Sequence 3396, Ap	1063	73.6	2.6	96202	4	US-09-949-016-16433	Sequence 16433, A
c 991	74.6	2.6	7988	4	US-09-710-279-3962	Sequence 3962, Ap	c1064	73.6	2.6	204	4	US-08-621-976-1323	Sequence 1323, Ap
c 992	74.6	2.6	7989	4	US-09-539-601-10	Sequence 10, Appl	1065	73.4	2.6	227	2	US-08-520-678A-28	Sequence 28, Appl
c 993	74.6	2.6	8001	4	US-09-539-601-7	Sequence 7, Appli	c1066	73.4	2.6	227	3	US-08-897-126-28	Sequence 28, Appl
c 994	74.6	2.6	8001	4	US-09-539-601-16	Sequence 16, Appl	c1067	73.4	2.6	601	4	US-09-949-016-25850	Sequence 25850, A
c 995	74.6	2.6	8001	4	US-09-539-601-22	Sequence 22, Appl	1068	73.4	2.6	601	4	US-09-949-016-55172	Sequence 55172, A
c 996	74.6	2.6	8001	4	US-09-539-601-28	Sequence 28, Appl	1069	73.4	2.6	4456	3	US-09-095-443-1	Sequence 1, Appli
c 997	74.6	2.6	8637	4	US-09-539-601-4	Sequence 4, Appli	1070	73.4	2.6	6755	3	US-08-931-939-4	Sequence 4, Appli
c 998	74.6	2.6	8638	4	US-10-029-907-7	Sequence 7, Appli	c1071	73.4	2.6	8648	4	US-10-029-907-5	Sequence 5, Appli
c 999	74.6	2.6	8638	4	US-10-029-907-24	Sequence 24, Appl	c1072	73.4	2.6	22301	4	US-09-949-016-12924	Sequence 12924, A
c1000	74.6	2.6	8638	4	US-10-029-907-25	Sequence 25, Appl	1073	73.4	2.6	23465	4	US-09-949-016-12487	Sequence 12487, A
c1001	74.6	2.6	8639	4	US-10-029-907-1	Sequence 1, Appli	1074	73.4	2.6	118868	4	US-09-949-016-15746	Sequence 15746, A
c1002	74.6	2.6	8649	4	US-09-539-601-13	Sequence 13, Appl	c1075	73.4	2.6	152331	3	US-09-128-155-16	Sequence 16, Appl
c1003	74.6	2.6	11076	4	US-09-539-601-1	Sequence 1, Appli	1076	73.2	2.6	250	4	US-09-621-976-18363	Sequence 18363, A
c1004	74.6	2.6	11076	4	US-09-539-601-19	Sequence 19, Appl	1077	73.2	2.6	1702	4	US-09-799-451-574	Sequence 574, App
c1005	74.6	2.6	11076	4	US-09-539-601-25	Sequence 25, Appl	1078	73.2	2.6	2329	4	US-09-800-729-11	Sequence 11, Appl
c1006	74.6	2.6	11076	4	US-09-539-601-31	Sequence 31, Appl	1079	73.2	2.6	6065	4	US-09-800-729-35	Sequence 35, Appl
c1007	74.6	2.6	11338	4	US-09-949-016-1583	Sequence 1583, A	1080	73.2	2.6	13146	2	US-08-724-354D-3	Sequence 3, Appli
c1008	74.6	2.6	21593	4	US-09-949-016-15799	Sequence 15799, A	c1081	73.2	2.6	8850	4	US-09-270-984A-3	Sequence 3, Appli
c1009	74.6	2.6	41743	4	US-09-949-016-13796	Sequence 13796, A	c1082	73.2	2.6	8850	4	US-09-949-016-13424	Sequence 13424, A
c1010	74.6	2.6	57267	4	US-09-949-016-11899	Sequence 11899, A	c1083	73.2	2.6	92155	4	US-09-949-016-17484	Sequence 17484, A
c1011	74.6	2.6	96878	4	US-09-949-016-12551	Sequence 12551, A	c1084	73.2	2.6	143550	4	US-09-949-016-14143	Sequence 14143, A
c1012	74.6	2.6	101015	4	US-09-949-016-16981	Sequence 16981, A	c1085	73.2	2.6	149543	4	US-09-949-016-15947	Sequence 15947, A
c1013	74.6	2.6	422592	4	US-09-949-016-14182	Sequence 14182, A	c1086	73.2	2.6	199471	4	US-09-949-016-14083	Sequence 14083, A
c1014	74.4	2.6	378	4	US-09-248-796A-11672	Sequence 11672, A	c1087	73.2	2.6	673	4	US-09-621-976-14963	Sequence 14963, A
c1015	74.4	2.6	1123	3	US-09-152-060-15	Sequence 15, Appl	c1088	73	2.6	271	2	US-08-731-272A-29	Sequence 29, Appl
c1016	74.4	2.6	1949	4	US-09-270-767-30986	Sequence 30986, A	c1089	73	2.6	601	4	US-09-949-016-201490	Sequence 201490, A
c1017	74.4	2.6	3290	4	US-09-270-767-14750	Sequence 14750, A	1090	73	2.6	601	4	US-09-949-016-201491	Sequence 201491, A
c1018	74.4	2.6	21862	4	US-09-949-016-17319	Sequence 17319, A	1091	73	2.6	1069	4	US-09-205-258-74	Sequence 74, Appl
c1019	74.4	2.6	49440	4	US-09-949-016-14150	Sequence 14150, A	1092	73	2.6	1709	4	US-09-426-783-6	Sequence 6, Appli
c1020	74.2	2.6	321	2	US-08-520-678A-23	Sequence 23, Appl	1093	73	2.6	2028	4	US-09-426-783-9	Sequence 9, Appli
c1021	74.2	2.6	321	3	US-08-897-126-23	Sequence 23, Appl	1094	73	2.6	2065	3	US-09-370-473-5	Sequence 5, Appli
c1022	74.2	2.6	472	4	US-09-270-767-12212	Sequence 2212, A	1095	73	2.6	2837	2	US-08-993-228-11	Sequence 11, Appl
c1023	74.2	2.6	601	4	US-09-949-016-32560	Sequence 32560, A	1096	73	2.6	4880	3	US-09-392-277-1	Sequence 1, Appli
c1024	74.2	2.6	601	4	US-09-949-016-60625	Sequence 60625, A	1097	73	2.6	4880	3	US-09-392-277-1	Sequence 1, Appli
c1025	74.2	2.6	601	4	US-09-949-016-155363	Sequence 155363, A	1098	73	2.6	4880	3	US-09-031-563-1	Sequence 1, Appli
c1026	74.2	2.6	1214	4	US-09-780-717-28	Sequence 28, Appl	1099	73	2.6	5125	3	US-09-258-000-1	Sequence 1, Appli
c1027	74.2	2.6	2083	4	US-09-716-129-41	Sequence 41, Appl	1100	73	2.6	5125	3	US-09-392-277-4	Sequence 4, Appli
c1028	74.2	2.6	102409	4	US-09-949-016-15148	Sequence 15148, A	1101	73	2.6	5125	4	US-09-258-000-4	Sequence 4, Appli
c1029	74.2	2.6	360470	4	US-09-949-016-13173	Sequence 13173, A	1102	73	2.6	61664	4	US-09-949-016-13308	Sequence 13308, A
c1030	74	2.6	347	4	US-09-621-976-16136	Sequence 16136, A	1103	73	2.6	86639	4	US-09-949-016-17397	Sequence 17397, A
c1031	74	2.6	601	4	US-09-949-016-21580	Sequence 21580, A	c1104	73	2.6	117838	4	US-09-949-016-17595	Sequence 17595, A
c1032	74	2.6	601	4	US-09-949-016-16416	Sequence 126416, A	c1105	73	2.6	139049	4	US-09-949-016-17595	Sequence 17595, A
c1033	74	2.6	601	4	US-09-949-016-127057	Sequence 127057, A	c1106	73	2.6	146095	4	US-09-949-016-17030	Sequence 17030, A
c1034	74	2.6	601	4	US-09-949-016-130332	Sequence 130332, A	1107	73	2.6	146095	4	US-09-949-016-12872	Sequence 12872, A
c1035	74	2.6	601	4	US-09-949-016-173109	Sequence 173109, A	1108	73	2.6	146104	4	US-09-949-016-13239	Sequence 13239, A
c1036	74	2.6	1206	3	US-09-465-558-53	Sequence 53, Appl	c1109	73	2.6	186959	4	US-09-949-016-13125	Sequence 13125, A
c1037	74	2.6	1637	4	US-09-205-258-178	Sequence 178, App	c1110	73	2.6	190078	4	US-09-949-016-12707	Sequence 12707, A
c1038	74	2.6	4055	4	US-09-620-312D-706	Sequence 706, App	c1111	73	2.6	202001	4	US-09-949-016-17026	Sequence 17026, A
c1039	74	2.6	8100	4	US-09-554-337-4	Sequence 4, Appli	1112	73	2.6	245286	4	US-09-734-674-3	Sequence 3, Appli
c1040	74	2.6	11517	1	US-07-920-281C-1	Sequence 1, Appli	1113	73	2.6	283538	4	US-09-949-016-15497	Sequence 15497, A
c1041	74	2.6	11517	3	US-08-466-277-1	Sequence 1, Appli	1114	73	2.6	413	3	US-09-949-016-13506	Sequence 13506, A
c1042	74	2.6	11517	3	US-09-688-842-1	Sequence 1, Appli	1115	72.8	2.6	510	4	US-09-227-357-71	Sequence 71, Appl
c1043	74	2.6	15538	4	US-09-554-337-1	Sequence 1, Appli	1116	72.8	2.6	601	4	US-09-248-796A-13735	Sequence 13735, A
c1044	74	2.6	20229	4	US-09-949-016-16549	Sequence 16649, A	c1117	72.8	2.6	601	4	US-09-949-016-127054	Sequence 127054, A
c1045	74	2.6	41062	4	US-09-949-016-12761	Sequence 12761, A	c1118	72.8	2.6	601	4	US-09-949-016-127056	Sequence 127056, A
c1046	74	2.6	41062	4	US-09-949-016-16796	Sequence 16796, A	c1119	72.8	2.6	601	4	US-09-949-016-127058	Sequence 127058, A
c1047	73.8	2.6	601	4	US-09-949-016-48520	Sequence 48520, A	c1120	72.8	2.6	601	4	US-09-949-016-127059	Sequence 127059, A
c1048	73.8	2.6	601	4	US-09-949-016-184917	Sequence 184917, A	c1121	72.8	2.6	601	4	US-09-949-016-127060	Sequence 127060, A
c1049	73.8	2.6	601	4	US-09-949-016-185072	Sequence 185072, A	c1122	72.8	2.6	601	4	US-09-949-016-127061	Sequence 127061, A

c1123	72.8	2.6	601	4	US-09-949-016-149677	Sequence 149677,	1196	72.2	2.5	601	4	US-09-949-016-55173	Sequence 55173, A
1124	72.8	2.6	601	4	US-09-949-016-184898	Sequence 184898,	1197	72.2	2.5	601	4	US-09-949-016-55174	Sequence 55174, A
1125	72.8	2.6	601	4	US-09-949-016-185053	Sequence 185053,	1198	72.2	2.5	601	4	US-09-949-016-122967	Sequence 122967, A
1126	72.8	2.6	1534	1	US-08-300-903A-6	Sequence 6, Appli	1199	72.2	2.5	601	4	US-09-949-016-123061	Sequence 123061, A
1127	72.8	2.6	1534	4	US-08-988-197-6	Sequence 6, Appli	1200	72.2	2.5	601	4	US-09-949-016-123155	Sequence 123155, A
1128	72.8	2.6	1534	4	US-10-385-072-6	Sequence 6, Appli	1201	72.2	2.5	601	4	US-09-949-016-123249	Sequence 123249, A
1129	72.8	2.6	1976	4	US-09-920-759-10	Sequence 10, Appli	1202	72.2	2.5	601	4	US-09-949-016-123343	Sequence 123343, A
1130	72.8	2.6	2291	4	US-09-220-132-114	Sequence 11, App	1203	72.2	2.5	601	4	US-09-949-016-123385	Sequence 123385, A
1131	72.8	2.6	2291	4	US-09-814-915A-95	Sequence 95, Appli	1204	72.2	2.5	601	4	US-09-949-016-123427	Sequence 123427, A
1132	72.8	2.6	8920	2	US-08-446-855A-1	Sequence 1, Appli	1205	72.2	2.5	601	4	US-09-949-016-123469	Sequence 123469, A
1133	72.8	2.6	8920	3	US-09-150-741-1	Sequence 1, Appli	1206	72.2	2.5	601	4	US-09-949-016-123511	Sequence 123511, A
1134	72.8	2.6	14554	4	US-09-949-016-15908	Sequence 15908, A	1207	72.2	2.5	601	4	US-09-949-016-123553	Sequence 123553, A
1135	72.8	2.6	23319	4	US-09-949-016-14407	Sequence 14407, A	1208	72.2	2.5	601	4	US-09-949-016-123595	Sequence 123595, A
c1136	72.8	2.6	53336	4	US-09-949-016-12500	Sequence 12500, A	1209	72.2	2.5	601	4	US-09-949-016-123637	Sequence 123637, A
c1137	72.8	2.6	53336	4	US-09-949-016-15092	Sequence 16092, A	1210	72.2	2.5	601	4	US-09-949-016-123679	Sequence 123679, A
c1138	72.8	2.6	56326	4	US-09-949-016-15648	Sequence 16468, A	1211	72.2	2.5	601	4	US-09-949-016-123721	Sequence 123721, A
1139	72.8	2.6	67479	4	US-09-949-016-11804	Sequence 11804, A	1212	72.2	2.5	601	4	US-09-949-016-123763	Sequence 123763, A
1140	72.8	2.6	71119	4	US-09-949-016-13358	Sequence 13358, A	c1213	72.2	2.5	974	4	US-09-270-767-14699	Sequence 14699, A
c1141	72.8	2.6	89892	4	US-09-949-016-13667	Sequence 13667, A	1214	72.2	2.5	1662	4	US-09-248-796A-3485	Sequence 2485, Ap
1142	72.8	2.6	312474	4	US-09-949-016-17434	Sequence 17434, A	1215	72.2	2.5	3238	3	US-08-123-934A-5	Sequence 5, Appli
1143	72.6	2.6	73	4	US-09-621-976-14729	Sequence 14729, A	1216	72.2	2.5	3238	4	PCT-US94-10080-5	Sequence 5, Appli
1144	72.6	2.6	601	4	US-09-949-016-48516	Sequence 48516, A	1217	72.2	2.5	3238	5	US-09-949-016-13342	Sequence 13342, A
1145	72.6	2.6	601	4	US-09-949-016-48521	Sequence 48521, A	1218	72.2	2.5	6029	4	US-09-949-016-12142	Sequence 12142, A
c1146	72.6	2.6	601	4	US-09-949-016-133438	Sequence 133438, A	1219	72.2	2.5	11093	4	US-09-949-016-12145	Sequence 12145, A
1147	72.6	2.6	787	4	US-09-621-976-1878	Sequence 1878, Ap	1220	72	2.5	72	4	US-09-621-976-10145	Sequence 10145, A
1148	72.6	2.6	2481	2	US-08-630-118A-1	Sequence 1, Appli	1221	72	2.5	72	4	US-09-621-976-14815	Sequence 14815, A
1149	72.6	2.6	2481	2	US-08-838-399-1	Sequence 1, Appli	1222	72	2.5	72	4	US-09-621-976-14842	Sequence 14842, A
1150	72.6	2.6	2481	3	US-09-235-839-1	Sequence 1, Appli	c1223	72	2.5	101	3	US-09-404-879A-293	Sequence 293, App
1151	72.6	2.6	2481	3	US-09-327-035-1	Sequence 1, Appli	c1224	72	2.5	101	4	US-09-338-933-293	Sequence 293, App
1152	72.6	2.6	2604	2	US-08-630-118A-3	Sequence 3, Appli	c1225	72	2.5	101	4	US-09-216-681-293	Sequence 293, App
1153	72.6	2.6	2604	2	US-08-838-399-3	Sequence 3, Appli	c1226	72	2.5	101	4	US-09-216-003A-293	Sequence 293, App
1154	72.6	2.6	2604	3	US-09-235-839-3	Sequence 3, Appli	c1227	72	2.5	101	4	US-09-667-857-293	Sequence 293, App
1155	72.6	2.6	2604	3	US-09-327-035-3	Sequence 3, Appli	1228	72	2.5	183	4	US-09-621-976-13606	Sequence 13606, A
1156	72.6	2.6	34372	4	US-09-949-016-13098	Sequence 13098, A	1229	72	2.5	358	4	US-09-621-976-997	Sequence 927, App
1157	72.6	2.6	34875	4	US-09-949-016-13099	Sequence 13099, A	c1230	72	2.5	509	3	US-09-030-607-202	Sequence 202, App
c1158	72.6	2.6	58768	4	US-09-949-016-13175	Sequence 13175, A	c1231	72	2.5	509	3	US-09-433-313-202	Sequence 202, App
c1159	72.6	2.6	152070	4	US-09-949-016-15402	Sequence 15402, A	c1232	72	2.5	509	3	US-09-352-616A-202	Sequence 202, App
c1160	72.6	2.6	236474	4	US-09-949-016-13418	Sequence 13418, A	c1233	72	2.5	509	3	US-09-232-149A-202	Sequence 202, App
1161	72.4	2.5	601	4	US-09-949-016-179789	Sequence 179789, A	c1234	72	2.5	509	4	US-09-159-812-202	Sequence 202, App
c1162	72.4	2.5	601	4	US-09-949-016-89635	Sequence 89635, A	c1235	72	2.5	509	4	US-09-636-215-202	Sequence 202, App
c1163	72.4	2.5	601	4	US-09-949-016-89636	Sequence 89636, A	c1236	72	2.5	509	4	US-09-685-166A-202	Sequence 202, App
c1164	72.4	2.5	601	4	US-09-949-016-126417	Sequence 126417, A	c1237	72	2.5	509	4	US-09-115-453-202	Sequence 202, App
c1165	72.4	2.5	601	4	US-09-949-016-127053	Sequence 127053, A	c1238	72	2.5	509	4	US-09-688-489-202	Sequence 202, App
c1166	72.4	2.5	601	4	US-09-949-016-127055	Sequence 127055, A	c1239	72	2.5	509	4	US-09-679-436-202	Sequence 202, App
1167	72.4	2.5	601	4	US-09-949-016-161232	Sequence 161232, A	c1240	72	2.5	509	4	US-09-759-143-202	Sequence 202, App
c1168	72.4	2.5	601	4	US-09-949-016-173108	Sequence 173108, A	c1241	72	2.5	509	4	US-09-651-236-202	Sequence 202, App
1169	72.4	2.5	601	4	US-09-949-016-184918	Sequence 184918, A	1242	72	2.5	601	4	US-09-949-016-32214	Sequence 32214, A
1170	72.4	2.5	601	4	US-09-949-016-185073	Sequence 185073, A	1243	72	2.5	601	4	US-09-949-016-32215	Sequence 32215, A
1171	72.4	2.5	991	3	US-08-924-747-25	Sequence 25, Appli	1244	72	2.5	601	4	US-09-949-016-32216	Sequence 32216, A
1172	72.4	2.5	991	3	US-09-247-373B-25	Sequence 25, Appli	1245	72	2.5	601	4	US-09-949-016-108014	Sequence 108014, A
1173	72.4	2.5	1398	3	US-09-296-715-25	Sequence 25, Appli	1246	72	2.5	601	4	US-09-949-016-108015	Sequence 108015, A
1174	72.4	2.5	1398	4	US-09-270-767-4082	Sequence 4082, Ap	1247	72	2.5	601	4	US-09-949-016-108016	Sequence 108016, A
1175	72.4	2.5	1398	4	US-09-270-767-13364	Sequence 13364, A	c1248	72	2.5	601	4	US-09-949-016-126415	Sequence 126415, A
1176	72.4	2.5	2187	3	US-09-127-219B-2	Sequence 2, Appli	1249	72	2.5	2158	1	US-07-602-608-1	Sequence 1, Appli
1177	72.4	2.5	15575	4	US-09-949-016-12634	Sequence 12634, A	1250	72	2.5	2158	1	US-08-261-578-1	Sequence 1, Appli
1178	72.4	2.5	15575	4	US-09-949-016-16568	Sequence 16568, A	1251	72	2.5	13118	4	US-09-949-016-14721	Sequence 14721, A
1179	72.4	2.5	20721	4	US-09-949-016-16257	Sequence 16257, A	1252	72	2.5	13648	4	US-09-949-016-12470	Sequence 12470, A
c1180	72.4	2.5	23927	4	US-09-949-016-14284	Sequence 14284, A	c1253	72	2.5	63247	4	US-09-949-016-16809	Sequence 16809, A
c1181	72.4	2.5	45484	4	US-09-949-016-12967	Sequence 12967, A	1254	71.8	2.5	146	4	US-09-621-976-16686	Sequence 16686, A
c1182	72.4	2.5	61913	4	US-09-949-016-15338	Sequence 15338, A	1255	71.8	2.5	536	1	US-08-341-568-1	Sequence 1, Appli
c1183	72.4	2.5	61922	4	US-09-949-016-11772	Sequence 11772, A	1256	71.8	2.5	536	2	US-08-911-020-1	Sequence 1, Appli
c1184	72.4	2.5	90472	4	US-09-949-016-14038	Sequence 14038, A	1257	71.8	2.5	601	4	US-09-949-016-122969	Sequence 122969, A
1185	72.2	2.5	146	4	US-09-621-976-16695	Sequence 16695, A	1258	71.8	2.5	601	4	US-09-949-016-123063	Sequence 123063, A
1186	72.2	2.5	243	1	US-07-922-723A-9	Sequence 9, Appli	1259	71.8	2.5	601	4	US-09-949-016-123157	Sequence 123157, A
1187	72.2	2.5	243	1	US-07-799-828C-9	Sequence 9, Appli	1260	71.8	2.5	601	4	US-09-949-016-123251	Sequence 123251, A
1188	72.2	2.5	243	1	US-08-074-275-9	Sequence 9, Appli	1261	71.8	2.5	601	4	US-09-949-016-123345	Sequence 123345, A
1189	72.2	2.5	243	1	US-08-480-366-9	Sequence 9, Appli	1262	71.8	2.5	601	4	US-09-949-016-123387	Sequence 123387, A
1190	72.2	2.5	243	2	US-07-952-277A-9	Sequence 9, Appli	1263	71.8	2.5	601	4	US-09-949-016-123429	Sequence 123429, A
1191	72.2	2.5	601	4	US-09-949-016-25851	Sequence 25851, A	1264	71.8	2.5	601	4	US-09-949-016-123471	Sequence 123471, A
1192	72.2	2.5	601	4	US-09-949-016-25852	Sequence 25852, A	1265	71.8	2.5	601	4	US-09-949-016-123513	Sequence 123513, A
1193	72.2	2.5	601	4	US-09-949-016-48517	Sequence 48517, A	1266	71.8	2.5	601	4	US-09-949-016-123555	Sequence 123555, A
1194	72.2	2.5	601	4	US-09-949-016-48518	Sequence 48518, A	1267	71.8	2.5	601	4	US-09-949-016-123597	Sequence 123597, A
1195	72.2	2.5	601	4	US-09-949-016-48519	Sequence 48519, A	1268	71.8	2.5	601	4	US-09-949-016-123639	Sequence 123639, A

1269	71.8	2.5	601	4	US-09-949-016-123681	Sequence 123681,	1342	71.4	2.5	278866	4	US-09-949-016-13924	Sequence 13924, A
1270	71.8	2.5	601	4	US-09-949-016-123723	Sequence 123723,	1343	71.4	2.5	278866	4	US-09-949-016-13925	Sequence 13925, A
1271	71.8	2.5	601	4	US-09-949-016-123765	Sequence 123765,	1344	71.4	2.5	278866	4	US-09-949-016-13926	Sequence 13926, A
c1272	71.8	2.5	601	4	US-09-949-016-182882	Sequence 128882,	1345	71.4	2.5	278866	4	US-09-949-016-14699	Sequence 14699, A
1273	71.8	2.5	732	3	US-09-149-476-66	Sequence 66, Appl	1346	71.4	2.5	278866	4	US-09-949-016-14700	Sequence 14700, A
1274	71.8	2.5	1844	4	US-10-003-392-7	Sequence 7, Appl	1347	71.4	2.5	278866	4	US-09-949-016-14701	Sequence 14701, A
1275	71.8	2.5	55195	4	US-09-949-016-15854	Sequence 15854, A	1348	71.4	2.5	278866	4	US-09-949-016-14702	Sequence 14702, A
1276	71.8	2.5	158942	4	US-09-949-016-12227	Sequence 12227, A	1349	71.4	2.5	278866	4	US-09-949-016-14703	Sequence 14703, A
1277	71.8	2.5	158950	4	US-09-949-016-12227	Sequence 12227, A	1350	71.2	2.5	72	4	US-08-621-976-9837	Sequence 9837, Ap
1278	71.6	2.5	72	4	US-09-621-976-15064	Sequence 15064, A	1351	71.2	2.5	145	4	US-08-621-976-16691	Sequence 16691, A
1279	71.6	2.5	253	4	US-09-621-976-12799	Sequence 12799, A	1352	71.2	2.5	261	4	US-09-248-796A-12701	Sequence 12701, A
1280	71.6	2.5	601	4	US-09-949-016-126130	Sequence 126130,	c1353	71.2	2.5	467	2	US-08-841-349-18	Sequence 18, Appl
1281	71.6	2.5	601	4	US-09-949-016-126131	Sequence 126131,	c1354	71.2	2.5	467	4	US-09-431-184A-18	Sequence 18, Appl
1282	71.6	2.5	601	4	US-09-949-016-126132	Sequence 126132,	1355	71.2	2.5	601	4	US-09-949-016-126134	Sequence 126134, A
1283	71.6	2.5	601	4	US-09-949-016-126133	Sequence 126133,	1356	71.2	2.5	601	4	US-09-949-016-126135	Sequence 126135, A
1284	71.6	2.5	601	4	US-09-949-016-126137	Sequence 126137,	1357	71.2	2.5	601	4	US-09-949-016-126136	Sequence 126136, A
1285	71.6	2.5	1485	3	US-09-372-422A-39	Sequence 39, Appl	c1358	71.2	2.5	3212	3	US-08-697-954-1	Sequence 1, Appl
1286	71.6	2.5	1810	4	US-09-800-729-73	Sequence 73, Appl	c1359	71.2	2.5	13372	4	US-09-949-016-16941	Sequence 16941, A
1287	71.6	2.5	1811	4	US-09-800-729-77	Sequence 77, Appl	c1360	71.2	2.5	27794	4	US-09-949-016-15133	Sequence 15133, A
1288	71.6	2.5	1813	5	PCT-US94-12883-3	Sequence 3, Appl	c1361	71.2	2.5	37254	4	US-09-949-016-15973	Sequence 15973, A
1289	71.6	2.5	2679	4	US-09-684-579-2	Sequence 2, Appl	1362	71	2.5	71	4	US-09-621-976-14905	Sequence 14905, A
1290	71.6	2.5	4239	4	US-09-815-048-1	Sequence 1, Appl	1363	71	2.5	1965	4	US-09-482-273-27	Sequence 27, Appl
c1291	71.6	2.5	5340	4	US-09-627-122-21	Sequence 21, Appl	1364	71	2.5	2964	4	US-09-578-063-25	Sequence 25, Appl
c1292	71.6	2.5	29121	4	US-09-949-016-11748	Sequence 11748, A	c1365	71	2.5	12951	4	US-09-949-016-14075	Sequence 14075, A
c1293	71.6	2.5	29122	4	US-09-949-016-13591	Sequence 13591, A	1366	71	2.5	101349	4	US-09-949-016-17433	Sequence 17433, A
1294	71.6	2.5	35007	4	US-09-949-016-15330	Sequence 15330, A	1367	70.8	2.5	234	4	US-09-248-796A-10692	Sequence 10692, A
c1295	71.6	2.5	44244	4	US-09-949-016-11743	Sequence 11743, A	c1368	70.8	2.5	388	2	US-08-623-906A-13	Sequence 13, Appl
c1296	71.6	2.5	44245	4	US-09-949-016-13579	Sequence 13579, A	1369	70.8	2.5	490	4	US-09-270-767-10524	Sequence 10524, A
c1297	71.6	2.5	140224	4	US-09-949-016-17002	Sequence 17002, A	c1370	70.8	2.5	553	4	US-09-270-767-11139	Sequence 11139, A
1298	71.4	2.5	80	1	US-07-920-281C-25	Sequence 25, Appl	c1371	70.8	2.5	601	4	US-09-949-016-105488	Sequence 105488, A
1299	71.4	2.5	80	3	US-08-466-277-25	Sequence 25, Appl	1372	70.8	2.5	601	4	US-09-949-016-139454	Sequence 139454, A
1300	71.4	2.5	80	4	US-09-688-842-25	Sequence 25, Appl	1373	70.8	2.5	705	4	US-09-270-767-5061	Sequence 5061, Ap
1301	71.4	2.5	601	4	US-09-949-016-47328	Sequence 47328, A	1374	70.8	2.5	705	4	US-09-270-767-20343	Sequence 20343, A
c1302	71.4	2.5	601	4	US-09-949-016-193437	Sequence 193437,	1375	70.8	2.5	2389	4	US-09-799-875-7	Sequence 7, Appl
c1303	71.4	2.5	601	4	US-09-949-016-199458	Sequence 199458,	1376	70.8	2.5	6078	3	US-09-173-914-1	Sequence 1, Appl
c1304	71.4	2.5	601	4	US-09-949-016-199461	Sequence 199461,	1377	70.8	2.5	6200	3	US-09-439-923-1	Sequence 1, Appl
1305	71.4	2.5	980	3	US-09-171-208-8	Sequence 8, Appl	1378	70.8	2.5	6200	4	US-09-711-202A-1	Sequence 1, Appl
1306	71.4	2.5	1138	4	US-09-800-729-44	Sequence 44, Appl	c1379	70.8	2.5	6200	4	US-09-711-205A-1	Sequence 1, Appl
1307	71.4	2.5	1578	3	US-09-416-050A-1	Sequence 1, Appl	c1380	70.8	2.5	117001	4	US-09-949-016-15684	Sequence 15684, A
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1313	71.4	2.5	2381	1	US-08-726-160-9	Sequence 9, Appl	1386	70.6	2.5	412	4	US-09-784-423-22	Sequence 22, Appl
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RESULT 2
US-10-067-422-2
; Sequence 2, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; FILE REFERENCE: PT004P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-422-2

Query Match 75.3%; Score 2142.2; DB 4; Length 2259;
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## RESULT 3

US-09-620-312D-969

; Sequence 969, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

```
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 969
; LENGTH: 2144
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (528)..(1607)
US-09-620-312D-969
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Query Match 69.9%; Score 1988.4; DB 4; Length 2144;

Best Local Similarity 97.1%; Pred. No. 0;

Matches 2056; Conservative 0; Mismatches 11; Indels 51; Gaps 1;

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QY 659 TCCTCACTCCAGTCTCTTCCACTCCGATCGCTCCAGAAATTTTGACGGTTTCCATGCC 718
Db 27 TCCCGGGTCGACCCACGGCTCCGCTCCGATGGCTCCAGAAATTTTGACGGTTTCCATGCC 86
QY 719 ATTTATGAGGAGATCACAGCATGCTCTCATCCCCCTTGTTCCATGAGGCGACGTGCGTC 778
Db 87 ATTTATGAGGAGATCACAGCATGCTCTCATCCCCCTTGTTCCATGAGGCGACGTGCGTC 146
QY 779 CTTGCAAGGCTGGATCTTACAAAGTGTGCTGCTTGGCAGGCTATATCGGCGAGCGCTGT 838
Db 147 CTTGCAAGGCTGGATCTTACAAAGTGTGCTGCTTGGCAGGCTATATCGGCGAGCGCTGT 206
QY 839 GAAATC-----TC 847
Db 207 GAAATCTTCTTGAGGCTGGGAAATCCAAATCAAGCGGTCAAGAGATTCAATGTCTGTC 266
QY 848 CTTGAGAAAGAAACTGCTTCAGACCTCGGGGCCCAAGTCAATGGGTACCGAGAAATAACA 907
Db 267 CTTGAGAAAGAAACTGCTTCAGACCTCGGGGCCCAAGTCAATGGGTACCGAGAAATAACA 326
QY 908 GGGGCCCTGGGCTTATCAACGAGCGCATGTCTAAATTTGGCACCGTGTGTCTTTCTTT 967
Db 327 GGGGCCCTGGGCTTATCAACGAGCGCATGTCTAAATTTGGCACCGTGTGTCTTTCTTT 386
QY 968 TGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCAGCAGAGATCGAGAG 1027
Db 387 TGTAACTCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCAGCAGAGATCGAGAG 446
QY 1028 TGGTCAGGGAACAGCCCATCTGCAATAAAAGCTCGCGAGAACCAAGATTTTCAGACCTG 1087
Db 447 TGGTCAGGGAACAGCCCATCTGCAATAAAAGCTCGCGAGAACCAAGATTTTCAGACCTG 506
QY 1088 GTGAGAGGAGAGTCTTCCGATGAGGTTTCAGTCAAGGGAGACACCATATACACAGCTA 1147
Db 507 GTGAGAGGAGAGTCTTCCGATGAGGTTTCAGTCAAGGGAGACACCATATACACAGCTA 566
QY 1148 TACTCAGGGCTTTCAGCAAGCAGAACTGCAAGTGGCCCTTACCAAGAGCCAGCCCTT 1207
Db 567 TACTCAGGGCTTTCAGCAAGCAGAACTGCAAGTGGCCCTTACCAAGAGCCAGCCCTT 626
QY 1208 CCTTTTGGAGATCTGCCCATGGATACCAACATCTGTCAATCCAGCTCCAGTATGAGTGC 1267
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627	CC	TTTGGAGATCTG	CCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGC	686			
1268	AT	CTACCCCTTTCTAC	CCGCCGCTCGGCGACGACGAGGAGCATCTCTGAGGACTCGGGAAG	1327			
687	AT	CTCACCTTTCTAC	CCGCCGCTCGGCGACGACGAGGAGCATCTCTGAGGACTCGGGAAG	746			
1328	TGG	AGTGGGCGGGCACC	ATCCTGCATCCCTATCTGCCGGGAAAATTGAGAAATCATCACTGCT	1387			
747	TGG	AGTGGGCGGGCACC	ATCCTGCATCCCTATCTGCCGGGAAAATTGAGAAATCATCACTGCT	806			
1388	CCA	AGAGCCCAAGGTTG	CGCTGCGCTGGCAGGACGACATCTACAGAGGAGCACCAGCGG	1447			
807	CCA	AGAGCCCAAGGTTG	CGCTGCGCTGGCAGGACGACATCTACAGAGGAGCACCAGCGG	866			
1448	GTG	CATGACCGCAGCCT	ACACAAGGAGCGTGTTCTCTAGTCTGACGCGTGCCCTGGTG	1507			
867	GTG	CATGACCGCAGCCT	ACACAAGGAGCGTGTTCTCTAGTCTGACGCGTGCCCTGGTG	926			
1508	AAT	GAGCGCACTGTG	TGGTGCGCCCATGTGTTACTGACCTGGGGAAAGTCAACCATG	1567			
927	AAT	GAGCGCACTGTG	TGGTGCGCGCTGCGCCACTGTGTTACTGACCTGGGGAAAGTCAACCATG	986			
1568	ATC	AAAGACAGCAGAC	CTGAAAGTTGTTTGGGGAAAATTCTACCGGGATGATGACCGGGAT	1627			
987	ATC	AAAGACAGCAGAC	CTGAAAGTTGTTTGGGGAAAATTCTACCGGGATGATGACCGGGAT	1046			
1628	GAG	AAGACCTCACAG	AGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACCCC	1687			
1047	GAG	AAGACCTCACAG	AGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACCCC	1106			
1688	ATC	CTGTTGATGTGA	CATCGCCATCCTGAAAGTCTCTAGACAAGGCCCTGTATCAGCACC	1747			
1107	ATC	CTGTTGATGTGA	CATCGCCATCCTGAAAGTCTCTAGACAAGGCCCTGTATCAGCACC	1166			
1748	CGA	GTCCAGCCCATCT	CGCTCGCTGCAGTGGGATCTCAGCACTTCCTCCAGGAGTCC	1807			
1167	CGA	GTCCAGCCCATCT	CGCTCGCTGCAGTGGGATCTCAGCACTTCCTCCAGGAGTCC	1226			
1808	CAC	ATCACTGTGGCT	GGAATGTCTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAAC	1867			
1227	CAC	ATCACTGTGGCT	GGAATGTCTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAAC	1286			
1868	GAC	ACATCGGCTCTG	GGGTGGTCAGTGTGGTGGAATCTCGCTGTGTGTGAGGAGCAGCAT	1927			
1287	GAC	ACATCGGCTCTG	GGGTGGTCAGTGTGGTGGAATCTCGCTGTGTGTGAGGAGCAGCAT	1346			
1928	GAG	GACCATGGCATCC	CAGTGAGTCTACATGATAAATGTTCTGTGCGCACTGGGACCC	1987			
1347	GAG	GACCATGGCATCC	CAGTGAGTCTACATGATAAATGTTCTGTGCGCACTGGGACCC	1406			
1988	ACT	GCCCCCTTCTGA	TATCTGCATCTGCAGACAGGAGGCATCGCGGTGTGTCTTCCCG	2047			
1407	ACT	GCCCCCTTCTGA	TATCTGCATCTGCAGACAGGAGGCATCGCGGTGTGTCTTCCCG	1466			
2048	GG	ACGAGCATCTCT	CTGAGCCA	CGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATGAT	2107		
1467	GG	ACGAGCATCTCT	CTGAGCCA	CGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATGAT	1526		
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1587	ATT	GAAAGAAATATG	AAATGAACCATG	CTCATGCACTCC	TTTGAGAGTGTTCGTGATAT	1646	
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1707	A	CTTGCTGTGCC	AGGCTTCTG	ACTTCA	GGGCAAAA	CTCAGTGAAGGGTGAGTAGAC	1766

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Db	1767	CTCCATTCGCTGGTAGGCTGATGCGCGCTCCACTACTAGGACAGGCCAATTGGAAAGATGCCA	1826
Qy	2408	GGGCTTCCAAAGAGTAGTTTCTTTCAAAGAGACCATATACAAACCTCTCCACTCCACT	2467
Db	1827	GGGCTTCCAAAGAGTAGTTTCTTTCAAAGAGACCATATACAAACCTCTCCACTCCACT	1886
Qy	2468	GACCTGGTGGTCTTCTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACACAGGGAAGA	2527
Db	1887	GACCTGGTGGTCTTCTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACACAGGGAAGA	1946
Qy	2528	TCTGGGCTTCATGAGGGCCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCTGTGGACA	2587
Db	1947	TCTGGGCTTCATGAGGGCCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCTGTGGACA	2006
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Db	2007	GCCCAGGGCAGCAGAGCTGGGATGTGTGTCATGCCTTTGTGTACATGGCCACACAGTACAGT	2066
Qy	2648	CTGGTCCCTTTTCTTCCCACTCTCTTGTCACACATTTTAAATAAAGGGTTGGCTTCTG	2707
Db	2067	CTGGTCCCTTTTCTTCCCACTCTCTTGTCACACATTTTAAATAAAGGGTTGGCTTCTG	2126
Qy	2708	AACACAAAAA	2725
Db	2127	AACACAAAAA	2144

## RESULT 4

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US-09-620-312D-1006
; Sequence 1006, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCES: Polypeptides
; FILE REFERENCES: 784C1P2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_Fl_genes Version 1.0
; SEQ ID NO 1006
; LENGTH: 2142
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (528)..(1604)
US-09-620-312D-1006

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Query Match 69.7%; Score 1984.8; DB 4; Length 2142;

Best Local Similarity 97.0%; Pred. No. 0;  
Matches 2053; Conservative 0; Mismatches 12; Indels 51; Gaps 1;

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QY 659 TCCTCAGTCCAGGCTCTTCCATCCGATGGCTCCAGAAATTTGACGGTTTCCATGCC 718
Db 27 TCCCGGTCGACCCACGCGTCCGCTCCGATCCGCTCCAGAAATTTTGAAGGTTTCCATGCC 86
QY 719 ATTTATGAGGAGATCACAGCATGCTCCATCCCTGTTTCCATGAGCGGACGTCGTC 778
Db 87 ATTTATGAGGAGATCACAGCATGCTCCATCCCTGTTTCCATGAGCGGACGTCGTC 146
QY 779 CTTGCAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGCTATATCGGCAGCGCTGT 838
Db 147 CTTGCAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGCTATATCGGCAGGCTGT 206
QY 839 GAAATC-----TC 847
Db 207 GAAATCTTCTGGGCTGGGAATCCAGATCAAGGGCTCAGAAATTCATTGTCTGTC 266
QY 848 CTTGAAGAAAGAACTGCTCAGACCTCGGGGCCAGTCAATGGGTACCAAGAAATAACA 907
Db 267 CTTGAAGAAAGAACTGCTCAGACCTCGGGGCCAGTCAATGGGTACCAAGAAATAACA 326
QY 908 GGGGCCCTGGCTTATCAACGGAGCCATGCTAAATTTGGCACCGTGTCTTTCTTT 967
Db 327 GGGGCCCTGGCTTATCAACGGAGCCATGCTAAATTTGGCACCGTGTCTTTCTTT 386
QY 968 TGTAAACAATCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGATGGAGAG 1027
Db 387 TGTAAACAATCTTATGTTCTTAGTGGCAATGAGAAAGAACTTGGCCAGCAGATGGAGAG 446
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QY 1088 GTGAAAGGAGATGTTCTCCGATGAGGTTTCAAGTCAAGGGAGACACCATTTACACAGCTA 1147
Db 507 GTGAAAGGAGATGTTCTCCGATGAGGTTTCAAGTCAAGGGAGACACCATTTACACAGCTA 566
QY 1148 TACTCAGCGGCTTTCAGCAGCAGAACTGCGAGTGGCCCTTCAAGAAAGCAGCCCTT 1207
Db 567 TACTCAGCGGCTTTCAGCAGCAGAACTGCGAGTGGCCCTTCAAGAAAGCAGCCCTT 626
QY 1208 CCCTTTGAGATCTGCCATGGATACCAACATCTGCATACCCAGCTCCAGTATCAGTGC 1267
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QY 1808 CACATCACTGTGGCTGGTGAATGTCTGGGAGAGCTGAGAGGCCCTGGCTTCAAGAAC 1867
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QY 1868 GACACATCGCTCTGGGGTGGTCAAGTGTGGAGTCCGCTGCTGTGAGGAGCAGAT 1927
Db 1287 GACACATCGCTCTGGGGTGGTCAAGTGTGGAGTCCGCTGCTGTGAGGAGCAGAT 1346
QY 1928 GAGGACCATGGCATCCCAAGTGAATCTCACTGATTAACATGTTCTGTGCCAGCTGGGAACCC 1987
Db 1347 GAGGACCATGGCATCCCAAGTGAATCTCACTGATTAACATGTTCTGTGCCAGCTGGGAACCC 1406
QY 1988 ACTGCCCCCTTCTGATATCTGCACTGAGAGACAGAGGAGCATCGCGCTGTCTTCCGG 2047
Db 1407 ACTGCCCCCTTCTGATATCTGCACTGAGAGACAGAGGAGCATCGCGCTGTCTTCCGG 1466
QY 2048 GGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATGAT 2107
Db 1467 GGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGCTCAGCTGGAGCTATGAT 1526
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QY 2348 CTCATTTCTGGTAGGCTGATGCGCGTCCACTACTAGCAGCAGCAATTTGAGAGATGCCA 2407
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Db 1947 TCTGGGCTTCATGAGGCCCTTTTGAAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACA 2006
QY 2588 GCCCAGGCGCAGCAGAGCTGGGATGTGGTGCATCCGCTTTGTGTACATGCGCACAGTACAGT 2647
Db 2007 GCCCAGGCGCAGCAGAGCTGGGATGTGGTGCATCCGCTTTGTGTACATGCGCACAGTACAGT 2066
QY 2648 CTGTGCTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAATGAGGTTGGCTTCTG 2707
Db 2067 CTGTGCTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAATGAGGTTGGCTTCTG 2126
QY 2708 AACTCAAAAAA 2723
Db 2127 AACTCAAAAAA 2142
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RESULT 5
US-09-280-116-179
; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 179
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: astacin/m 12a metalloproteases
US-09-280-116-179

Query Match      16.8%; Score 479.4; DB 3; Length 505;
Best Local Similarity 99.4%; Pred. No. 8.4e-103; Indels 2; Gaps 2;
Matches 502; Conservative 0; Mismatches 1;

Qy 331 CTTGGATGACCTTCTATGTGAAGGGGTTCTACTGTGCAGAGTCCGAGCAGGCTGTGACGG 390
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Qy 391 AGGAGACTGCATGCCATGTGGCAGGTTCTGAGAGCCCAAGGTCAGATTTGTTGGA 450
Db      |||||
Qy 61  AGGAGACTGCATGCCATGTGGCAGGTTCTGAGAGCCCAAGGTCAGATTTGTTGGA 120
Db      |||||
Qy 451 AAGCTATCCCTAAATGCTCACTGGAATGACCACTTCACTGAACCTGGGTTGTCTAT 510
Db      |||||
Qy 121 AAGCTATCCCTAAATGCTCACTGGAATGACCACTTCACTGAACCTGGGTTGTCTAT 180
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Qy 241 TGAGTTTCGTGATGAGACAACCCGATGGCCAGATCATCAAGCGTGTCTGTGGCAAGA 300
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Db      |||||
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Db      |||||
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Db      |||||
Qy 751 CCCTGTTTTCATGACGCAAGTGGTCTCTGACAAAGCTGATCTTAC-AAGTGTGCT 809
Db      |||||
Qy 421 CCCTGTTTTCATGACGCAAGTGGTCTCTGACAAAGCTGATCTTACAAAGTGTGCT 480
Db      |||||
Qy 810 GCTTGGCAGGCTATCTGGGAGCG 834
Db      |||||
Qy 481 GCTTGGCAGGCTATCTGGGAGCG 505
Db      |||||

RESULT 6
US-09-835-811-1
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL0012228
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; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match      4.9%; Score 140.8; DB 4; Length 1696;
Best Local Similarity 87.5%; Pred. No. 4.9e-23; Indels 0; Gaps 0;
Matches 154; Conservative 0; Mismatches 22;

Qy 2671 CTTGTACACATTTAATAAAATAAGGGTTGGCTTCTGAACACACAAAAA 2730
Db      |||||
Qy 1473 CTTGTCCCTCCCAAGATTAAGGATCACTGTATAGATTAAAAA 1532
Db      |||||
Qy 2731 AAAAAA 2790
Db      |||||
Qy 1533 AAAAAA 1592
Db      |||||
Qy 2791 AAAAAA 2846
Db      |||||
Qy 1593 AAAAAA 1648
Db      |||||

RESULT 7
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESS: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match      4.9%; Score 140; DB 1; Length 240;
Best Local Similarity 86.1%; Pred. No. 2.8e-23;
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Qy 2829 AAAAAAAAAAAAAAAAAA 2846  
Db 100 AAAAAAAAAAAAAAAAAA 83

## RESULT 11

US-09-970-966-53/c  
; Sequence 53, Application US/09970966  
; Patent No. 6720146  
; GENERAL INFORMATION:  
; APPLICANT: Stolk, John A.  
; APPLICANT: Molesh, David Alan  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.484C6  
; CURRENT APPLICATION NUMBER: US/09/970,966  
; CURRENT FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; FEATURE:  
; LOCATION: 224-225, 228, 235, 240, 246, 257, 266, 274, 279, 281, 282,  
; LOCATION: 283, 285, 287, 288, 290, 291, 292, 293, 294, 295, 296, 297,  
; LOCATION: 300, 301, 303, 307, 311, 313, 314, 317, 318, 319, 320, 321,  
; LOCATION: 323, 324, 328, 329, 330, 336, 337, 338, 339, 340, 341  
; OTHER INFORMATION: n = A,T,C or G  
; NAME/KEY: misc feature  
; LOCATION: 342-343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 356,  
; LOCATION: 357, 358, 359, 362, 363, 364, 365, 367, 373, 380, 381,  
; LOCATION: 382, 385, 387, 388, 389, 390, 392  
; OTHER INFORMATION: n = A,T,C or G

## US-09-970-966-53

Query Match 4.9%; Score 138.4; DB 4; Length 396;  
Best Local Similarity 79.3%; Pred. No. 8.5e-23;  
Matches 157; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
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Db 280 TTTATATTTTCTTTCTTTTGTGATTTAAANAAGGNAANNAANNAANTAA 221  
Qy 2709 ACTACAAAAAATAA 2768  
Db 220 AA 161  
Qy 2769 AA 2828  
Db 160 AA 101  
Qy 2829 AAAAAAAAAAAAAAAAAA 2846  
Db 100 AAAAAAAAAAAAAAAAAA 83

## RESULT 12

US-09-370-838-151  
; Sequence 151, Application US/09370838  
; Patent No. 6444425  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Raodoh  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
; FILE REFERENCE: 210121.475C1

; CURRENT APPLICATION NUMBER: US/09/370,838  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: US 09/285,323  
; EARLIER FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 289  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 151  
; LENGTH: 3275  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-370-838-151

Query Match 4.9%; Score 138.2; DB 3; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 2.8e-22;  
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Qy 2688 AAAATAAGGTTGGCTTCTGAACCTACAAAAAATAAAAAAAAAAAAAAAAAA 2747  
Db 3111 AATAAAGTTACATGCACAAAAAATAAAAAAAAAAAAAAAAAA 3170  
Qy 2748 AA 2807  
Db 3171 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3230  
Qy 2808 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846  
Db 3231 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3269

## RESULT 13

US-09-854-133-151  
; Sequence 151, Application US/09854133  
; Patent No. 6759508  
; GENERAL INFORMATION:  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Raodoh  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 210121.475C10  
; CURRENT APPLICATION NUMBER: US/09/854,133  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 735  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 151  
; LENGTH: 3275  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-854-133-151

Query Match 4.9%; Score 138.2; DB 4; Length 3275;  
Best Local Similarity 91.8%; Pred. No. 2.8e-22;  
Matches 146; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Qy 2688 AAAATAAGGTTGGCTTCTGAACCTACAAAAAATAAAAAAAAAAAAAAAAAA 2747  
Db 3111 AATAAAGTTACATGCACAAAAAATAAAAAAAAAAAAAAAAAA 3170  
Qy 2748 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2807  
Db 3171 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3230  
Qy 2808 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2846  
Db 3231 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3269

## RESULT 14

US-09-797-906-1  
; Sequence 1, Application US/09797906  
; Patent No. 6329188

GENERAL INFORMATION:  
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEINASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001151CIP  
; CURRENT APPLICATION NUMBER: US/09/797,906  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1798  
; TYPE: DNA  
; ORGANISM: Human  
US-09-797-906-1

Query Match 4.8%; Score 137.8; DB 3; Length 1798;  
Best Local Similarity 95.3%; Pred. No. 2.6e-22;  
Matches 142; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 2698 TTGGCTTCTGAACTACAAAAA 2757  
DB 1635 TTGGCAGTGGAAAAA 1694  
QY 2758 AAAAAA 2817  
DB 1695 AAAAAA 1754  
QY 2818 AAAAAA 2846  
DB 1755 AAAAAA 1783

RESULT 15  
US-09-014-969-14  
; Sequence 14, Application US/09014969  
; Patent No. 5965397  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavalie, Edward R.  
; APPLICANT: Racie, Lisa A.  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Agostino, Michael J.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09,14,969  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sprunger, Suzanne A.  
; REGISTRATION NUMBER: 41,323  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8284  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 2447 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-014-969-14

Query Match 4.8%; Score 137; DB 2; Length 2447;  
Best Local Similarity 84.9%; Pred. No. 4.6e-22;  
Matches 152; Conservative 1; Mismatches 26; Indels 0; Gaps 0;  
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DB 2208 TTGTACTTTAAATGTGACAAATAAACCTTTTGGGAGAAAAA 2267  
QY 2728 AAAAAA 2787  
DB 2268 AAAAAA 2327  
QY 2788 AAAAAA 2846  
DB 2328 AAAAAA 2386

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OM nucleic - nucleic search, using sw model

Run on: May 6, 2005, 13:19:57 ; Search time 1080 Seconds  
(without alignments)  
16113.018 Million cell updates/sec

Perfect score: 2846  
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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624	2846	100.0	2846	16	US-10-063-742-37
739	2846	100.0	2846	19	US-10-972-317-37
740	2714.4	95.4	2845	15	US-10-101-510-644
741	2292.4	80.5	2632	17	US-10-274-639-38
742	2292.4	80.5	2632	17	US-10-333-574-38
743	2197.6	77.2	2306	14	US-10-004-551-3
744	2197.6	77.2	2306	16	US-10-098-871-25
745	2142.2	75.3	2259	13	US-10-067-422-2
746	1988.4	69.9	2144	15	US-10-037-270-969
747	1988.4	69.9	2144	17	US-10-117-722-969
Sequence 230, App					
Sequence 169, App					
Sequence 37, Appl					
Sequence 3, Appl					
Sequence 644, App					
Sequence 38, Appl					
Sequence 3, Appl					
Sequence 25, Appl					
Sequence 969, App					

Sequence 1006, Ap	69.7	2142	15	US-10-037-270-1006	Sequence 1006, Ap
Sequence 1006, Ap	69.7	2142	17	US-10-117-722-1006	Sequence 1006, Ap
Sequence 1, Appl	60.5	1867	14	US-10-004-551-1	Sequence 1, Appl
Sequence 29, Appl	548	18	15	US-10-101-510-29	Sequence 29, Appl
Sequence 1083, Ap	14.4	997	11	US-09-876-143-1083	Sequence 1083, Ap
Sequence 789, App	337	9	9	US-09-954-531-789	Sequence 789, App
Sequence 1223, Ap	337	9	9	US-09-954-531-1223	Sequence 1223, Ap
Sequence 1856, Ap	337	19	19	US-10-843-641A-1856	Sequence 1856, Ap
Sequence 2290, Ap	337	19	19	US-10-843-641A-2290	Sequence 2290, Ap
Sequence 6744, Ap	337	19	19	US-09-918-995-6744	Sequence 6744, Ap
Sequence 12276, A	9.8	297	17	US-10-242-535A-12276	Sequence 12276, A
Sequence 12276, A	9.8	297	17	US-10-085-783A-12276	Sequence 12276, A
Sequence 696, App	432	11	11	US-09-876-143-696	Sequence 696, App
Sequence 4638, Ap	286	18	18	US-10-723-860-4638	Sequence 4638, Ap
Sequence 275184, A	7.7	554	13	US-10-027-632-275184	Sequence 275184, A
Sequence 275184, A	7.7	554	17	US-10-027-632-275184	Sequence 275184, A
Sequence 1, Appl	369	10	10	US-09-903-393-1	Sequence 1, Appl
Sequence 13303, A	5.1	476	18	US-10-021-323-13303	Sequence 13303, A
Sequence 3350, Ap	5.1	1423	18	US-10-767-795-3350	Sequence 3350, Ap
Sequence 15, Appl	5.1	2057	17	US-10-266-829-15	Sequence 15, Appl
Sequence 115991, A	5.1	2177	18	US-10-425-115-115991	Sequence 115991, A
Sequence 62402, A	5.1	603	18	US-10-425-115-62402	Sequence 62402, A
Sequence 636, App	5.1	608	18	US-10-021-323-636	Sequence 636, App
Sequence 92182, A	5.1	683	18	US-10-425-115-92182	Sequence 92182, A
Sequence 16822, A	5.1	483	18	US-10-021-323-16822	Sequence 16822, A
Sequence 58681, A	5.1	381	18	US-10-357-930-58681	Sequence 58681, A
Sequence 138, App	5.1	597	18	US-10-021-323-138	Sequence 138, App
Sequence 44930, A	5.1	375	18	US-10-357-930-44930	Sequence 44930, A
Sequence 47693, A	5.1	488	18	US-10-425-115-47693	Sequence 47693, A
Sequence 11054, A	5.1	517	18	US-10-021-323-11054	Sequence 11054, A
Sequence 8671, Ap	5.1	547	18	US-10-021-323-8671	Sequence 8671, Ap
Sequence 7767, Ap	5.1	1999	18	US-10-723-860-7767	Sequence 7767, Ap
Sequence 92368, A	5.0	411	18	US-10-425-115-92368	Sequence 92368, A
Sequence 49593, A	5.0	2070	17	US-10-424-599-49593	Sequence 49593, A
Sequence 6195, Ap	5.0	547	18	US-10-021-323-6195	Sequence 6195, Ap
Sequence 128443, A	5.0	1400	17	US-10-424-599-128443	Sequence 128443, A
Sequence 12621, A	5.0	433	18	US-10-425-115-12621	Sequence 12621, A
Sequence 1714, Ap	5.0	2226	17	US-10-374-780A-1714	Sequence 1714, Ap
Sequence 1354, Ap	5.0	2226	17	US-10-412-699B-1354	Sequence 1354, Ap
Sequence 11004, A	5.0	458	18	US-10-021-323-11004	Sequence 11004, A
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Sequence 1125, A	5.0	565	18	US-10-021-323-1125	Sequence 1125, A
Sequence 16890, A	5.0	1301	18	US-10-021-323-16890	Sequence 16890, A
Sequence 179473, A	5.0	540	18	US-10-425-115-179473	Sequence 179473, A
Sequence 23149, A	5.0	2922	18	US-10-357-930-23149	Sequence 23149, A
Sequence 2253, Ap	5.0	560	18	US-10-021-323-2253	Sequence 2253, Ap
Sequence 134227, A	5.0	315	18	US-10-425-115-134227	Sequence 134227, A
Sequence 13784, A	5.0	397	9	US-09-960-352-13784	Sequence 13784, A
Sequence 37, Appl	5.0	409	9	US-09-822-849A-37	Sequence 37, Appl
Sequence 47977, A	5.0	519	17	US-10-424-599-47977	Sequence 47977, A
Sequence 56601, A	5.0	524	18	US-10-425-115-56601	Sequence 56601, A
Sequence 56643, A	5.0	544	18	US-10-357-930-56643	Sequence 56643, A
Sequence 26, Appl	5.0	681	9	US-09-822-830A-26	Sequence 26, Appl
Sequence 17062, A	5.0	496	18	US-10-021-323-17062	Sequence 17062, A
Sequence 7873, Ap	5.0	542	18	US-10-425-115-7873	Sequence 7873, Ap
Sequence 110165, A	5.0	684	18	US-10-425-115-110165	Sequence 110165, A
Sequence 5254, Ap	5.0	1215	9	US-10-723-860-5254	Sequence 5254, Ap
Sequence 8890, Ap	5.0	257	9	US-09-960-352-8890	Sequence 8890, Ap
Sequence 48241, A	5.0	2289	18	US-10-425-115-48241	Sequence 48241, A
Sequence 7683, Ap	5.0	2575	18	US-10-723-860-7683	Sequence 7683, Ap
Sequence 2841, Ap	5.0	487	18	US-10-021-323-2841	Sequence 2841, Ap
Sequence 4626, Ap	5.0	774	19	US-10-487-901-4626	Sequence 4626, Ap
Sequence 1463, Ap	5.0	8392	15	US-10-311-455-1463	Sequence 1463, Ap
Sequence 91, Appl	5.0	11416	15	US-10-311-455-91	Sequence 91, Appl
Sequence 19, Appl	5.0	11416	17	US-10-221-613-19	Sequence 19, Appl
Sequence 13342, A	5.0	16033	15	US-10-311-455-13342	Sequence 13342, A
Sequence 21207, A	5.0	286	9	US-09-960-352-21207	Sequence 21207, A
Sequence 23843, A	5.0	560	18	US-10-425-115-23843	Sequence 23843, A
Sequence 23843, A	5.0	609	18	US-10-437-963-23843	Sequence 23843, A
Sequence 20806, A	5.0	1123	18	US-10-739-930-20806	Sequence 20806, A
Sequence 51691, A	5.0	547	18	US-10-437-963-51691	Sequence 51691, A
Sequence 15266, A	5.0	904	18	US-10-425-115-15266	Sequence 15266, A
Sequence 15266, A	5.0	1245	18	US-10-425-115-15266	Sequence 15266, A



821	141.2	5.0	1678	18	US-10-425-115-71345	Sequence 71345, A	894	140	4.9	3101	17	US-10-424-599-95057	Sequence 95067, A
c 822	141.2	5.0	6775	18	US-10-433-793-189	Sequence 189, App	895	140	4.9	3931	15	US-10-723-860-5012	Sequence 5012, App
c 823	141	5.0	403	18	US-10-425-115-155989	Sequence 155989, App	896	140	4.9	3973	15	US-10-311-455-141	Sequence 144, App
824	141	5.0	421	18	US-10-425-115-167936	Sequence 167936, A	c 897	140	4.9	40324	18	US-10-433-793-179	Sequence 179, App
825	141	5.0	737	17	US-10-424-599-69307	Sequence 69307, A	139.8	139.8	4.9	516	18	US-10-437-963-99239	Sequence 99239, A
826	141	5.0	936	17	US-10-424-599-69900	Sequence 69900, A	139.8	139.8	4.9	528	17	US-10-424-599-37260	Sequence 37260, A
827	141	5.0	2265	18	US-10-425-115-28893	Sequence 28893, A	139.8	139.8	4.9	545	18	US-10-021-323-6889	Sequence 6889, App
828	141	5.0	4824	18	US-10-723-860-5191	Sequence 5191, App	901	139.8	4.9	564	17	US-10-424-599-39558	Sequence 39558, A
c 829	140.8	4.9	165	9	US-09-764-846-344	Sequence 344, App	902	139.8	4.9	1047	17	US-10-021-323-8346	Sequence 8346, App
830	140.8	4.9	165	10	US-09-764-872-709	Sequence 709, App	902	139.8	4.9	1047	17	US-10-366-288-47	Sequence 47, Appl
831	140.8	4.9	165	10	US-09-764-891-7491	Sequence 7491, App	904	139.8	4.9	1416	17	US-10-295-027-688	Sequence 688, App
832	140.8	4.9	165	10	US-09-764-891-9815	Sequence 9815, App	904	139.8	4.9	2235	19	US-10-887-553A-987	Sequence 987, App
c 833	140.8	4.9	165	14	US-10-091-483-344	Sequence 344, App	906	139.8	4.9	7115	18	US-10-723-860-7372	Sequence 7372, App
834	140.8	4.9	165	15	US-10-205-428-956	Sequence 956, App	907	139.6	4.9	432	18	US-10-425-115-94211	Sequence 94211, A
835	140.8	4.9	341	18	US-10-021-323-451	Sequence 451, App	908	139.6	4.9	432	18	US-10-357-930-57078	Sequence 57078, A
836	140.8	4.9	355	18	US-10-021-323-8650	Sequence 850, App	c 909	139.6	4.9	490	18	US-10-021-323-10245	Sequence 10245, A
837	140.8	4.9	489	18	US-10-021-323-6774	Sequence 6774, App	c 910	139.6	4.9	545	18	US-10-021-323-6099	Sequence 6099, App
838	140.8	4.9	489	18	US-10-021-323-9165	Sequence 9165, App	c 911	139.6	4.9	578	18	US-10-021-323-7450	Sequence 7450, App
839	140.8	4.9	502	18	US-10-357-930-57784	Sequence 57784, A	912	139.6	4.9	698	9	US-09-764-846-131	Sequence 131, App
840	140.8	4.9	516	18	US-10-021-323-16986	Sequence 16986, A	913	139.6	4.9	698	14	US-10-091-483-131	Sequence 131, App
841	140.8	4.9	571	18	US-10-021-323-10114	Sequence 10114, A	914	139.6	4.9	736	17	US-10-424-599-60906	Sequence 60906, A
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c 846	140.8	4.9	469	18	US-10-021-323-16830	Sequence 16830, A	919	139.6	4.9	2549	18	US-10-723-860-5438	Sequence 5438, App
848	140.6	4.9	549	18	US-10-437-963-43799	Sequence 43799, A	920	139.6	4.9	1749	18	US-10-723-860-6482	Sequence 6482, App
c 849	140.6	4.9	1233	18	US-10-425-115-82555	Sequence 82555, A	921	139.4	4.9	437	17	US-10-424-599-87401	Sequence 87401, A
c 850	140.6	4.9	1504	18	US-10-425-115-63627	Sequence 63627, A	922	139.4	4.9	509	18	US-10-021-323-6707	Sequence 6707, App
851	140.6	4.9	1521	17	US-10-172-118-1450	Sequence 1450, App	923	139.4	4.9	515	18	US-10-425-115-169633	Sequence 169633, A
852	140.6	4.9	1521	17	US-10-342-887-1450	Sequence 1450, App	924	139.4	4.9	516	18	US-10-021-323-10534	Sequence 10534, A
853	140.6	4.9	1576	18	US-10-723-860-5808	Sequence 5808, App	c 925	139.4	4.9	552	18	US-10-021-323-17351	Sequence 17351, A
c 854	140.6	4.9	1803	17	US-10-374-780A-1279	Sequence 1279, App	926	139.4	4.9	1880	18	US-10-425-115-44753	Sequence 44753, A
856	140.6	4.9	1811	17	US-10-424-599-59218	Sequence 59218, A	c 927	139.2	4.9	3673778	16	US-10-312-841-2	Sequence 2, Appli
857	140.6	4.9	2525	17	US-10-424-599-101605	Sequence 101605, A	928	139.2	4.9	431	18	US-10-021-323-15260	Sequence 15260, A
858	140.6	4.9	2809	17	US-10-172-118-340	Sequence 340, App	929	139.2	4.9	467	18	US-10-437-963-94117	Sequence 94117, A
859	140.6	4.9	3505	17	US-10-342-887-340	Sequence 340, App	930	139.2	4.9	571	18	US-10-021-323-7115	Sequence 7115, App
c 860	140.6	4.9	3505	17	US-10-389-566-204	Sequence 204, App	931	139.2	4.9	575	17	US-10-424-599-71318	Sequence 71318, A
861	140.4	4.9	327	9	US-09-960-352-4630	Sequence 4630, App	932	139.2	4.9	937	17	US-10-424-599-69518	Sequence 69518, A
862	140.4	4.9	381	18	US-10-021-323-10489	Sequence 10489, A	933	139.2	4.9	1071	17	US-10-170-385-338	Sequence 338, App
c 863	140.4	4.9	495	18	US-10-021-323-2679	Sequence 2679, App	934	139.2	4.9	1235	18	US-10-425-115-165957	Sequence 165957, A
864	140.4	4.9	515	17	US-10-424-599-106126	Sequence 106126, App	935	139.2	4.9	1466	18	US-10-425-115-176985	Sequence 176985, A
865	140.4	4.9	576	17	US-10-424-599-126135	Sequence 126135, A	936	139.2	4.9	1975	18	US-10-425-115-176985	Sequence 176985, A
c 866	140.4	4.9	592	18	US-10-425-115-105613	Sequence 105613, A	937	139.2	4.9	2190	17	US-10-425-115-80851	Sequence 80851, A
868	140.4	4.9	899	18	US-10-437-963-27088	Sequence 27088, A	938	139.2	4.9	2190	17	US-10-424-599-9903	Sequence 9903, App
869	140.4	4.9	945	18	US-10-425-115-13415	Sequence 13415, A	939	139.2	4.9	4237	9	US-09-745-763-20	Sequence 20, Appl
870	140.4	4.9	1176	18	US-10-425-115-60769	Sequence 60769, A	c 940	139.2	4.9	21354	17	US-10-221-744A-512	Sequence 512, App
c 871	140.4	4.9	1198	9	US-09-789-561-55	Sequence 55, Appl	941	139	4.9	422	18	US-10-425-115-108647	Sequence 108647, A
872	140.4	4.9	1362	17	US-10-424-599-37296	Sequence 37296, A	942	139	4.9	439	18	US-10-357-930-57531	Sequence 57531, A
873	140.4	4.9	1958	17	US-10-424-599-60709	Sequence 60709, A	943	139	4.9	537	18	US-10-021-323-7228	Sequence 7228, App
874	140.4	4.9	2094	18	US-10-425-115-51614	Sequence 51614, A	c 944	139	4.9	557	18	US-10-425-115-148098	Sequence 148098, A
c 875	140.4	4.9	11729	15	US-10-311-455-868	Sequence 868, App	945	139	4.9	564	18	US-10-425-115-177666	Sequence 177666, A
c 876	140.2	4.9	260	17	US-10-242-535A-40371	Sequence 40371, A	946	139	4.9	582	18	US-10-425-115-83069	Sequence 83069, A
877	140.2	4.9	638	17	US-10-085-783A-40371	Sequence 40371, A	947	139	4.9	645	18	US-10-425-115-116277	Sequence 116277, A
878	140.2	4.9	1495	17	US-10-424-599-125433	Sequence 125433, A	948	139	4.9	654	17	US-10-424-599-129198	Sequence 129198, A
c 879	140.2	4.9	242	9	US-09-960-373-3873	Sequence 3873, App	949	139	4.9	716	19	US-10-764-420-422	Sequence 422, App
c 880	140	4.9	359	18	US-10-425-115-99058	Sequence 99058, A	950	139	4.9	2050	18	US-10-723-860-6437	Sequence 6437, App
881	140	4.9	564	18	US-10-021-323-7972	Sequence 7972, App	951	139	4.9	2520	17	US-10-389-566-205	Sequence 205, App
882	140	4.9	630	18	US-10-425-115-95100	Sequence 95100, A	952	139	4.9	5845	15	US-10-311-455-1635	Sequence 1635, App
883	140	4.9	684	18	US-10-425-115-168572	Sequence 168572, A	c 953	139	4.9	7306	15	US-10-311-455-1610	Sequence 1610, App
884	140	4.9	760	18	US-10-357-930-29499	Sequence 29499, A	c 954	139	4.9	12007	15	US-10-311-455-690	Sequence 690, App
885	140	4.9	973	17	US-10-424-599-58879	Sequence 58879, A	c 955	139	4.9	3673778	16	US-10-312-841-1	Sequence 1, Appli
886	140	4.9	1068	18	US-10-437-963-86611	Sequence 86611, A	956	138.8	4.9	359	18	US-10-437-963-76171	Sequence 76171, A
c 887	140	4.9	1110	18	US-10-437-963-46659	Sequence 46659, A	957	138.8	4.9	466	17	US-10-424-599-71764	Sequence 71764, A
c 888	140	4.9	1163	17	US-10-424-599-86284	Sequence 86284, A	958	138.8	4.9	486	18	US-10-021-323-8307	Sequence 8307, App
c 889	140	4.9	1603	18	US-10-357-930-22091	Sequence 22091, A	959	138.8	4.9	496	18	US-10-021-323-4109	Sequence 4109, App
890	140	4.9	1603	18	US-10-357-930-23103	Sequence 23103, A	960	138.8	4.9	526	18	US-10-425-115-137716	Sequence 137716, A
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893	140	4.9	1603	18	US-10-357-930-28971	Sequence 28971, A	963	138.8	4.9	718	18	US-10-425-115-154975	Sequence 154975, A
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							965	138.8	4.9	924	18	US-10-425-115-173094	Sequence 173094, A
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967	138.8	4.9	936	11	US-09-938-671-47	Sequence 47, Appl	1040	138	4.8	2372	18	US-10-425-115-58985	Sequence 58985, A
968	138.8	4.9	936	19	US-10-935-098-47	Sequence 47, Appl	c1041	138	4.8	2585	18	US-10-425-115-54177	Sequence 54177, A
969	138.8	4.9	1070	18	US-10-425-115-61473	Sequence 61473, A	c1042	138	4.8	8946	15	US-10-311-455-884	Sequence 884, App
970	138.8	4.9	1182	18	US-10-425-115-129960	Sequence 129960, A	c1043	138	4.8	113515	15	US-10-311-455-2147	Sequence 2147, App
c 971	138.8	4.9	1306	18	US-10-425-115-83709	Sequence 83709, A	1044	137.8	4.8	375	17	US-10-424-599-58586	Sequence 58586, A
972	138.8	4.9	1929	8	US-10-425-115-161709	Sequence 161709, A	1045	137.8	4.8	388	17	US-10-424-599-131162	Sequence 131162, A
973	138.8	4.9	2753	9	US-09-789-561-15	Sequence 15, Appl	1046	137.8	4.8	522	18	US-10-021-323-869	Sequence 869, App
974	138.8	4.9	2753	19	US-10-883-936-15	Sequence 15, Appl	1047	137.8	4.8	524	18	US-10-425-115-109499	Sequence 109499, A
c 975	138.8	4.9	15832	14	US-10-239-676-106	Sequence 106, App	1048	137.8	4.8	526	18	US-10-425-115-130137	Sequence 130137, A
c 976	138.8	4.9	15832	15	US-10-311-455-1316	Sequence 1316, App	1049	137.8	4.8	587	18	US-10-425-115-172648	Sequence 172648, A
c 977	138.8	4.9	15832	15	US-10-240-453-110	Sequence 118, App	1050	137.8	4.8	619	18	US-10-425-115-102831	Sequence 102831, A
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c 979	138.6	4.9	313	18	US-10-021-323-13390	Sequence 13390, A	1052	137.8	4.8	684	18	US-10-425-115-62433	Sequence 62433, A
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981	138.6	4.9	514	18	US-10-425-115-74503	Sequence 74503, A	1054	137.8	4.8	1159	18	US-10-425-115-6815	Sequence 6815, App
982	138.6	4.9	538	18	US-10-021-323-870	Sequence 870, App	1055	137.8	4.8	2333	17	US-10-424-599-127867	Sequence 127867, A
983	138.6	4.9	545	17	US-10-424-599-4829	Sequence 4829, App	1056	137.8	4.8	2617	17	US-10-425-115-151022	Sequence 151022, A
984	138.6	4.9	578	17	US-10-424-599-133291	Sequence 133291, A	c1057	137.8	4.8	5195	15	US-10-311-455-894	Sequence 894, App
985	138.6	4.9	583	18	US-10-767-795-134	Sequence 134, App	c1058	137.8	4.8	6944	15	US-10-172-086-112	Sequence 112, App
986	138.6	4.9	595	18	US-10-425-115-175716	Sequence 175716, A	c1059	137.8	4.8	6944	18	US-10-311-507-114	Sequence 114, App
987	138.6	4.9	640	18	US-10-021-323-8853	Sequence 8853, App	c1060	137.8	4.8	6944	18	US-10-480-846-112	Sequence 112, App
c 988	138.6	4.9	893	14	US-10-198-846-7225	Sequence 7225, App	1061	137.6	4.8	325	17	US-10-424-599-59828	Sequence 59828, A
c 989	138.6	4.9	893	14	US-10-357-930-4784	Sequence 4784, App	1062	137.6	4.8	389	18	US-10-437-963-8873	Sequence 8873, App
c 990	138.6	4.9	2134	18	US-10-425-115-176649	Sequence 176649, A	c1063	137.6	4.8	406	10	US-09-814-353-4900	Sequence 4900, App
991	138.6	4.9	3055	18	US-10-425-115-128140	Sequence 128140, A	c1064	137.6	4.8	406	10	US-09-814-353-11195	Sequence 11195, A
c 992	138.6	4.9	14006	15	US-10-311-455-1931	Sequence 1931, App	c1065	137.6	4.8	411	18	US-10-021-323-7694	Sequence 7694, App
c 993	138.4	4.9	396	9	US-09-825-294-53	Sequence 53, Appl	c1066	137.6	4.8	419	9	US-09-960-352-11234	Sequence 11234, A
c 994	138.4	4.9	396	15	US-09-970-966-53	Sequence 53, Appl	1067	137.6	4.8	479	18	US-10-425-115-158896	Sequence 158896, A
c 995	138.4	4.9	396	15	US-10-212-677-53	Sequence 53, Appl	1068	137.6	4.8	485	18	US-10-021-323-8174	Sequence 8174, App
c 996	138.4	4.9	396	17	US-10-361-811-53	Sequence 53, Appl	1069	137.6	4.8	490	18	US-10-021-323-16197	Sequence 16197, A
c 997	138.4	4.9	396	17	US-10-369-186-53	Sequence 53, Appl	1070	137.6	4.8	512	18	US-10-425-115-1891	Sequence 1891, App
998	138.4	4.9	524	17	US-10-424-599-11691	Sequence 11691, A	1071	137.6	4.8	538	18	US-10-021-323-14752	Sequence 14752, A
999	138.4	4.9	567	18	US-10-021-323-8240	Sequence 8240, App	1072	137.6	4.8	556	18	US-10-357-930-40082	Sequence 40082, A
c1000	138.4	4.9	583	18	US-10-021-323-6081	Sequence 6081, App	1073	137.6	4.8	556	18	US-10-357-930-40082	Sequence 40182, A
c1001	138.4	4.9	602	18	US-10-425-115-61525	Sequence 61525, A	1074	137.6	4.8	556	18	US-10-357-930-42124	Sequence 42124, A
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1004	138.2	4.9	767	17	US-10-424-599-45104	Sequence 45104, A	1077	137.6	4.8	600	18	US-10-425-115-76887	Sequence 76887, A
1005	138.4	4.9	1211	18	US-10-739-930-4124	Sequence 4124, App	1078	137.6	4.8	655	17	US-10-424-599-107600	Sequence 107600, A
1006	138.4	4.9	1316	18	US-10-425-115-109626	Sequence 109626, A	1079	137.6	4.8	697	18	US-10-425-115-20836	Sequence 20836, A
1007	138.4	4.9	2921	9	US-09-925-301-223	Sequence 223, App	1080	137.6	4.8	751	18	US-10-425-115-71448	Sequence 71448, A
1008	138.4	4.9	3569	18	US-10-767-701-14981	Sequence 14981, A	1081	137.6	4.8	1278	18	US-10-425-115-58302	Sequence 58302, A
c1009	138.4	4.9	7486	18	US-10-433-793-80	Sequence 80, Appl	c1082	137.6	4.8	1671	15	US-10-311-455-761	Sequence 761, App
c1010	138.4	4.9	7369	18	US-10-473-126-131	Sequence 131, App	1083	137.4	4.8	231	17	US-10-242-535A-30412	Sequence 30412, A
c1011	138.4	4.9	7369	19	US-10-486-319A-34	Sequence 34, Appl	1084	137.4	4.8	231	17	US-10-085-783A-30412	Sequence 30412, A
c1012	138.4	4.9	10369	15	US-10-311-455-365	Sequence 365, App	1085	137.4	4.8	464	15	US-10-106-698-307	Sequence 307, App
c1013	138.4	4.9	10369	17	US-10-221-714A-25	Sequence 25, Appl	1086	137.4	4.8	506	18	US-10-021-323-2311	Sequence 2311, App
1014	138.2	4.9	325	18	US-10-021-323-8658	Sequence 858, App	1087	137.4	4.8	601	18	US-10-425-115-170572	Sequence 170572, A
1015	138.2	4.9	334	17	US-10-424-599-120644	Sequence 120644, A	1088	137.4	4.8	605	17	US-10-424-599-39289	Sequence 39289, A
c1016	138.2	4.9	351	10	US-09-814-353-17579	Sequence 17579, A	1089	137.4	4.8	606	18	US-10-437-963-54715	Sequence 54715, A
1017	138.2	4.9	452	18	US-10-021-323-4768	Sequence 4768, App	1090	137.4	4.8	627	17	US-10-424-599-50144	Sequence 50144, A
c1018	138.2	4.9	485	18	US-10-021-323-6802	Sequence 6802, App	1091	137.4	4.8	640	17	US-10-424-599-122753	Sequence 122753, A
1019	138.2	4.9	552	18	US-10-425-115-42027	Sequence 42027, A	1092	137.4	4.8	641	17	US-10-424-599-117136	Sequence 117136, A
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1022	138.2	4.9	768	18	US-10-425-115-98337	Sequence 98337, A	c1095	137.4	4.8	1103	18	US-10-425-115-68317	Sequence 68317, A
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1026	138.2	4.9	2785	18	US-10-723-860-5447	Sequence 5447, App	c1099	137.2	4.8	368	18	US-10-425-115-138566	Sequence 138566, A
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1028	138.2	4.9	3275	15	US-10-854-133-151	Sequence 151, App	c1101	137.2	4.8	394	18	US-10-425-115-118177	Sequence 118177, A
1029	138.2	4.9	3275	15	US-10-144-649A-151	Sequence 151, App	c1102	137.2	4.8	408	9	US-09-960-352-6263	Sequence 6263, App
1030	138.2	4.9	3454	18	US-10-723-860-6412	Sequence 6412, App	c1103	137.2	4.8	472	18	US-10-425-115-88743	Sequence 88743, A
c1031	138.2	4.9	6436	15	US-10-311-455-654	Sequence 654, App	c1104	137.2	4.8	502	18	US-10-021-323-11431	Sequence 11431, A
c1032	138	4.8	499	18	US-10-021-323-1716	Sequence 1716, App	c1105	137.2	4.8	549	18	US-10-021-323-7101	Sequence 7101, App
c1033	138	4.8	560	18	US-10-021-323-3016	Sequence 3016, App	1106	137.2	4.8	568	17	US-10-424-599-117111	Sequence 117111, A
c1034	138	4.8	574	18	US-10-021-323-7391	Sequence 7391, App	1107	137.2	4.8	568	18	US-10-425-115-22899	Sequence 22899, A
1035	138	4.8	577	18	US-10-425-115-89366	Sequence 89366, A	1108	137.2	4.8	569	18	US-10-437-963-88900	Sequence 88900, A
c1036	138	4.8	592	14	US-10-198-846-8340	Sequence 8340, App	1109	137.2	4.8	573	18	US-10-425-115-31452	Sequence 31452, A
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1038	138	4.8	1137	18	US-10-739-930-635	Sequence 635, App	1111	137.2	4.8	633	17	US-10-425-115-8940	Sequence 8940, App
1039	138	4.8	2022	18	US-10-739-930-4367	Sequence 4367, App	1112	137.2	4.8	647	18	US-10-425-115-170206	Sequence 170206, A

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c1114	137.2	4.8	711	17	US-10-424-599-42333	Sequence 42333, A	1187	136.6	4.8	1583	18	US-10-425-115-57459	Sequence 57459, A
1115	137.2	4.8	714	17	US-10-424-599-80204	Sequence 80204, A	1188	136.6	4.8	2094	17	US-10-424-599-133718	Sequence 133718, A
1116	137.2	4.8	1078	18	US-10-425-115-13215	Sequence 13215, A	1189	136.6	4.8	2207	18	US-10-425-115-145441	Sequence 145441, A
c1117	137.2	4.8	1285	17	US-10-424-599-115563	Sequence 115563, A	c1130	136.6	4.8	2235	17	US-10-424-599-70027	Sequence 70027, A
c1118	137.2	4.8	1302	18	US-10-425-115-56162	Sequence 56162, A	c1131	136.6	4.8	2248	18	US-10-425-115-65796	Sequence 65796, A
c1119	137.2	4.8	1533	18	US-10-732-860-7968	Sequence 7968, Ap	c1132	136.6	4.8	11394	15	US-10-240-453-96	Sequence 96, Appl
1120	137.2	4.8	1617	18	US-10-425-115-164014	Sequence 164014, A	c1133	136.6	4.8	2140405	13	US-10-027-633-76212	Sequence 76212, A
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1122	137.2	4.8	1808	9	US-09-989-920-46	Sequence 46, Appl	c1135	136.4	4.8	333	17	US-10-424-599-53217	Sequence 53217, A
1123	137.2	4.8	2009	18	US-10-425-115-1808	Sequence 1808, Ap	1136	136.4	4.8	430	24	US-10-437-963-34803	Sequence 34803, A
c1124	137.2	4.8	2096	18	US-10-425-115-72738	Sequence 72738, A	1137	136.4	4.8	424	18	US-10-425-115-52807	Sequence 52807, A
c1125	137.2	4.8	3177	15	US-10-311-455-6234	Sequence 624, App	1138	136.4	4.8	446	9	US-09-960-352-3400	Sequence 3400, Ap
1126	137	4.8	3178	18	US-10-021-323-6340	Sequence 6340, App	1139	136.4	4.8	447	18	US-10-425-115-148961	Sequence 148961, A
1127	137	4.8	338	18	US-10-425-115-65485	Sequence 65485, A	c1200	136.4	4.8	469	18	US-10-021-323-6668	Sequence 6668, Ap
1128	137	4.8	339	18	US-10-425-115-98529	Sequence 98529, A	1136	136.4	4.8	516	18	US-10-357-930-55908	Sequence 55908, A
1129	137	4.8	372	18	US-10-425-115-24788	Sequence 24788, A	c1202	136.4	4.8	539	10	US-09-814-353-17862	Sequence 17862, A
1130	137	4.8	430	18	US-10-425-115-170993	Sequence 170993, A	1137	136.4	4.8	539	17	US-10-424-599-76890	Sequence 76890, A
1131	137	4.8	497	18	US-10-357-930-58292	Sequence 58292, A	c1204	136.4	4.8	553	18	US-10-021-323-7987	Sequence 7987, Ap
1132	137	4.8	554	18	US-10-425-115-23306	Sequence 23306, A	1205	136.4	4.8	601	17	US-10-424-599-59636	Sequence 59636, A
1133	137	4.8	561	18	US-10-425-115-169551	Sequence 169551, A	1206	136.4	4.8	617	17	US-10-424-599-71934	Sequence 71934, A
1134	137	4.8	626	18	US-10-425-115-6250	Sequence 6250, Ap	1207	136.4	4.8	822	17	US-10-424-599-111916	Sequence 11916, A
1135	137	4.8	1140	18	US-10-437-963-26438	Sequence 26438, A	1208	136.4	4.8	1519	18	US-10-425-115-17631	Sequence 17631, A
c1136	137	4.8	2142	17	US-10-424-599-118533	Sequence 118533, A	1209	136.4	4.8	1875	17	US-10-374-780A-1941	Sequence 1941, Ap
c1137	137	4.8	2197	18	US-10-425-115-18496	Sequence 18496, A	c1210	136.4	4.8	5586	17	US-10-257-166-86	Sequence 86, Appl
c1138	137	4.8	2700	18	US-10-723-860-5126	Sequence 5126, Ap	c1211	136.4	4.8	24259	17	US-10-021-323-3385	Sequence 3385, Ap
c1139	137	4.8	6172	15	US-10-240-485-126	Sequence 126, App	1212	136.2	4.8	450	18	US-10-021-323-4616	Sequence 4616, Ap
c1140	136.8	4.8	241	9	US-09-960-352-5777	Sequence 5777, Ap	c1213	136.2	4.8	459	18	US-10-357-930-54303	Sequence 54303, A
1141	136.8	4.8	421	18	US-10-021-323-7658	Sequence 7658, Ap	1214	136.2	4.8	481	18	US-10-357-930-56267	Sequence 56267, A
1142	136.8	4.8	456	9	US-09-960-352-9659	Sequence 9659, Ap	1215	136.2	4.8	510	18	US-10-767-795-5097	Sequence 5097, Ap
1143	136.8	4.8	463	17	US-10-424-599-101158	Sequence 101158, A	1216	136.2	4.8	518	18	US-10-021-323-4634	Sequence 4634, Ap
1144	136.8	4.8	520	18	US-10-425-115-132906	Sequence 132906, A	c1217	136.2	4.8	528	18	US-10-021-323-8131	Sequence 8131, Ap
1145	136.8	4.8	543	18	US-10-425-115-148211	Sequence 148211, A	c1218	136.2	4.8	541	18	US-10-021-323-11946	Sequence 11946, A
1146	136.8	4.8	570	18	US-10-357-930-59133	Sequence 59133, A	1220	136.2	4.8	558	18	US-10-437-963-8817	Sequence 8817, Ap
1147	136.8	4.8	591	18	US-10-021-323-13007	Sequence 13007, A	1221	136.2	4.8	1015	18	US-10-425-115-54818	Sequence 54818, A
1148	136.8	4.8	612	17	US-10-424-599-50936	Sequence 50936, A	1222	136.2	4.8	1093	17	US-10-424-599-95648	Sequence 95648, A
1149	136.8	4.8	677	18	US-10-425-115-131288	Sequence 131288, A	1223	136.2	4.8	1138	18	US-10-425-115-108606	Sequence 108606, A
1150	136.8	4.8	762	17	US-10-424-599-132177	Sequence 3277, A	1224	136.2	4.8	1323	18	US-10-425-115-54043	Sequence 54043, A
1151	136.8	4.8	831	9	US-09-729-674-67	Sequence 67, Appl	1225	136.2	4.8	1405	18	US-10-425-115-42749	Sequence 42749, A
1152	136.8	4.8	831	18	US-10-913-553-67	Sequence 67, Appl	1226	136.2	4.8	1638	17	US-10-424-599-96402	Sequence 96402, A
1153	136.8	4.8	1091	18	US-10-723-860-6015	Sequence 6015, Ap	1227	136.2	4.8	2481	18	US-10-425-115-440	Sequence 440, App
1154	136.8	4.8	1133	18	US-10-425-115-59679	Sequence 59679, A	c1228	136.2	4.8	24259	17	US-10-221-714A-415	Sequence 415, App
1155	136.8	4.8	1170	18	US-10-425-115-136412	Sequence 136412, A	1229	136	4.8	138	17	US-10-242-535A-50216	Sequence 50216, App
1156	136.8	4.8	1492	18	US-10-425-115-103271	Sequence 103271, A	1230	136	4.8	138	17	US-10-085-783A-50216	Sequence 50216, A
1157	136.8	4.8	2091	18	US-10-425-115-93227	Sequence 93227, A	1231	136	4.8	362	18	US-10-425-115-56607	Sequence 56607, A
1158	136.8	4.8	2148	17	US-10-739-930-2257	Sequence 2257, Ap	1232	136	4.8	419	17	US-10-424-599-58948	Sequence 58948, A
c1159	136.8	4.8	2370	17	US-10-424-599-44604	Sequence 44604, A	1233	136	4.8	443	17	US-10-424-599-18435	Sequence 18435, A
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1161	136.8	4.8	3758	18	US-10-437-963-81706	Sequence 81706, A	1235	136	4.8	487	18	US-10-425-115-144831	Sequence 144831, A
c1162	136.8	4.8	6161	15	US-10-311-455-384	Sequence 384, App	c1236	136	4.8	489	18	US-10-021-323-4517	Sequence 4517, Ap
c1163	136.8	4.8	6192	17	US-10-473-126-277	Sequence 408, App	c1237	136	4.8	508	18	US-10-021-323-5403	Sequence 5403, Ap
c1164	136.8	4.8	7369	18	US-10-473-126-277	Sequence 277, App	1238	136	4.8	526	18	US-10-021-323-14764	Sequence 14764, A
c1165	136.8	4.8	7369	19	US-10-486-319A-56	Sequence 56, Appl	c1239	136	4.8	527	18	US-10-021-323-16206	Sequence 16206, A
1166	136.6	4.8	212	17	US-10-242-535A-22243	Sequence 22243, A	c1239	136	4.8	586	18	US-10-437-963-45637	Sequence 45637, A
1167	136.6	4.8	212	17	US-10-085-783A-22243	Sequence 22243, A	1240	136	4.8	615	18	US-10-425-115-172581	Sequence 172581, A
c1168	136.6	4.8	220	9	US-09-960-352-14522	Sequence 14522, A	c1241	136	4.8	643	17	US-10-424-599-97217	Sequence 97217, A
1169	136.6	4.8	394	18	US-10-357-930-13555	Sequence 13555, A	1242	136	4.8	658	18	US-10-425-115-51887	Sequence 51887, A
1170	136.6	4.8	408	18	US-10-357-930-34697	Sequence 34697, A	1243	136	4.8	688	18	US-10-425-115-131293	Sequence 131293, A
1171	136.6	4.8	426	18	US-10-357-930-43554	Sequence 43554, A	1244	136	4.8	871	18	US-10-425-115-177814	Sequence 177814, A
1172	136.6	4.8	426	18	US-10-021-323-9484	Sequence 9484, Ap	1245	136	4.8	947	18	US-10-425-115-97521	Sequence 97521, A
1173	136.6	4.8	484	18	US-10-357-930-58027	Sequence 58027, A	c1246	136	4.8	1012	18	US-10-425-115-25975	Sequence 25975, A
1174	136.6	4.8	531	17	US-10-424-599-54674	Sequence 54674, A	1247	136	4.8	1086	18	US-10-425-115-168545	Sequence 168545, A
1175	136.6	4.8	539	18	US-10-425-115-152949	Sequence 152949, A	c1248	136	4.8	1233	17	US-10-424-599-44264	Sequence 44264, A
1176	136.6	4.8	545	18	US-10-425-115-38204	Sequence 38204, A	1249	136	4.8	1243	18	US-10-425-115-133539	Sequence 133710, A
1177	136.6	4.8	554	18	US-10-425-115-882	Sequence 882, App	1250	136	4.8	1712	18	US-10-425-115-13539	Sequence 13539, A
1178	136.6	4.8	566	18	US-10-767-701-17472	Sequence 17472, A	1251	136	4.8	1806	18	US-10-775-920-425	Sequence 225, App
1179	136.6	4.8	584	18	US-10-425-115-33678	Sequence 33678, A	1252	136	4.8	2323	18	US-10-425-115-19557	Sequence 19557, A
1180	136.6	4.8	588	18	US-10-437-963-55397	Sequence 55397, A	1253	136	4.8	3908	18	US-10-425-115-70814	Sequence 70814, A
1181	136.6	4.8	596	17	US-10-424-599-18370	Sequence 18370, A	1254	136	4.8	385	18	US-10-425-115-125187	Sequence 125187, A
c1182	136.6	4.8	599	14	US-10-081-846-8885	Sequence 8885, Ap	c1255	135.8	4.8	396	18	US-10-357-930-57615	Sequence 57615, A
1183	136.6	4.8	627	18	US-10-021-323-73	Sequence 73, Appl	1256	135.8	4.8	432	17	US-10-424-599-83231	Sequence 83231, A
1184	136.6	4.8	701	17	US-10-424-599-66331	Sequence 66331, A	1257	135.8	4.8	443	18	US-10-021-323-6814	Sequence 6814, Ap
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1260	135.8	4.8	522	18	US-10-425-115-7487	Sequence 7487, App	c1333	135.2	4.8	378	18	US-10-425-115-80509	Sequence 80509, A
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1264	135.8	4.8	574	18	US-10-021-323-11147	Sequence 11147, A	c1337	135.2	4.8	446	18	US-10-425-115-136246	Sequence 136246, A
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1266	135.8	4.8	593	18	US-10-021-323-7120	Sequence 7120, App	c1339	135.2	4.8	538	18	US-10-425-115-93124	Sequence 93124, A
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1271	135.8	4.8	2172	17	US-10-424-599-88491	Sequence 88491, A	c1344	135.2	4.8	1868	18	US-10-425-115-165307	Sequence 165307, A
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1274	135.8	4.8	2501	18	US-10-473-126-364	Sequence 364, App	c1347	135	4.7	195	17	US-10-282-122A-13382	Sequence 13382, A
1275	135.8	4.8	4001	15	US-10-173-086-96	Sequence 96, Appl	c1348	135	4.7	240	17	US-10-242-535A-8132	Sequence 8132, App
1276	135.8	4.8	4001	18	US-10-311-507-10	Sequence 10, Appl	c1349	135	4.7	240	17	US-10-085-783A-8132	Sequence 8132, App
1277	135.8	4.8	4001	18	US-10-480-846-96	Sequence 96, Appl	c1350	135	4.7	341	18	US-10-425-115-77243	Sequence 77243, A
1278	135.8	4.8	5306	15	US-10-311-455-484	Sequence 484, App	c1351	135	4.7	344	18	US-10-425-115-165946	Sequence 165946, A
1279	135.8	4.8	6134	18	US-10-433-793-170	Sequence 170, App	c1352	135	4.7	368	18	US-10-021-323-5024	Sequence 5024, App
1280	135.8	4.8	7061	15	US-10-311-455-969	Sequence 969, App	c1353	135	4.7	384	18	US-10-425-115-101577	Sequence 101577, A
1281	135.8	4.8	7061	17	US-10-221-613-147	Sequence 147, App	c1354	135	4.7	417	18	US-10-357-930-9115	Sequence 9115, App
1282	135.8	4.8	14798	15	US-10-311-455-1005	Sequence 1005, App	c1355	135	4.7	422	18	US-10-425-115-54417	Sequence 54417, A
1283	135.8	4.8	14798	15	US-10-311-455-1692	Sequence 1692, App	c1356	135	4.7	444	18	US-10-425-115-66130	Sequence 66130, A
1284	135.8	4.8	35962	18	US-10-473-126-98	Sequence 98, Appl	c1357	135	4.7	506	17	US-10-424-599-122103	Sequence 122103, A
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1290	135.6	4.8	468	18	US-10-425-115-95424	Sequence 95424, A	c1363	135	4.7	606	17	US-10-424-599-54586	Sequence 54586, A
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1292	135.6	4.8	631	18	US-10-425-115-140103	Sequence 140103, A	c1365	135	4.7	1128	18	US-10-437-963-65728	Sequence 65728, A
1293	135.6	4.8	660	17	US-10-424-599-24054	Sequence 24054, A	c1366	135	4.7	1360	17	US-10-424-599-81801	Sequence 81801, A
1294	135.6	4.8	722	17	US-10-424-599-61867	Sequence 61867, A	c1367	135	4.7	1395	18	US-10-425-115-143733	Sequence 143733, A
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1297	135.6	4.8	817	18	US-10-437-963-69665	Sequence 69665, A	c1370	134.8	4.7	435	18	US-10-021-323-11676	Sequence 11676, A
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1299	135.6	4.8	1038	18	US-10-425-115-149229	Sequence 149229, App	c1372	134.8	4.7	515	18	US-10-357-930-54538	Sequence 54538, A
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1302	135.6	4.8	1459	18	US-10-818-809-3	Sequence 3, Appl	c1375	134.8	4.7	608	17	US-10-424-599-90628	Sequence 90628, A
1303	135.6	4.8	1468	18	US-10-425-115-155843	Sequence 155843, A	c1376	134.8	4.7	1125	18	US-10-425-115-99739	Sequence 99739, A
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1307	135.6	4.8	2099	18	US-10-425-115-87145	Sequence 87145, A	c1380	134.8	4.7	1447	18	US-10-437-963-46106	Sequence 46106, A
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FN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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PD 20-FEB-2003.  
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RESULT 33  
ID ACD18627 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 34  
ID ACA58828 standard; cDNA; 2846 BP.  
DE cDNA encoding human secreted polypeptide PRO1344.  
FN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 35  
ID ABX98237 standard; cDNA; 2846 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.  
FN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;



RESULT 36  
ID ACC13988 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 37  
ID AC009768 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 38  
ID ACC88513 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 39  
ID ACD21253 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 40  
ID ABX75625 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
FN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 41  
ID ACA64004 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
FN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 42  
ID ABX97828 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 43  
ID ACA97304 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 44  
ID ACA57767 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
FN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 45  
ID ACD14295 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 46  
ID ACC91078 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 47  
ID ACC8820 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 48  
ID ACD07017 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US20030308353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 49  
ID ACA67468 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 50  
ID ACC81523 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 51  
ID ACA91268 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
FN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 52  
ID ACC89127 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 53  
ID ACC86483 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 54  
ID ACC89741 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 55  
ID ACC92920 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 56  
ID ABX80775 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 57  
ID ACA72548 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 58  
ID ACA89066 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 59  
ID ACA69802 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 60  
ID ACA96945 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 61  
ID ACA90941 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 62  
ID ACA70723 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 63  
ID ACA95233 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 64  
ID ACD4284 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 65  
ID ACC86176 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 66  
ID ACD45167 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 67  
ID ACC90048 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 68  
ID ACD12656 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 69  
ID ACF19886 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 70  
ID ABX76830 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 71  
ID ACA73162 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 72  
ID ACA68705 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 73  
ID ACA74549 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 74  
ID ACA70416 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 75  
ID ACD14602 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
Pred. No. 0;  
RESULT 76  
ID ACA93715 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.

PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 77  
ID ACA69274 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 78  
ID ABX98739 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 79  
ID ACC81216 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 80  
ID ACA95540 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 81  
ID ACD04458 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 82  
ID ACC87899 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 83  
ID ACF12561 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 84  
ID ACH66262 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 85  
ID ABX79455 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 86  
ID ACA96276 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #85.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 87  
ID ACA65050 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 88  
ID ACA73776 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 89  
ID ACA74188 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 90  
ID ACA96583 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 91  
ID ACD10689 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 92  
ID AC91385 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 93  
ID ACA93476 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 94  
ID ACD02720 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 95  
ID ACC87285 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 8; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 96  
ID ACC85869 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027262-A1.

PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 97  
ID ACA74856 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 98  
ID ACA65357 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 99  
ID ACA94174 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 100  
ID ACA97918 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 101  
ID ACA91420 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 102  
ID ACA90634 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 103  
ID ACD16181 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 104  
ID ACD17342 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 105  
ID ACC91999 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 106  
ID ACD02316 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC. 100.0%; Score 2846; DB 8; Length 2846;  
Query Match

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 107  
ID ACA74856 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 108  
ID ACA91727 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 109  
ID ACA71371 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 110  
ID AC090771 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 111  
ID ACA65781 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO protein #85.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 112  
ID ACA68944 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC. 100.0%; Score 2846; DB 8; Length 2846;  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 113  
ID ACA92974 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 114  
ID ACA94926 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 115  
ID ACD16488 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 116  
ID ACD15567 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 8; Length 2846;  
RESULT 117

ID ACA98466 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #19.  
 FN US2003027993-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 8; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 118  
 ID ABX17058 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #55.  
 FN US2002123463-A1.  
 PD 05-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 8; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 119  
 ID ABX16670 standard; cDNA; 2846 BP.  
 DE Human cDNA encoding secreted/transmembrane protein #85.  
 FN US2002127584-A1.  
 PD 12-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 8; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 120  
 ID ACA67913 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 FN US2002177164-A1.  
 PD 28-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 121  
 ID ACA63391 standard; cDNA; 2846 BP.  
 DE cDNA encoding human PRO polypeptide #19.  
 FN US2003023042-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 122  
 ID ACA97611 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #85.  
 FN US2003032115-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 123  
 ID ACA99060 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 FN US2003032140-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 124  
 ID ACC91692 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003040076-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 125  
 ID ACP11103 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 FN US2003008352-A1.  
 PD 09-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 126  
 ID ACD14953 standard; cDNA; 2846 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #85.  
 FN US2003044922-A1.

PD 06-MAR-2003.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 127  
 ID ACA88362 standard; cDNA; 2846 BP.  
 DE Human secreted and transmembrane polypeptide PRO1344 cDNA.  
 FN US2002197615-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 128  
 ID ACD81869 standard; cDNA; 2846 BP.  
 DE cDNA encoding human PRO1344 polypeptide.  
 FN US2003017981-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 129  
 ID ACD11717 standard; cDNA; 2846 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #85.  
 FN US2003032118-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 130  
 ID ACC95846 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003036135-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 131  
 ID ACF16409 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003054455-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 132  
 ID ACF02527 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003049741-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 133  
 ID ACF02834 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003049743-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 134  
 ID ACF21421 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003049769-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 135  
 ID ACF10105 standard; cDNA; 2846 BP.  
 DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
 FN US2003068743-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 2846; DB 9; Length 2846;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 136

ID ACF77998 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 137  
ID ACD46703 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 138  
ID ACD49466 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 139  
ID ACF28233 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 140  
ID ACD88923 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 141  
ID ACD84318 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 142  
ID ACD9092 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 143  
ID ADA77921 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 144  
ID ACF48834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 145  
ID ACD09154 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 146  
ID ACF11947 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 147  
ID ACF41181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 148  
ID ACF15795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 149  
ID ACF16102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 150  
ID ADB17094 standard; cDNA; 2846 BP.  
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 151  
ID ACD31929 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 152  
ID ACF18737 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 153  
ID ACF09184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 154  
ID ACF78305 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 155  
ID ACF51904 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 156  
ID ACF26391 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 157  
ID ACF24184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 158  
ID ACF63495 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 159  
ID ACF50369 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 160  
ID ACH07840 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 161  
ID ACF13646 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 162  
ID ACD41572 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 163  
ID ADA37741 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 164

ID ACF31985 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 165  
ID ACF23263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 166  
ID ACF39953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 167  
ID ACD45475 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 168  
ID ACF53132 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 169  
ID ACF27312 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 170  
ID ACF45150 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 171  
ID ACF29768 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 172  
ID ACD89844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ACD84625 standard; cDNA; 2846 BP.



DE Human PRO polynucleotide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 174  
ID ACD98785 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 175  
ID ACF77077 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 176  
ID ACF76770 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 177  
ID ACF49755 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 178  
ID ACF50062 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 179  
ID ADA21427 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 180  
ID ACD09461 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 181  
ID ACD08540 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 182  
ID ACH03594 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 183

ID ACF12254 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 184  
ID ACC94762 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 185  
ID ACD22481 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 186  
ID ACF15181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 187  
ID ACC97276 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 188  
ID ACC92306 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 189  
ID ACF13953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 190  
ID ACF14260 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 191  
ID ADA10214 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 192  
ID ACF09491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 193  
ID ACD45782 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 194  
ID ACD47931 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 195  
ID ACD67662 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 196  
ID ACF25470 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 197  
ID ACF29154 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 198  
ID ACD84932 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 199  
ID ACD84011 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 200  
ID ACD88002 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 201  
ID ACF30689 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 202  
ID ACF32292 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 203  
ID ACH1952 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 204  
ID ACH12259 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 205  
ID ADA19899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 206  
ID ACD40651 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 207  
ID ADS17282 standard; cDNA; 2846 BP.  
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.  
FN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 208  
ID ADA17758 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
FN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 209  
ID ACF18123 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 210  
ID ACF08570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 211  
ID ACF31371 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 212  
ID ACF52211 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 213  
ID ACD50080 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 214  
ID ACF38783 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 215  
ID ACF26698 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 216  
ID ACF24798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 217  
ID ACF46378 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 218  
ID ACF27926 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 219  
ID ACD89230 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 220  
ID ACF63802 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 221  
ID ACF60442 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 222  
ID ACH12566 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 223  
ID ACH09989 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 224  
ID ACD03844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 225  
ID ACD10382 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 226  
ID ACD12024 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 227  
ID ACF42409 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 228  
ID ADA27866 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 229  
ID ACF18430 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
RESULT 230  
ID ACF63802 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

ID ACF02220 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 231  
ID ACF21728 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 232  
ID ACF10412 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 233  
ID ACF33864 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 234  
ID ACF44826 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 235  
ID ACD90458 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 236  
ID ACD91071 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 237  
ID ACF30382 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 238  
ID ACD87081 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 239  
ID ACF60135 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

FN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 240  
ID ACF46685 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 241  
ID ACF75542 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 242  
ID ADA79713 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003073173-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 243  
ID ACF17202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 244  
ID ACF22956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 245  
ID ACF07956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 246  
ID ACF08263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 247  
ID ACF40567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;  
RESULT 248  
ID ACF53746 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 9; Length 2846;  
Pred. No. 0;

RESULT 249  
ID ACD47010 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 250  
ID ACF47913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 251  
ID ACF47299 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 252  
ID ACF46071 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 253  
ID ACD86160 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 254  
ID ACF52518 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 255  
ID ACF52825 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 256  
ID ACF64818 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 257  
ID ACF76463 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 258  
ID ACF61363 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 259  
ID ACF61670 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 260  
ID ACD30701 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 261  
ID ACD31622 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 262  
ID ACD32543 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 263  
ID ADA20071 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 264  
ID ACD82108 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 265  
ID ACF17509 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 266  
ID ADA94446 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 267  
ID ACF07342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;

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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 268
ID ACF20500 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ACF20807 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 270
ID ACF21114 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 271
ID ACF47606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 272
ID ACF47606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 273
ID ACF53439 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 274
ID ACD86774 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 275
ID ACH05022 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 276
ID ACF44519 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 277
ID ADA81440 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 278
ID ACD22174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 279
ID ACD24521 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
FN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 280
ID ACD39724 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 281
ID ACD40031 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
FN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 282
ID ACF13339 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 283
ID ACF03141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ACF78612 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ACF13333 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ACF50676 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
FN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 2846; DB 9; Length 2846;
Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 287  
ID ACP34171 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 288  
ID ACD46396 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 289  
ID ACD48238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 290  
ID ACP27619 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 291  
ID ACP24491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 292  
ID ACD85546 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 293  
ID ACD90151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 294  
ID ACD83704 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 295  
ID ACP49141 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
ID ACH07226 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 297  
ID ACH07533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 298  
ID ACH08147 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 299  
ID ACH11338 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 300  
ID ACH11645 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 301  
ID ACH10296 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 302  
ID ACF01299 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 303  
ID ACF40874 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 304  
ID ACD24214 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044518-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 305  
ID ACD31315 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003032132-A1.  
PD 13-FEB-2003.



Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 306  
ID ACF17816 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 307  
ID ADA38671 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 308  
ID ACF32599 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 309  
ID ACF40260 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 310  
ID ACF48220 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 311  
ID ACF38169 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 312  
ID ACF25105 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 313  
ID ACF27005 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 314  
ID ACF29461 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 315  
ID ACD87695 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 316  
ID ACF76156 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 317  
ID ACF49448 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 318  
ID ACF43905 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 319  
ID ACH06250 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 320  
ID ACH06557 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 321  
ID ADA83238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 322  
ID ACC92613 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 323  
ID ACC93227 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 324  
ID ACF19272 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.



RESULT 344  
ID ACF39090 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 345  
ID ACF28847 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 346  
ID ACD90764 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 347  
ID ACD86467 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 348  
ID ACH05329 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 349  
ID ACF65125 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 350  
ID ADB20281 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 351  
ID ACF43598 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 352  
ID ACH09068 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 353  
ID ACH09375 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 354  
ID ADA78533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 355  
ID ACF09798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 356  
ID ACF50983 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 357  
ID ACF23877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 358  
ID ACD88309 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 359  
ID ACH09682 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 360  
ID ACH10603 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 361  
ID ACD11410 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 362  
ID ACC96460 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003044924-A1.

PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 363  
ID ACC98490 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 364  
ID ACF11795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 365  
ID ACF16716 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 366  
ID ACD32236 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 367  
ID ACD30394 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 368  
ID ACD41265 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 369  
ID ACF07649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 370  
ID ACF31064 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 371  
ID ACF77384 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 372  
ID ACF11026 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 373  
ID ACF32906 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 374  
ID ACF26084 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 375  
ID ACD83397 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 376  
ID ACF23570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 377  
ID ACF42984 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 378  
ID ACF43291 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 379  
ID ACH05943 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
FN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 380  
ID ACH08761 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 381  
ID ACC90355 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027273-A1.

PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 382  
ID ACF10719 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 383  
ID ACC93534 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 384  
ID ACC96153 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 385  
ID ACD24828 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 386  
ID ACF01913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003045739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 387  
ID ACF22035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 388  
ID ACF22649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 389  
ID ACF08877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 390  
ID ACF33213 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 391  
ID ACD10075 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

ID ACF54667 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 392  
ID ACF48527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 393  
ID ACD47317 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 394  
ID ACD49159 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 395  
ID ACF37862 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 396  
ID ACF30075 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 397  
ID ACD87388 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 398  
ID ACF61977 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 399  
ID ACH10910 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 400  
ID ACD10075 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 401  
ID ACD16800 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 402  
ID ACF65430 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 403  
ID ACC99097 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 404  
ID ACF00491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 405  
ID ACD40958 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 406  
ID ACF14567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 407  
ID ACF22342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 408  
ID ACF78919 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 409  
ID ACF11640 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003073177-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 410  
ID ACF44212 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003104556-A1.  
PD 05-JUN-2003.

ID ADA22353 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 411  
ID ACF51597 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003064442-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 412  
ID ACF33520 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003064450-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 413  
ID ACD49773 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068731-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 414  
ID ACF37555 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 415  
ID ACF28540 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003068754-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 416  
ID ACD8616 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 417  
ID ACF75235 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 418  
ID ACF61056 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 419  
ID ACF44212 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding CDNA, SEQ ID NO:169.  
PN US2003104556-A1.  
PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 420  
ID ACH08454 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 421  
ID ACD39420 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 422  
ID ACC93841 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 423  
ID ACD20946 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 424  
ID ACF06728 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044919-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 425  
ID ACD20639 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 426  
ID ACD22788 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 427  
ID ACF41488 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 428  
ID ADA06519 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 429  
ID ADA39212 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 430  
ID ACF07035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 431  
ID ACF77691 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 432  
ID ACD46089 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 433  
ID ACF46992 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 434  
ID ACF54360 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 435  
ID ACF45764 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 436  
ID ACF45457 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 437  
ID ACF38476 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 438  
ID ACD89537 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;



Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 439  
ID ACD85239 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 440  
ID ACD85853 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 441  
ID ACF75949 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 442  
ID ACF60749 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 443  
ID ACH05636 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 444  
ID ADA82604 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 445  
ID ADB85610 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 446  
ID ADB96238 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 447  
ID ACF55895 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 9; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 448  
ID ACF55281 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 449  
ID ADB85912 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 450  
ID ACF56202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 451  
ID ACF56509 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 452  
ID ADB68289 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 453  
ID ADB68096 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 454  
ID ACF55588 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 455  
ID ACF54974 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 456  
ID ADB90913 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 457  
ID ADC57710 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.

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PN US2003027754-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 458
ID ADC55074 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 459
ID ADC11941 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 460
ID ADC06993 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 461
ID ADC56363 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 462
ID ADC17172 standard; cDNA; 2846 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 37).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 463
ID ADC07418 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 464
ID ADC11408 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 465
ID ADC14870 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 466
ID ADC52365 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 467
ID ADC14530 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 468
ID ADD08062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 469
ID ADC81887 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 470
ID ADD07529 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 471
ID ADC82420 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #55.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 472
ID ADD05642 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 473
ID ADD08600 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 474
ID ADD06849 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 475
ID ADC83096 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 476
ID ADS55203 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;
RESULT 477
ID ADD36041 standard; cDNA; 2846 BP.
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DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003105298-A1.
PD	05-JUN-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 478	
ID	ADDF56161 standard; cDNA; 2846 BP.
DE	Human PRO polynucleotide #65.
PN	US2003077594-A1.
PD	24-APR-2003.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 479	
ID	ADD54599 standard; cDNA; 2846 BP.
DE	Human PRO polynucleotide #65.
PN	US2002132253-A1.
PD	19-SEP-2002.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 480	
ID	ADE26753 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003087304-A1.
PD	08-MAY-2003.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 481	
ID	ADE26220 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003087305-A1.
PD	08-MAY-2003.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 482	
ID	ADF67157 standard; cDNA; 2846 BP.
DE	Human PRO1344 nucleotide sequence SEQ ID NO:230.
PN	US2002198148-A1.
PD	26-DEC-2002.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 483	
ID	ADG01042 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003078387-A1.
PD	24-APR-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 484	
ID	ADG08595 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180793-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 485	
ID	ADG02637 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003207397-A1.
PD	06-NOV-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 486	
ID	ADG01344 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003207399-A1.
PD	06-NOV-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 487	
ID	ADF95519 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003207398-A1.
PD	06-NOV-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 488	
ID	ADF95216 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180795-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 489	
ID	ADG12334 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003207392-A1.
PD	06-NOV-2003.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 490	
ID	ADH24069 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180918-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 491	
ID	ADH34095 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180858-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 492	
ID	ADH29928 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180859-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 493	
ID	ADH23899 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180919-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 494	
ID	ADH08994 standard; cDNA; 2846 BP.
DE	Human PRO polynucleotide #85.
PN	US2003207395-A1.
PD	06-NOV-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2846;
Best Local Similarity	100.0%; Pred. No. 0;
RESULT 495	
ID	ADG85303 standard; cDNA; 2846 BP.
DE	Novel human secreted and transmembrane protein PRO1344 CDNA.
PN	US2003180904-A1.
PD	25-SEP-2003.
PA	(GETH ) GENENTECH INC.
Query Match	100.0%; Score 2846; DB 10; Length 2

RESULT 496  
ID ADH24579 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 497  
ID ADH37435 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 498  
ID ADH02024 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 499  
ID ADH37605 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 500  
ID ADG85643 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 501  
ID ADH24239 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 502  
ID ADH38533 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 503  
ID ADG83654 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 504  
ID ADH29462 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 505

ID ADH27578 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 506  
ID ADH37775 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 507  
ID ADH37952 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 508  
ID ADH57372 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 509  
ID ADH53514 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 510  
ID ADH53684 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 511  
ID ADH52020 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 512  
ID ADH49875 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 513  
ID ADI25385 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 514  
ID ADH90178 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 515  
ID ADI1594 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 516  
ID ADH9729 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 517  
ID ADI35411 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
FN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 518  
ID ADI03577 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 519  
ID ADI11934 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 520  
ID ADH90008 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 521  
ID ADH99903 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 522  
ID ADH98409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 523  
ID ADI11084 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181682-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 524  
ID ADI11594 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 525  
ID ADH98239 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 526  
ID ADH98579 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 527  
ID ADH98069 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 528  
ID ABX78612 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #95.  
FN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 529  
ID ACA75584 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 530  
ID ACA71064 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
FN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 531  
ID ACC87592 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 532  
ID ACC86978 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
FN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 533  
ID ACD04151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 534  
ID ABX77859 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein related PCR primer #50.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 535  
ID ABX80271 standard; DNA; 2846 BP.  
DE Human secreted or transmembrane protein related PCR primer #50.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 536  
ID ACA69177 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 537  
ID ACA69482 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 538  
ID ACA90327 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 539  
ID ACC89434 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 540  
ID ABX90248 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 541  
ID ACA98225 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 542  
ID ACA93867 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 543  
ID ACD15260 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044923-A1.

PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 544  
ID ACD08847 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 545  
ID ACC96767 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 546  
ID ACF15488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 547  
ID ABX64094 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 548  
ID ACA72855 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 549  
ID ACD03027 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 550  
ID ACD01842 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 551  
ID ACA92034 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 552  
ID ADI05057 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 553  
ID ADI03407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181654-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 554  
ID ADI04802 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 555  
ID ADH78256 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 556  
ID ADI19600 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 557  
ID ADH90348 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 558  
ID ADI03067 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 559  
ID ADH77916 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 560  
ID ADH97899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 561  
ID ADI01284 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 562  
ID ADI01979 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 563  
ID ADI03237 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 564  
ID ADI11424 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 565  
ID ADI02326 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 566  
ID ADI11764 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 567  
ID ADI05401 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 568  
ID ADH79473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 569  
ID ADI19430 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 570  
ID ADI05231 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 2846; DB 10; Length 2846;  
RESULT 571  
ID ADH79643 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.



Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 572  
ID ADI01469 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 573  
ID ADI01639 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 574  
ID ADI01809 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 575  
ID ADH79813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 576  
ID ADI04631 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 577  
ID ADI02767 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 578  
ID ADH78086 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 579  
ID ADH78086 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 580  
ID ADI25895 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 581  
ID ADI25725 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 582  
ID ADI25895 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 581  
ID ADH98749 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 582  
ID ADH79590 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 583  
ID ADL32775 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 11; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 584  
ID ADM30309 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 11; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 585  
ID ADL93721 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 11; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 586  
ID ADC52175 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 587  
ID ADE74306 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 588  
ID ADE74918 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 589  
ID ADF35356 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 590  
ID ADG11606 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.

PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 591  
ID ADF96131 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 592  
ID ADG04402 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 593  
ID ADG00562 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 594  
ID ADH06437 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 595  
ID ADH06437 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 596  
ID ADG68958 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 597  
ID ADH27748 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 598  
ID ADH25089 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 599  
ID ADH33721 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 600  
ID ADG82818 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 601  
ID ADH02364 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 602  
ID ADH07971 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 603  
ID ADG69368 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 604  
ID ADH39189 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 605  
ID ADH26099 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 606  
ID ADG83929 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 607  
ID ADH19476 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 608  
ID ADG85473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 609  
ID ADH06267 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 610  
ID ADH30097 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 611  
ID ADH24409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 612  
ID ADH33068 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
FN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 613  
ID ADG69538 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 614  
ID ADH07801 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 615  
ID ADG85813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 616  
ID ADH39359 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 617  
ID ADH33551 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 618  
ID ADH33891 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 619  
ID ADH01101 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 620  
ID ADG69708 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 621  
ID ADH20969 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
FN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 622  
ID ADH02194 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
FN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 623  
ID ADG69198 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 624  
ID ADG85983 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 625  
ID ADH24919 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 626  
ID ADH39536 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 627  
ID ADH39536 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
FN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;

ID ADH20009 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 628  
ID ADH02534 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 629  
ID ADG69028 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 630  
ID ADH07631 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 631  
ID ADG86153 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 632  
ID ADH24749 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 633  
ID ADH25797 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 634  
ID ADH38363 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 635  
ID ADH57202 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 636  
ID ADH52190 standard; cDNA; 2846 BP.

DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 637  
ID ADH49556 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 638  
ID ADH90518 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 639  
ID ADI11254 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 640  
ID ADH98919 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 641  
ID ADI02149 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 642  
ID ADH90688 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 643  
ID ADJ54807 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 644  
ID ADJ98563 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181797-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 645  
ID ADJ98733 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 646  
ID ADH78892 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 647  
ID ADJ99126 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 648  
ID ADJ99296 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US20031817196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 649  
ID ADJ98914 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 650  
ID ADH79062 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 651  
ID ADK00922 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 652  
ID ADK14443 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 653  
ID ADJ64578 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 654  
ID ADM31474 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2004048334-A1.

PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 655  
ID ADM36521 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 656  
ID ADM40326 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 657  
ID ADM80892 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 658  
ID ADM37934 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2846; DB 12; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 659  
ID ADK65407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.2%; Score 2795; DB 10; Length 2846;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 660  
ID ADA00368 standard; cDNA; 2843 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 95.7%; Score 2723; DB 9; Length 2843;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 661  
ID ACA67289 standard; cDNA; 2848 BP.  
DE cDNA encoding human secreted polypeptide PRO1344.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 91.6%; Score 2606; DB 8; Length 2848;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 662  
ID ACA89307 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 91.0%; Score 2591; DB 8; Length 2846;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 663  
ID AB235533 standard; cDNA; 2845 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 644.  
PN WO200274979-A2.  
PD 26-SEP-2002.

PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 89.8%; Score 2556; DB 6; Length 2845;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 664  
ID ADL06663 standard; DNA; 2650 BP.  
DE Human 3T3 cell conversion promoter FP938 DNA.  
FN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match 84.1%; Score 2394; DB 10; Length 2650;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 665  
ID ADL06661 standard; cDNA; 2650 BP.  
DE Human 3T3 cell conversion promoter FP938 cDNA.  
FN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match 84.1%; Score 2394; DB 10; Length 2650;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 666  
ID AAA39951 standard; cDNA; 2747 BP.  
DE Human TANGO 215 cDNA.  
FN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 83.4%; Score 2373; DB 3; Length 2747;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 667  
ID AAF74433 standard; cDNA; 2306 BP.  
DE Human PRO2 nucleotide sequence SEQ ID NO:3.  
FN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 71.8%; Score 2043; DB 4; Length 2306;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 668  
ID ' AA01222 standard; cDNA; 2306 BP.  
DE DNA encoding human secreted protein, POLY13.  
FN WO200119856-A2.  
PD 22-MAR-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 71.8%; Score 2043; DB 5; Length 2306;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 669  
ID ADP41309 standard; cDNA; 2311 BP.  
DE Human CD-like molecule HSXDF41 cDNA, SEQ ID NO:108.  
FN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 71.2%; Score 2027; DB 7; Length 2311;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 670  
ID ADH89027 standard; cDNA; 2305 BP.  
DE Human POLYX polynucleotide #13.  
FN US2003198958-A1.  
PD 23-OCT-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (FERN/) FERNANDES E.  
PA (HERR/) HERRMANN J L.  
PA (LIUX/) LIU X.  
PA (YANG/) YANG M.  
PA (BOLD/) BOLDOS F L.  
PA (SMIT/) SMITHSON G.  
PA (RAST/) RASTELLI L.  
Query Match 67.5%; Score 1922; DB 12; Length 2305;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 671  
ID AAA39952 standard; cDNA; 2163 BP.  
DE Human TANGO 215 coding sequence cDNA.  
FN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 67.0%; Score 1908; DB 3; Length 2163;

Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 672  
ID AAI60862 standard; cDNA; 2040 BP.  
DE Human polynucleotide SEQ ID NO 4851.  
FN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 66.1%; Score 1882; DB 4; Length 2040;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 673  
ID AAI59076 standard; cDNA; 2144 BP.  
DE Human polynucleotide SEQ ID NO 1279.  
FN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 66.1%; Score 1880; DB 4; Length 2144;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 674  
ID ADQ9299 standard; cDNA; 2144 BP.  
DE DNA encoding human GPCR-like protein seqid 969.  
FN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 66.1%; Score 1880; DB 5; Length 2144;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 675  
ID ADB49059 standard; cDNA; 2144 BP.  
DE Novel human cDNA SEQ ID NO 969.  
FN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 66.1%; Score 1880; DB 9; Length 2144;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 676  
ID AAI59113 standard; cDNA; 2142 BP.  
DE Human polynucleotide SEQ ID NO 1316.  
FN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 64.2%; Score 1827; DB 4; Length 2142;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 677  
ID ADQ99336 standard; cDNA; 2142 BP.  
DE DNA encoding human GPCR-like protein seqid 1006.  
FN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 64.2%; Score 1827; DB 5; Length 2142;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 678  
ID ADB49096 standard; cDNA; 2142 BP.  
DE Novel human cDNA SEQ ID NO 1006.  
FN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 64.2%; Score 1827; DB 9; Length 2142;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 679  
ID AAD33261 standard; cDNA; 2022 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:35.  
FN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 63.1%; Score 1795; DB 6; Length 2022;  
Best Local Similarity 99.8%; Pred. No. 0;

RESULT 680  
ID AAC90025 standard; cDNA; 2259 BP.  
DE Clone HFPEY75 coding sequence.  
FN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 62.8%; Score 1787; DB 3; Length 2259;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 681  
ID AAH47256 standard; cDNA; 2784 BP.  
DE Human serine protease-like protein encoding cDNA (hc-PLACE1009992).  
FN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.4%; Score 1747; DB 4; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 682  
ID AAH15142 standard; cDNA; 2784 BP.  
DE Human cDNA sequence SEQ ID NO:13201.  
FN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.4%; Score 1747; DB 4; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 683  
ID ADN04639 standard; cDNA; 2784 BP.  
DE Antiproliferative cDNA sequence #529.  
FN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 61.4%; Score 1747; DB 12; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 684  
ID ADS85021 standard; DNA; 2784 BP.  
DE Human atopic dermatitis-related gene sequence SeqID23.  
FN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 61.4%; Score 1747; DB 13; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 685  
ID ADS85033 standard; DNA; 2784 BP.  
DE Human atopic dermatitis-related gene sequence SeqID35.  
FN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 61.4%; Score 1747; DB 13; Length 2784;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 686  
ID AAD30584 standard; cDNA; 2632 BP.  
DE Human protease, PRTS-17 cDNA.  
FN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 58.7%; Score 1672; DB 6; Length 2632;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 687  
ID AAF74432 standard; cDNA; 1867 BP.  
DE Human PRO1 nucleotide sequence SEQ ID NO:1.  
FN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 57.4%; Score 1633; DB 4; Length 1867;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 688  
ID AAH47258 standard; cDNA; 2289 BP.  
DE Human serine protease-like protein coding sequence.  
FN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 47.1%; Score 1340; DB 4; Length 2289;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 689  
ID AAD3241 standard; cDNA; 1101 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:15.  
FN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 27.9%; Score 795; DB 6; Length 1101;  
Best Local Similarity 99.9%; Pred. No. 3.2e-250;  
RESULT 690  
ID AAH99144 standard; cDNA; 1058 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 1001.  
FN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 18.8%; Score 534; DB 4; Length 1058;  
Best Local Similarity 100.0%; Pred. No. 5.3e-165;  
RESULT 691  
ID AAS68826 standard; cDNA; 1058 BP.  
DE DNA encoding novel human diagnostic protein #22630.  
FN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 18.8%; Score 534; DB 5; Length 1058;  
Best Local Similarity 100.0%; Pred. No. 5.3e-165;  
RESULT 692  
ID AAH08069 standard; cDNA; 705 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:4904.  
FN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 18.3%; Score 522; DB 4; Length 705;  
Best Local Similarity 100.0%; Pred. No. 4.8e-161;  
RESULT 693  
ID AAI60899 standard; cDNA; 438 BP.  
DE Human polynucleotide SEQ ID NO 4888.  
FN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.8%; Score 393; DB 4; Length 438;  
Best Local Similarity 100.0%; Pred. No. 7.1e-119;  
RESULT 694  
ID ABK30409 standard; cDNA; 505 BP.  
DE Human G-protein-coupled protease #179.  
FN US6331427-B1.  
PD 18-DEC-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 13.0%; Score 370; DB 6; Length 505;  
Best Local Similarity 99.8%; Pred. No. 2.2e-111;  
RESULT 695  
ID ABL63519 standard; DNA; 337 BP.  
DE Breast cancer related gene sequence SEQ ID NO:1856.  
FN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 11.8%; Score 337; DB 6; Length 337;  
Best Local Similarity 100.0%; Pred. No. 1.5e-100;  
RESULT 696  
ID ABL63953 standard; DNA; 337 BP.  
DE Breast cancer related gene sequence SEQ ID NO:2290.  
FN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 11.8%; Score 337; DB 6; Length 337;  
Best Local Similarity 100.0%; Pred. No. 1.5e-100;  
RESULT 697  
ID ABK30334 standard; cDNA; 2886 BP.  
DE Human G-protein-coupled protease #104.  
FN US6331427-B1.  
PD 18-DEC-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 11.6%; Score 329; DB 6; Length 2886;  
Best Local Similarity 99.8%; Pred. No. 3.5e-98;



RESULT 698  
ID AB234917 standard; cDNA; 548 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 29.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 11.0%; Score 314; DB 6; Length 548;  
Pred. No. 4.2e-93;  
RESULT 699  
ID AAD33260 standard; cDNA; 477 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:34.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Score 247; DB 6; Length 477;  
Pred. No. 3.2e-71;  
RESULT 700  
ID ACH19532 standard; cDNA; 403 BP.  
DE Human adult lung cDNA #535.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 100.0%; Score 232; DB 9; Length 403;  
Pred. No. 2.7e-66;  
RESULT 701  
ID ADQ21818 standard; DNA; 286 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4638.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 100.0%; Score 202; DB 12; Length 286;  
Pred. No. 1.8e-56;  
RESULT 702  
ID AAX40465 standard; cDNA; 340 BP.  
DE Human secreted protein 5' EST SEQ ID No: 65.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Query Match  
Best Local Similarity 6.4%; Score 181; DB 2; Length 340;  
Pred. No. 1.2e-49;  
RESULT 703  
ID ADI43251 standard; DNA; 2226 BP.  
DE Plant transcription factor polynucleotide #1150.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match  
Best Local Similarity 4.8%; Score 136; DB 12; Length 2226;  
Pred. No. 3.8e-35;  
RESULT 704  
ID ADQ02941 standard; cDNA; 2226 BP.  
DE Soybean orthologue of Thalecress transcription factor, cDNA #174.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.

PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAWARA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match  
Best Local Similarity 4.8%; Score 136; DB 12; Length 2226;  
Pred. No. 3.8e-35;  
RESULT 705  
ID ABK28222 standard; DNA; 11394 BP.  
DE DNA transcription associated complementary genomic DNA #48.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 100.0%; Score 136; DB 6; Length 11394;  
Pred. No. 2.5e-35;  
RESULT 706  
ID AAK89974 standard; DNA; 165 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3550.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;  
Pred. No. 1.5e-34;  
RESULT 707  
ID AAK90168 standard; DNA; 165 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3744.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;  
Pred. No. 1.5e-34;  
RESULT 708  
ID AAK89381 standard; DNA; 165 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 2957.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;  
Pred. No. 1.5e-34;  
RESULT 709  
ID AAK73944 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28756.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;  
Pred. No. 1.5e-34;  
RESULT 710  
ID AAK78761 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33573.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;  
Pred. No. 1.5e-34;  
RESULT 711  
ID AAK81312 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36124.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 135; DB 4; Length 165;  
Pred. No. 1.5e-34;

Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 712  
ID AAK79574 standard; DNA; 165 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34386.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 713  
ID AAL07127 standard; DNA; 165 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9815.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 714  
ID AAL04803 standard; DNA; 165 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7491.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 715  
ID ABA08161 standard; DNA; 165 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 956.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 716  
ID ABL97697 standard; DNA; 165 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2349.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 4; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 717  
ID AAS29235 standard; DNA; 165 BP.  
DE Genomic sequence #78 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 5; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 718  
ID ABA17044 standard; DNA; 165 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9375.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 5; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 719  
ID AAL16672 standard; DNA; 165 BP.  
DE Human pancreatic related protein-encoding exon, SEQ ID NO:36.  
PN WO200155327-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 5; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 720  
ID AAS39812 standard; DNA; 165 BP.  
DE Genomic sequence #231 encoding human colon associated polypeptide.  
PN WO200155302-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 5; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;

RESULT 721  
ID ABS68375 standard; DNA; 165 BP.  
DE Human DNA-binding protein genomic DNA sequence #78.  
PN US2002102638-A1.  
PD 01-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 135; DB 6; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 722  
ID ADB32772 standard; DNA; 165 BP.  
DE Human novel colon related polypeptide DNA SEQ ID NO 709.  
PN US2003050231-A1.  
PD 13-MAR-2003.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 135; DB 9; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 723  
ID ADC25497 standard; cDNA; 165 BP.  
DE Human cDNA from extracellular matrix gene 80 #9.  
PN US2003049650-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 10; Length 165;  
Best Local Similarity 100.0%; Pred. No. 1.5e-34;  
RESULT 724  
ID AAI87804 standard; cDNA; 398 BP.  
DE Human polynucleotide SEQ ID NO 7864.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 135; DB 4; Length 398;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
RESULT 725  
ID ACN49835 standard; cDNA; 450 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-E4, SEQ:4616.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 135; DB 13; Length 450;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
RESULT 726  
ID ACN53191 standard; cDNA; 564 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-B10, SEQ:7972.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 135; DB 13; Length 564;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 727  
ID AAF91862 standard; cDNA; 2753 BP.  
DE Human secreted protein-encoding gene 5 cDNA clone HDP1E85, SEQ ID NO:15.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 135; DB 4; Length 2753;  
Best Local Similarity 100.0%; Pred. No. 7.7e-35;  
RESULT 728  
ID ABA93725 standard; cDNA; 3028 BP.  
DE Human differentiation/development cDNA clone amy2\_2b19.  
PN WO200198454-A2.  
PD 27-DEC-2001.  
PA (GERU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 4.7%; Score 135; DB 6; Length 3028;

Best Local Similarity 100.0%; Pred. No. 7.5e-35;  
RESULT 729  
ID ACF34512 standard; DNA; 3028 BP.  
DE Gene encoding angiogenesis protein BNO146.  
FN WO2003027285-A1.  
PD 03-APR-2003.  
PA (BTON-) BIONOMICS LTD.  
Query Match 4.7%; Score 135; DB 8; Length 3028;  
Best Local Similarity 100.0%; Pred. No. 7.5e-35;  
RESULT 730  
ID ABK34669 standard; cDNA; 3415 BP.  
DE Human cDNA for novel secreted protein, SEQ ID 438.  
FN WO200177290-A2.  
PD 18-OCT-2001.  
PA (GBMY) GENETICS INST INC.  
Query Match 4.7%; Score 135; DB 6; Length 3415;  
Best Local Similarity 100.0%; Pred. No. 7.3e-35;  
RESULT 731  
ID ADQ22192 standard; DNA; 3931 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5012.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 135; DB 12; Length 3931;  
Best Local Similarity 100.0%; Pred. No. 7e-35;  
RESULT 732  
ID ADS54096 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 20.  
FN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 10; Length 4316;  
Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
RESULT 733  
ID ADS54224 standard; DNA; 4316 BP.  
DE Pretreated genomic DNA region 148.  
FN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 10; Length 4316;  
Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
RESULT 734  
ID ADS89522 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:538.  
FN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 13; Length 4316;  
Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
RESULT 735  
ID ADS89248 standard; DNA; 4316 BP.  
DE Oligonucleotide of the invention SEQ ID NO:264.  
FN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 13; Length 4316;  
Best Local Similarity 100.0%; Pred. No. 6.9e-35;  
RESULT 736  
ID ABU32921 standard; DNA; 5195 BP.  
DE Human immune system associated gene SEQ ID NO: 894.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 6; Length 5195;  
Best Local Similarity 100.0%; Pred. No. 6.6e-35;  
RESULT 737  
ID ABL32511 standard; DNA; 5306 BP.  
DE Human immune system associated gene SEQ ID NO: 484.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 6; Length 5306;  
Best Local Similarity 100.0%; Pred. No. 6.5e-35;

RESULT 738  
ID ABN80041 standard; DNA; 5387 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 58.  
FN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 6; Length 5387;  
Best Local Similarity 100.0%; Pred. No. 6.5e-35;  
RESULT 739  
ID ABK34027 standard; DNA; 6944 BP.  
DE Human DNA for staging of Astrocytomas, complement, #57.  
FN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 6; Length 6944;  
Best Local Similarity 100.0%; Pred. No. 6.1e-35;  
RESULT 740  
ID ADA20447 standard; DNA; 6944 BP.  
DE Prostate tumour related genomic DNA complement sample #56.  
FN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 8; Length 6944;  
Best Local Similarity 100.0%; Pred. No. 6.1e-35;  
RESULT 741  
ID ADA84254 standard; DNA; 6944 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.  
FN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 8; Length 6944;  
Best Local Similarity 100.0%; Pred. No. 6.1e-35;  
RESULT 742  
ID ABN80146 standard; DNA; 14920 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 163.  
FN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 6; Length 14920;  
Best Local Similarity 100.0%; Pred. No. 5e-35;  
RESULT 743  
ID ABL34174 standard; DNA; 113515 BP.  
DE Human immune system associated gene SEQ ID NO: 2147.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 135; DB 6; Length 113515;  
Best Local Similarity 100.0%; Pred. No. 3.1e-35;  
RESULT 744  
ID ABX36136 standard; cDNA; 181 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #1301.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.7%; Score 134; DB 8; Length 181;  
Best Local Similarity 100.0%; Pred. No. 3.2e-34;  
RESULT 745  
ID ACN53869 standard; cDNA; 355 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-B10, SEQ:8650.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 355;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
RESULT 746  
ID ABV58662 standard; cDNA; 381 BP.  
DE Human prostate expression marker cDNA 58653.

PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 134; DB 5; Length 381;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
RESULT 747  
ID ACN55708 standard; cDNA; 381 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-027-Q6-N6-E10, SEQ:10489.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 381;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
RESULT 748  
ID AAI88514 standard; cDNA; 389 BP.  
DE Human polynucleotide SEQ ID NO 8574.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 134; DB 4; Length 389;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
RESULT 749  
ID ABV57596 standard; cDNA; 396 BP.  
DE Human prostate expression marker cDNA 57587.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 134; DB 5; Length 396;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
RESULT 750  
ID ABK34899 standard; cDNA; 409 BP.  
DE Human cDNA encoding secreted protein #37.  
PN WO200177288-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match 4.7%; Score 134; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
RESULT 751  
ID ACN54703 standard; cDNA; 426 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-D2, SEQ:9484.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 426;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
RESULT 752  
ID ACN60479 standard; cDNA; 431 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-023-Q6-K6-D10, SEQ:15260.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 431;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
RESULT 753  
ID ACN56223 standard; cDNA; 458 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-A12, SEQ:11004.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 458;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;

RESULT 754  
ID ACN60136 standard; cDNA; 481 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 481;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 755  
ID ACN61841 standard; cDNA; 483 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-021-Q6-N6-F8, SEQ:16622.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 483;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 756  
ID ABV57059 standard; cDNA; 490 BP.  
DE Human prostate expression marker cDNA 57050.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 134; DB 5; Length 490;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 757  
ID ACN49328 standard; cDNA; 496 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-K6-E6, SEQ:4109.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 496;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 758  
ID ACN50622 standard; cDNA; 508 BP.  
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-E9, SEQ:5403.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 759  
ID ACN51926 standard; cDNA; 509 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-G11, SEQ:6707.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 509;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 760  
ID ACN49853 standard; cDNA; 518 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-031-Q6-N6-G11, SEQ:4634.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 518;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;

Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 761  
ID ACN59971 standard; cDNA; 538 BP.  
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-036-Q1-K6-H1, SEQ:14752.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 538;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 762  
ID ACN55464 standard; cDNA; 540 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-N6-A3, SEQ:10245.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 763  
ID ACN51318 standard; cDNA; 545 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-F6, SEQ:6099.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 545;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 764  
ID ACN53206 standard; cDNA; 553 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-003-Q1-N6-D8, SEQ:7987.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 765  
ID ACN48235 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-021-Q1-N6-B5, SEQ:3016.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 766  
ID ACN45362 standard; cDNA; 570 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A5, SEQ:143.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 570;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 767  
ID ACN52669 standard; cDNA; 578 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-017-Q1-N6-A11, SEQ:7450.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 578;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 768  
ID ADR59353 standard; cDNA; 583 BP.  
DE Cotton cDNA sequence, SEQ ID 134.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 4.7%; Score 134; DB 13; Length 583;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 769  
ID ACN45357 standard; cDNA; 597 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-A11, SEQ:138.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 597;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 770  
ID ACN56642 standard; cDNA; 598 BP.  
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-001-Q1-N6-H1, SEQ:11423.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 598;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 771  
ID ACN45855 standard; cDNA; 608 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-009-Q1-K6-G7, SEQ:636.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 608;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 772  
ID ACN50609 standard; cDNA; 616 BP.  
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-N6-D5, SEQ:5390.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 134; DB 13; Length 616;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 773  
ID AAC68125 standard; cDNA; 809 BP.  
DE Human secreted protein cDNA sequence #45.  
PN WO200058335-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 4.7%; Score 134; DB 3; Length 809;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
RESULT 774  
ID AAX89609 standard; cDNA; 831 BP.  
DE Human secreted protein clone bg570\_1 encoding cDNA.  
PN WO9935253-A1.  
PD 15-JUL-1999.

PA (GEMY ) GENETICS INST INC.  
 Query Match 4.7%; Score 134; DB 2; Length 831;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
 RESULT 775  
 ID AAS59240 standard; cDNA; 831 BP.  
 DE Human cDNA encoding a secreted protein bg570\_1.  
 PN W0200175068-A2.  
 PD 11-OCT-2001.  
 PA (GEMY ) GENETICS INST INC.  
 Query Match 4.7%; Score 134; DB 4; Length 831;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
 RESULT 776  
 ID ABA90909 standard; cDNA; 831 BP.  
 DE Human polynucleotide SEQ ID NO 67.  
 PN US2001039335-A1.  
 PD 08-NOV-2001.  
 PA (JACO/) JACOBS K.  
 PA (MCCO/) MCCOY J M.  
 PA (LAVA/) LAVALLIE E R.  
 PA (COLL/) COLLINS-RACIE L A.  
 PA (EVAN/) EVANS C.  
 PA (MERB/) MERBERG D.  
 PA (TREA/) TREACY M.  
 PA (AGOS/) AGOSTINO M J.  
 PA (STEI/) STEININGER R J.  
 PA (SPAU/) SPAULDING V.  
 PA (WONG/) WONG G G.  
 PA (CLAR/) CLARK H.  
 PA (PECH/) FECHTEL K.  
 Query Match 4.7%; Score 134; DB 6; Length 831;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
 RESULT 777  
 ID ADQ22074 standard; DNA; 980 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.  
 PN W02004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.7%; Score 134; DB 12; Length 980;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-34;  
 RESULT 778  
 ID ADM32854 standard; DNA; 1084 BP.  
 DE DNA sequence of a human adenosine monophosphate deaminase (AMPD).  
 PN W02004024880-A2.  
 PD 25-MAR-2004.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 4.7%; Score 134; DB 12; Length 1084;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-34;  
 RESULT 779  
 ID ADQ23195 standard; DNA; 1091 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6015.  
 PN W02004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.7%; Score 134; DB 12; Length 1091;  
 Best Local Similarity 100.0%; Pred. No. 2e-34;  
 RESULT 780  
 ID AAD02119 standard; cDNA; 1459 BP.  
 DE Maize RAD51 orthologue #2 cDNA.  
 PN W0200068370-A2.  
 PD 16-NOV-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 4.7%; Score 134; DB 4; Length 1459;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 781  
 ID ADR25589 standard; DNA; 1521 BP.  
 DE Breast cancer prognosis marker #1450.  
 PN W02004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 4.7%; Score 134; DB 13; Length 1521;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 782

ID ADP50501 standard; cDNA; 1521 BP.  
 DE Human PRO cDNA sequence SEQ ID NO:1027.  
 PN W02004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.7%; Score 134; DB 13; Length 1521;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 783  
 ID ADQ22988 standard; DNA; 1576 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.  
 PN W02004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 4.7%; Score 134; DB 12; Length 1576;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 784  
 ID ABV28953 standard; cDNA; 1603 BP.  
 DE Human prostate expression marker cDNA 28944.  
 PN W0200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 1603;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 785  
 ID ABV22100 standard; cDNA; 1603 BP.  
 DE Human prostate expression marker cDNA 22091.  
 PN W0200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 1603;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 786  
 ID ABV23114 standard; cDNA; 1603 BP.  
 DE Human prostate expression marker cDNA 23105.  
 PN W0200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 1603;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 787  
 ID ABV27940 standard; cDNA; 1603 BP.  
 DE Human prostate expression marker cDNA 27931.  
 PN W0200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 134; DB 5; Length 1603;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 RESULT 788  
 ID ADM47653 standard; DNA; 1708 BP.  
 DE Polynucleotide sequence #71 useful in producing transgenic plants.  
 PN US2003233670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE/) EDGERTON M D.  
 PA (CHOW/) CHOMET P S.  
 PA (LACC/) LACCETTI L B.  
 Query Match 4.7%; Score 134; DB 12; Length 1708;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
 RESULT 789  
 ID ADI42816 standard; DNA; 1803 BP.  
 DE Plant transcription factor polynucleotide #820.  
 PN US2004019927-A1.  
 PD 29-JAN-2004.  
 PA (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIAN/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAK/) HAAKE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.

PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 4.7%; Score 134; DB 12; Length 1803;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 790  
ID AD003025 standard; cDNA; 1803 BP.  
DE Corn orthologue of Thalecress transcription factor, cDNA #126.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIANG/) JIANG C.  
PA (SAMA/) SAWAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 4.7%; Score 134; DB 12; Length 1803;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 791  
ID ADN95834 standard; DNA; 1999 BP.  
DE Human BEC/LEC-related gene sequence SeqID758.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 4.7%; Score 134; DB 11; Length 1999;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 792  
ID ADQ24947 standard; DNA; 1999 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7767.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 134; DB 12; Length 1999;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 793  
ID ADP23790 standard; cDNA; 1999 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:968.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 134; DB 13; Length 1999;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 794  
ID ACN39804 standard; cDNA; 2074 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA325989, SEQ ID NO:4174.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 134; DB 13; Length 2074;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
RESULT 795  
ID ADP56341 standard; cDNA; 2401 BP.  
DE Human PRO cDNA sequence SEQ ID NO:2317.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 134; DB 13; Length 2401;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
RESULT 796

ID ADQ22618 standard; DNA; 2499 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5438.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 134; DB 12; Length 2499;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
RESULT 797  
ID ADJ48201 standard; DNA; 2520 BP.  
DE Maize oil-associated gene #19.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 4.7%; Score 134; DB 12; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 1.7e-34;  
RESULT 798  
ID ADP04916 standard; cDNA; 2789 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 511.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 4.7%; Score 134; DB 12; Length 2789;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 799  
ID ADR24479 standard; DNA; 2809 BP.  
DE Breast cancer prognosis marker #340.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 4.7%; Score 134; DB 13; Length 2809;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 800  
ID AAZ07192 standard; cDNA; 3275 BP.  
DE Human lung tumour protein SAL-25 5' cDNA sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 134; DB 2; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 801  
ID AAC79145 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific cDNA #98.  
PN WO2000060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 134; DB 3; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 802  
ID AAD23220 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific protein SAL-25 cDNA.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 134; DB 4; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 803  
ID ADP66459 standard; cDNA; 3275 BP.  
DE Human lung tumour-specific related cDNA, SEQ ID No 151.  
PN WO200292001-A2.  
PD 21-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 134; DB 10; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 804  
ID ADE87713 standard; cDNA; 3275 BP.  
DE Human lung tumour antigen cDNA #98.  
PN US2003118599-A1.  
PD 26-JUN-2003.



PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 134; DB 10; Length 3275;  
Best Local Similarity 100.0%; Pred. No. 1.6e-34;  
RESULT 805  
ID ADQ2371 standard; DNA; 4824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5191.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 134; DB 12; Length 4824;  
Best Local Similarity 100.0%; Pred. No. 1.4e-34;  
RESULT 806  
ID ABL32788 standard; DNA; 6171 BP.  
DE Human immune system associated gene SEQ ID NO: 761.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 6171;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 807  
ID ABQ67050 standard; DNA; 6486 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 80.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 6486;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 808  
ID AAX33181 standard; DNA; 6644 BP.  
DE Base sequence of the plasmid prx-ires-bar.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.  
Query Match 4.7%; Score 134; DB 2; Length 6644;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 809  
ID ADQ24552 standard; DNA; 7115 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7372.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 134; DB 12; Length 7115;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 810  
ID ACF62807 standard; DNA; 7369 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:56.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 8; Length 7369;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 811  
ID AB210137 standard; DNA; 7369 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #277.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 8; Length 7369;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 812  
ID AAX33182 standard; DNA; 7372 BP.  
DE Base sequence of the plasmid prx-bcl-xl-bar.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.  
Query Match 4.7%; Score 134; DB 2; Length 7372;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 813  
ID AAX33180 standard; DNA; 7797 BP.  
DE Cowpox virus bar full length gene sequence.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.

Query Match 4.7%; Score 134; DB 2; Length 7797;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
RESULT 814  
ID AAX33184 standard; DNA; 7996 BP.  
DE Base sequence of the plasmid prx-Bcl 2-i-hcd 25.  
PN WO9913073-A2.  
PD 18-MAR-1999.  
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.  
Query Match 4.7%; Score 134; DB 2; Length 7996;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
RESULT 815  
ID ABK40074 standard; DNA; 8899 BP.  
DE Human chemically pretreated gene sequence #78 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 8899;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
RESULT 816  
ID ABL32837 standard; DNA; 8899 BP.  
DE Human immune system associated gene SEQ ID NO: 810.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 8899;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
RESULT 817  
ID ABL32911 standard; DNA; 8946 BP.  
DE Human immune system associated gene SEQ ID NO: 884.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 8946;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
RESULT 818  
ID ADL26832 standard; cDNA; 12178 BP.  
DE Rat L-NAME-related actin-associated cytoskeleton protein LACS cDNA.  
PN WO2004022753-A1.  
PD 18-MAR-2004.  
PA (ANGE-) ANGES MG INC.  
Query Match 4.7%; Score 134; DB 13; Length 12178;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 819  
ID AAV09036 standard; RNA; 12827 BP.  
DE Equine arteritis virus partial RNA genome sequence.  
PN WO9802549-A1.  
PD 22-JAN-1998.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 4.7%; Score 134; DB 2; Length 12827;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 820  
ID AAV09039 standard; DNA; 15528 BP.  
DE Equine arteritis virus expression vector pEAV030.  
PN WO9802549-A1.  
PD 22-JAN-1998.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 4.7%; Score 134; DB 2; Length 15528;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 821  
ID AAS45399 standard; DNA; 15832 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #52.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 4; Length 15832;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 822  
ID ABL33343 standard; DNA; 15832 BP.  
DE Human immune system associated gene SEQ ID NO: 1316.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 15832;

Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 823  
ID AAL04801 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7489.  
FN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 134; DB 6; Length 15832;  
Best Local Similarity 100.0%; Pred. No. 1.1e-34;  
RESULT 824  
ID ABO67149 standard; DNA; 40324 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 179.  
FN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 134; DB 6; Length 40324;  
Best Local Similarity 100.0%; Pred. No. 8.4e-35;  
RESULT 825  
ID AAS35937 standard; DNA; 148 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1437.  
FN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 826  
ID AAK89970 standard; DNA; 148 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3546.  
FN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 827  
ID AA162624 standard; DNA; 148 BP.  
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 274.  
FN WO200155324-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 828  
ID AAK78753 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33565.  
FN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 829  
ID AAK81310 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36122.  
FN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 830  
ID AAK73937 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28749.  
FN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 831  
ID AAK79569 standard; DNA; 148 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34381.  
FN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;

RESULT 832  
ID AAL04801 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7489.  
FN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 833  
ID AAL06718 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9406.  
FN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 834  
ID AAL07121 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9809.  
FN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 835  
ID AAL05015 standard; DNA; 148 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7703.  
FN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 836  
ID ABA08155 standard; DNA; 148 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 950.  
FN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 837  
ID ABL97695 standard; DNA; 148 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2347.  
FN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 838  
ID ABL97908 standard; DNA; 148 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2560.  
FN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 839  
ID AAS29186 standard; DNA; 148 BP.  
DE Genomic sequence #29 encoding novel human DNA-binding protein.  
FN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 840  
ID AAS29163 standard; DNA; 148 BP.  
DE Genomic sequence #6 encoding novel human DNA-binding protein.  
FN WO200155162-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 841

ID AAS29228 standard; DNA; 148 BP.  
DE Genomic sequence #71 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 842  
ID AAS29176 standard; DNA; 148 BP.  
DE Genomic sequence #19 encoding novel human DNA-binding protein.  
PN WO200155162-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 843  
ID ABA17037 standard; DNA; 148 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9368.  
PN WO200159063-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 844  
ID AAD16668 standard; DNA; 148 BP.  
DE Human pancreatic related protein-encoding exon, SEQ ID NO:32.  
PN WO200155327-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 845  
ID ABS68316 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #19.  
PN US2002102638-A1.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 846  
ID ABS68303 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #6.  
PN US2002102638-A1.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 847  
ID ABS68326 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #29.  
PN US2002102638-A1.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 848  
ID ABS68368 standard; DNA; 148 BP.  
DE Human DNA-binding protein genomic DNA sequence #71.  
PN US2002102638-A1.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 4.7%; Score 133; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 849  
ID ADA41651 standard; DNA; 148 BP.

DE Human secreted protein related DNA.  
PN WO2002102993-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 8; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 850  
ID ADC25448 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 53 #4.  
PN US2003049650-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 851  
ID ADC25490 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 80 #2.  
PN US2003049650-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 852  
ID ADC25425 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 14 #3.  
PN US2003049650-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 853  
ID ADC25438 standard; cDNA; 148 BP.  
DE Human cDNA from extracellular matrix gene 25 #2.  
PN US2003049650-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 854  
ID ADC74709 standard; DNA; 148 BP.  
DE Human secreted protein-related DNA - SEQ ID 1342.  
PN WO2003038063-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 855  
ID ADE46631 standard; DNA; 148 BP.  
DE Human cardiovascular system related genomic DNA #197.  
PN US2003059908-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 856  
ID ADA57783 standard; DNA; 148 BP.  
DE BAC fragment containing human secreted protein gene #537.  
PN WO2002102994-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 10; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 857  
ID ADN41714 standard; DNA; 148 BP.  
DE Novel human secreted protein polynucleotide seqid 836.  
PN US2004044191-A1.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KIYAW/) KIYAW H.  
PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.  
PA (LAPL/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLUSE/) OLSEN H.  
PA (EBNER/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 12; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 858  
ID ADJ08049 standard; DNA; 148 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID1437.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 148;  
Best Local Similarity 100.0%; Pred. No. 7.1e-34;  
RESULT 859  
ID AAF24360 standard; DNA; 160 BP.  
DE Retroviral recombination assay coding sequence fragment #5.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 5; Length 160;  
Best Local Similarity 100.0%; Pred. No. 7e-34;  
RESULT 860  
ID AAF24365 standard; DNA; 172 BP.  
DE Retroviral recombination assay coding sequence fragment #10.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 5; Length 172;  
Best Local Similarity 100.0%; Pred. No. 6.9e-34;  
RESULT 861  
ID AAF24361 standard; DNA; 178 BP.  
DE Retroviral recombination assay coding sequence fragment #6.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 5; Length 178;  
Best Local Similarity 100.0%; Pred. No. 6.8e-34;  
RESULT 862  
ID AAT13475 standard; RNA; 191 BP.  
DE Capture probe for detection of target sequence by chimeraic probe.  
PN EP707076-A1.  
PD 17-APR-1996.  
PA (STAD) AMOCO CORP.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 2; Length 191;  
Best Local Similarity 100.0%; Pred. No. 6.7e-34;  
RESULT 863  
ID ACA25512 standard; DNA; 195 BP.  
DE Prokaryotic essential gene #7169.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 8; Length 195;  
Best Local Similarity 100.0%; Pred. No. 6.7e-34;  
RESULT 864  
ID ADP85921 standard; DNA; 196 BP.  
DE Synthetic construct #5.  
PN US2004110205-A1.  
PD 10-JUN-2004.  
PA (WANG/) WANG H.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 12; Length 196;  
Best Local Similarity 100.0%; Pred. No. 6.7e-34;  
RESULT 865  
ID AAV41451 standard; cDNA; 202 BP.  
DE Nucleotide sequence of the 3' portion of the BL229\_22 clone.  
PN WO9821332-A2.  
PD 22-MAY-1998.

PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 6.6e-34;  
RESULT 866  
ID AAF98423 standard; cDNA; 202 BP.  
DE Human cDNA clone BL229\_22 3' sequence SEQ ID 81.  
PN WO200119988-A1.  
PD 22-MAR-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 5; Length 202;  
Best Local Similarity 100.0%; Pred. No. 6.6e-34;  
RESULT 867  
ID AAF24363 standard; DNA; 208 BP.  
DE Retroviral recombination assay coding sequence fragment #8.  
PN WO200104360-A2.  
PD 18-JAN-2001.  
PA (UABR-) UAB RES FOUND.  
PA (TRAN-) TRANZYME INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 5; Length 208;  
Best Local Similarity 100.0%; Pred. No. 6.6e-34;  
RESULT 868  
ID ABX49357 standard; cDNA; 220 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #14522.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 8; Length 220;  
Best Local Similarity 100.0%; Pred. No. 6.5e-34;  
RESULT 869  
ID AAC98734 standard; cDNA; 225 BP.  
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:744.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 3; Length 225;  
Best Local Similarity 100.0%; Pred. No. 6.4e-34;  
RESULT 870  
ID AAT76782 standard; DNA; 240 BP.  
DE Staphylococcus aureus exfoliative toxin A gene capture probe.  
PN US5627054-A.  
PD 06-MAY-1997.  
PA (USSA) US SEC OF ARMY.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 2; Length 240;  
Best Local Similarity 100.0%; Pred. No. 6.3e-34;  
RESULT 871  
ID ABX38708 standard; cDNA; 242 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3873.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 8; Length 242;  
Best Local Similarity 100.0%; Pred. No. 6.3e-34;  
RESULT 872  
ID ABX48177 standard; cDNA; 286 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #13342.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 8; Length 286;  
Best Local Similarity 100.0%; Pred. No. 6.1e-34;  
RESULT 873  
ID ADL35477 standard; DNA; 305 BP.  
DE Human filamin A alpha-related functional screen hit DNA 3.  
PN WO2004019893-A2.

Query Match	4.7%;	Score 133;	DB 5;	Length 351;
Best Local Similarity	100.0%;	Pred. No. 5.8e-34;		
RESULT 881				
ID ABX43106 standard; cDNA; 365 BP.				
DE Bovine EST associated with lactation/muscle/fat deposition #8271.				
PN US2002137139-A1.				
PD 26-SEP-2002.				
PA (BYAT/) BYATT J C.				
PA (MATH/) MATHIALAGAN N.				
PA (TAON/) TAO N.				
PA (WAR/) WARREN W C.				
Query Match	4.7%;	Score 133;	DB 8;	Length 365;
Best Local Similarity	100.0%;	Pred. No. 5.7e-34;		
RESULT 882				
ID ABV44911 standard; cDNA; 375 BP.				
DE Human prostate expression marker cDNA 44902.				
PN WO200160860-A2.				
PD 23-AUG-2001.				
PA (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.				
Query Match	4.7%;	Score 133;	DB 5;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 5.7e-34;		
RESULT 883				
ID RAI87526 standard; cDNA; 382 BP.				
DE Human polynucleotide SEQ ID NO 7586.				
PN WO200164835-A2.				
PD 07-SEP-2001.				
PA (HYSE-) HYSEQ INC.				
Query Match	4.7%;	Score 133;	DB 4;	Length 382;
Best Local Similarity	100.0%;	Pred. No. 5.6e-34;		
RESULT 884				
ID AAI85202 standard; cDNA; 390 BP.				
DE Human polynucleotide SEQ ID NO 5262.				
PN WO200164835-A2.				
PD 07-SEP-2001.				
PA (HYSE-) HYSEQ INC.				
Query Match	4.7%;	Score 133;	DB 4;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 5.6e-34;		
RESULT 885				
ID ABV13564 standard; cDNA; 394 BP.				
DE Human prostate expression marker cDNA 13555.				
PN WO200160860-A2.				
PD 23-AUG-2001.				
PA (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.				
Query Match	4.7%;	Score 133;	DB 5;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 5.6e-34;		
RESULT 886				
ID AAF94862 standard; cDNA; 396 BP.				
DE Human ovarian cancer associated coding sequence SEQ ID NO: 53.				
PN WO200118046-A2.				
PD 15-MAR-2001.				
PA (CORI-) CORIXA CORP.				
Query Match	4.7%;	Score 133;	DB 4;	Length 396;
Best Local Similarity	100.0%;	Pred. No. 5.6e-34;		
RESULT 887				
ID ABL44812 standard; cDNA; 396 BP.				
DE Ovarian carcinoma sequence isolate 24368.				
PN US2002004491-A1.				
PD 10-JAN-2002.				
PA (XUG/) XU J.				
PA (STOL/) STOLK J A.				
PA (ALGA/) ALGATE P A.				
PA (FLIN/) FLING S P.				
Query Match	4.7%;	Score 133;	DB 6;	Length 396;
Best Local Similarity	100.0%;	Pred. No. 5.6e-34;		
RESULT 888				
ID ABT03129 standard; cDNA; 396 BP.				
DE Human ovarian carcinoma associated coding sequence SEQ ID NO: 53.				
PN WO200239885-A2.				
PD 23-MAY-2002.				
PA (CORI-) CORIXA CORP.				
Query Match	4.7%;	Score 133;	DB 6;	Length 396;
Best Local Similarity	100.0%;	Pred. No. 5.6e-34;		
RESULT 889				

ID ADM10722 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma-associated cDNA 24368.  
PN US2003206918-A1.  
PD 06-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 133; DB 11; Length 396;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 890  
ID ADJ11052 standard; cDNA; 396 BP.  
DE Representative human ovarian carcinoma cDNA SeqID 53.  
PN US2003232056-A1.  
PD 18-DEC-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 133; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 891  
ID ADM43313 standard; cDNA; 396 BP.  
DE Human ovarian carcinoma cDNA #53.  
PN US2003129192-A1.  
PD 10-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.7%; Score 133; DB 12; Length 396;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 892  
ID AA188388 standard; cDNA; 398 BP.  
DE Human polynucleotide SEQ ID NO 8448.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 133; DB 4; Length 398;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 893  
ID ACN53082 standard; cDNA; 398 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-021-Q1-N6-F7, SEQ:7863.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 398;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 894  
ID ADL37305 standard; DNA; 406 BP.  
DE Human ovarian cancer DNA marker #11195.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 895  
ID ADI72158 standard; DNA; 406 BP.  
DE Human ovarian cancer DNA marker #4900.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 406;  
Best Local Similarity 100.0%; Pred. No. 5.6e-34;  
RESULT 896  
ID ABV43535 standard; cDNA; 408 BP.  
DE Human prostate expression marker cDNA 43526.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 408;  
Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 897  
ID ABV34679 standard; cDNA; 408 BP.  
DE Human prostate expression marker cDNA 34670.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 408;

Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 898  
ID ACN52913 standard; cDNA; 411 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-019-Q1-N6-D10, SEQ:7694.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 411;  
Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 899  
ID ACN52877 standard; cDNA; 421 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 421;  
Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 900  
ID ACN56895 standard; cDNA; 435 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-011-Q6-N6-E2, SEQ:11676.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 435;  
Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 901  
ID ACN52033 standard; cDNA; 443 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-H4, SEQ:6814.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 443;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 902  
ID ABX38235 standard; cDNA; 446 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3400.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WAOR/) WARREN W C.  
Query Match 4.7%; Score 133; DB 8; Length 446;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 903  
ID AA183052 standard; cDNA; 452 BP.  
DE Human polynucleotide SEQ ID NO 3112.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 133; DB 4; Length 452;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 904  
ID ACN49987 standard; cDNA; 452 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-033-Q6-N6-F5, SEQ:4768.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.

Query Match 4.7%; Score 133; DB 13; Length 452;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 905  
ID AAI80464 standard; cDNA; 456 BP.  
DE Human polynucleotide SEQ ID NO 524.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.7%; Score 133; DB 4; Length 456;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 906  
ID ABX4494 standard; cDNA; 456 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9659.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.7%; Score 133; DB 8; Length 456;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 907  
ID ACN62049 standard; cDNA; 469 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-024-Q6-N6-E4, SEQ:16830.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 469;  
Best Local Similarity 100.0%; Pred. No. 5.4e-34;  
RESULT 908  
ID ACN58522 standard; cDNA; 476 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-010-Q6-K6-Cl1, SEQ:13303.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 476;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 909  
ID ACN51993 standard; cDNA; 478 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-E1, SEQ:6774.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 478;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 910  
ID ABV56248 standard; cDNA; 481 BP.  
DE Human prostate expression marker cDNA 56239.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 481;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 911  
ID ACN53393 standard; cDNA; 485 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-C5, SEQ:8174.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;

RESULT 912  
ID ACN52021 standard; cDNA; 485 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-N6-G4, SEQ:6802.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 485;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 913  
ID ACN53606 standard; cDNA; 486 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-F5, SEQ:8387.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 486;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 914  
ID ACN48060 standard; cDNA; 487 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-018-Q1-N6-F4, SEQ:2841.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 487;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 915  
ID ACN54384 standard; cDNA; 489 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-K6-F9, SEQ:9165.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 916  
ID ACN49736 standard; cDNA; 489 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-026-Q6-N6-B11, SEQ:4517.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 917  
ID ACN61416 standard; cDNA; 490 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 490;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 918  
ID ACN47898 standard; cDNA; 495 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-016-Q1-N6-E4, SEQ:2679.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.



PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E. 4.7%; Score 133; DB 13; Length 495;  
Query Match 100.0%; Pred. No. 5.3e-34;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 919  
ID ACN62281 standard; cDNA; 496 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-027-Q6-N6-E4, SEQ:17062.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 496;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 920  
ID ACN46935 standard; cDNA; 499 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-005-Q1-N6-D10, SEQ:1716.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 499;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 921  
ID ABV59092 standard; cDNA; 501 BP.  
DE Human prostate expression marker cDNA 59083.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MTLL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 501;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 922  
ID ACN56650 standard; cDNA; 502 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-001-Q1-N6-H7, SEQ:11431.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 502;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 923  
ID ACN47530 standard; cDNA; 506 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-012-Q1-K6-F1, SEQ:2311.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 506;  
Best Local Similarity 100.0%; Pred. No. 5.3e-34;  
RESULT 924  
ID ADK64316 standard; cDNA; 510 BP.  
DE Cotton cDNA sequence, SEQ ID 5097.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 4.7%; Score 133; DB 13; Length 510;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 925  
ID ACN55753 standard; cDNA; 516 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-N6-B12, SEQ:10534.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E. 4.7%; Score 133; DB 13; Length 516;  
Query Match 100.0%; Pred. No. 5.2e-34;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 926  
ID ACN55333 standard; cDNA; 517 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-K6-E7, SEQ:10114.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 517;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 927  
ID ACN46088 standard; cDNA; 522 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A5, SEQ:869.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 522;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 928  
ID ACN61425 standard; cDNA; 527 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-015-Q1-N6-H7, SEQ:16206.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 527;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 929  
ID ACN47028 standard; cDNA; 528 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-006-Q1-N6-B12, SEQ:1809.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 528;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 930  
ID ACN53350 standard; cDNA; 528 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-006-Q1-N6-F8, SEQ:8131.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 528;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 931  
ID ACN46089 standard; cDNA; 538 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-K6-A6, SEQ:870.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.7%; Score 133; DB 13; Length 538;  
Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 932  
ID ACN57165 standard; cDNA; 541 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-014-Q6-N6-G1, SEQ:11946.

PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 541;  
100.0%; Pred. No. 5.2e-34;  
RESULT 933  
ID ACN521102 standard; cDNA; 542 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-E12, SEQ:6883.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 542;  
100.0%; Pred. No. 5.2e-34;  
RESULT 934  
ID ACN521108 standard; cDNA; 545 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-F7, SEQ:6889.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 545;  
100.0%; Pred. No. 5.2e-34;  
RESULT 935  
ID ACN51414 standard; cDNA; 547 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-K6-G6, SEQ:6195.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 547;  
100.0%; Pred. No. 5.2e-34;  
RESULT 936  
ID ACN62109 standard; cDNA; 547 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 547;  
100.0%; Pred. No. 5.2e-34;  
RESULT 937  
ID ACN53890 standard; cDNA; 547 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 547;  
100.0%; Pred. No. 5.2e-34;  
RESULT 938  
ID ACN52320 standard; cDNA; 549 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-B10, SEQ:7101.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 549;  
100.0%; Pred. No. 5.2e-34;

Best Local Similarity 100.0%; Pred. No. 5.2e-34;  
RESULT 939  
ID ACN62570 standard; cDNA; 552 BP.  
DE Cotton developing fibre EST Clone ID: LIB3830-001-Q1-N6-A1, SEQ:17351.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 552;  
100.0%; Pred. No. 5.1e-34;  
RESULT 940  
ID ACN49708 standard; cDNA; 554 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-025-Q6-N6-F6, SEQ:4489.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 554;  
100.0%; Pred. No. 5.1e-34;  
RESULT 941  
ID ACN47785 standard; cDNA; 557 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-015-Q1-N6-A5, SEQ:2566.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 557;  
100.0%; Pred. No. 5.1e-34;  
RESULT 942  
ID ACN47472 standard; cDNA; 560 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-011-Q1-N6-C9, SEQ:2253.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 560;  
100.0%; Pred. No. 5.1e-34;  
RESULT 943  
ID ABV57899 standard; cDNA; 565 BP.  
DE Human prostate expression marker cDNA 57890.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 565;  
100.0%; Pred. No. 5.1e-34;  
RESULT 944  
ID ACN56344 standard; cDNA; 565 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-034-Q6-N6-B10, SEQ:11125.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 565;  
100.0%; Pred. No. 5.1e-34;  
RESULT 945  
ID ACN53459 standard; cDNA; 567 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-A7, SEQ:8240.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.

Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 567;  
RESULT 946  
ID ACN87735 standard; DNA; 599 BP.  
DE Breast cancer related marker, seq id 8885.  
FN US2003099974-A1.  
PA (MILL-) MILLENNIUM PHARM INC.  
PD 29-MAY-2003.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 5; Length 570;  
RESULT 947  
ID ACN52090 standard; cDNA; 571 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B9, SEQ:6871.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 571;  
RESULT 948  
ID ACN52610 standard; cDNA; 574 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-G6, SEQ:7391.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 574;  
RESULT 949  
ID ACN51300 standard; cDNA; 583 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-C2, SEQ:6081.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 583;  
RESULT 950  
ID ACN58226 standard; cDNA; 591 BP.  
DE Cotton gynoeceum tissue EST Clone ID: LIB3829-008-Q6-K6-G6, SEQ:13007.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 591;  
RESULT 951  
ID ACN87190 standard; DNA; 592 BP.  
DE Breast cancer related marker, seq id 8340.  
FN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 11; Length 592;  
RESULT 952  
ID ACN49504 standard; cDNA; 593 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-034-Q6-K6-G11, SEQ:4285.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 593;  
RESULT 953  
ID ACN87735 standard; DNA; 599 BP.  
DE Breast cancer related marker, seq id 8885.  
FN US2003099974-A1.  
PA (MILL-) MILLENNIUM PHARM INC.  
PD 29-MAY-2003.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 11; Length 599;  
RESULT 954  
ID ACN45292 standard; cDNA; 627 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-A11, SEQ:73.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 627;  
RESULT 955  
ID ACN54072 standard; cDNA; 640 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 640;  
RESULT 956  
ID AAC80551 standard; cDNA; 658 BP.  
DE Human secreted protein gene 21 SEQ ID NO:31.  
FN WO200058467-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 3; Length 658;  
RESULT 957  
ID AAC59098 standard; cDNA; 667 BP.  
DE Human secreted protein coding sequence SEQ ID NO: 60.  
FN WO200055171-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 3; Length 667;  
RESULT 958  
ID AAD05318 standard; cDNA; 671 BP.  
DE Human secreted protein-encoding gene 19 cDNA clone HWLF064, SEQ ID NO:29.  
FN WO200134626-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 4; Length 671;  
RESULT 959  
ID AAS62239 standard; cDNA; 681 BP.  
DE cDNA sequence #26 encoding novel human secreted protein.  
FN WO200177291-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 6; Length 681;  
RESULT 960  
ID AAK88206 standard; cDNA; 698 BP.  
DE Human digestive system antigen coding sequence SEQ ID NO: 522.  
FN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 4; Length 698;  
RESULT 961  
ID AAS29150 standard; cDNA; 698 BP.  
DE cDNA encoding for human DNA-binding protein #121.

Query Match  
Best Local Similarity 4.7%; Score 133; DB 11; Length 599;  
RESULT 954  
ID ACN45292 standard; cDNA; 627 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-K6-A11, SEQ:73.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 627;  
RESULT 955  
ID ACN54072 standard; cDNA; 640 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-K6-G11, SEQ:8853.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 13; Length 640;  
RESULT 956  
ID AAC80551 standard; cDNA; 658 BP.  
DE Human secreted protein gene 21 SEQ ID NO:31.  
FN WO200058467-A1.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 3; Length 658;  
RESULT 957  
ID AAC59098 standard; cDNA; 667 BP.  
DE Human secreted protein coding sequence SEQ ID NO: 60.  
FN WO200055171-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 3; Length 667;  
RESULT 958  
ID AAD05318 standard; cDNA; 671 BP.  
DE Human secreted protein-encoding gene 19 cDNA clone HWLF064, SEQ ID NO:29.  
FN WO200134626-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 4; Length 671;  
RESULT 959  
ID AAS62239 standard; cDNA; 681 BP.  
DE cDNA sequence #26 encoding novel human secreted protein.  
FN WO200177291-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 6; Length 681;  
RESULT 960  
ID AAK88206 standard; cDNA; 698 BP.  
DE Human digestive system antigen coding sequence SEQ ID NO: 522.  
FN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 4.7%; Score 133; DB 4; Length 698;  
RESULT 961  
ID AAS29150 standard; cDNA; 698 BP.  
DE cDNA encoding for human DNA-binding protein #121.

PN WO200155162-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 133; DB 5; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-34;  
 RESULT 962  
 ID AAD16659 standard; cDNA; 698 BP.  
 DE Human novel protein-encoding cDNA clone HVAET61, SEQ ID NO:13.  
 PN WO200155327-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 133; DB 5; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-34;  
 RESULT 963  
 ID ABS68290 standard; cDNA; 698 BP.  
 DE cDNA encoding human DNA-binding protein #121.  
 PN US2002102638-A1.  
 PD 01-AUG-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 4.7%; Score 133; DB 6; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-34;  
 RESULT 964  
 ID ADC25284 standard; cDNA; 698 BP.  
 DE Human cDNA from extracellular matrix gene 121.  
 PN US2003049650-A1.  
 PD 13-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 133; DB 10; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-34;  
 RESULT 965  
 ID ACD92384 standard; cDNA; 700 BP.  
 DE Human colon cancer cell expressed cDNA #796.  
 PN US2002155438-A1.  
 PD 24-OCT-2002.  
 PA (SIMP/) SIMPSON A J G.  
 PA (NETO/) NETO E D.  
 PA (BREN/) BRENTANI R R.  
 Query Match 4.7%; Score 133; DB 10; Length 700;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-34;  
 RESULT 966  
 ID ADP23585 standard; cDNA; 733 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:763.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH) GENENTECH INC.  
 Query Match 4.7%; Score 133; DB 13; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-34;  
 RESULT 967  
 ID ABV29481 standard; cDNA; 760 BP.  
 DE Human prostate expression marker cDNA 29472.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.7%; Score 133; DB 5; Length 760;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-34;  
 RESULT 968  
 ID ADX57243 standard; DNA; 774 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #4626.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.  
 PA (DOWC) DOW AGROSCIENCES LLC.  
 Query Match 4.7%; Score 133; DB 10; Length 774;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-34;  
 RESULT 969  
 ID AAA64638 standard; DNA; 801 BP.  
 DE Partial sequence MEL3 associated with melanoma and thyroid tumors.  
 PN WO200050595-A2.  
 PD 31-AUG-2000.  
 PA (GOUT/) GOUT I.  
 PA (RODN/) RODNIN N.

PA (FILO/) FILOENKO V.  
 PA (MATS/) MATSUKA G.  
 PA (SCAN/) SCANLAN M.  
 PA (OLDL/) OLD L.  
 PA (BILY/) BILYNSKY B.  
 Query Match 4.7%; Score 133; DB 3; Length 801;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-34;  
 RESULT 970  
 ID AB282489 standard; cDNA; 805 BP.  
 DE Human secreted protein cDNA #SEQ ID 36.  
 PN WO200268628-A1.  
 PD 06-SEP-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 133; DB 6; Length 805;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-34;  
 RESULT 971  
 ID AAF31060 standard; cDNA; 872 BP.  
 DE Rat clone 701291473H1 coding sequence.  
 PN WO200102557-A1.  
 PD 11-JAN-2001.  
 PA (JANC) JANSSEN PHARM NV.  
 Query Match 4.7%; Score 133; DB 4; Length 872;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
 RESULT 972  
 ID ADF81828 standard; DNA; 873 BP.  
 DE Leukemia-related DNA sequence #2384.  
 PN WO2003039443-A2.  
 PD 15-MAY-2003.  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
 PA (HAPE/) HAPERLACH T.  
 PA (SCHO/) SCHOECH C.  
 PA (KERN/) KERN W.  
 Query Match 4.7%; Score 133; DB 10; Length 873;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
 RESULT 973  
 ID AAC59297 standard; cDNA; 887 BP.  
 DE Human secreted protein cDNA #21.  
 PN WO200056753-A1.  
 PD 28-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 133; DB 3; Length 887;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
 RESULT 974  
 ID AAI87708 standard; cDNA; 903 BP.  
 DE Human polynucleotide SEQ ID NO 7768.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 133; DB 4; Length 903;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
 RESULT 975  
 ID AAA64642 standard; DNA; 905 BP.  
 DE Partial sequence MEL7 associated with melanoma and thyroid tumors.  
 PN WO200050595-A2.  
 PD 31-AUG-2000.  
 PA (GOUT/) GOUT I.  
 PA (RODN/) RODNIN N.  
 PA (FILO/) FILOENKO V.  
 PA (MATS/) MATSUKA G.  
 PA (SCAN/) SCANLAN M.  
 PA (OLDL/) OLD L.  
 PA (BILY/) BILYNSKY B.  
 Query Match 4.7%; Score 133; DB 3; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-34;  
 RESULT 976  
 ID AA206226 standard; DNA; 936 BP.  
 DE Human secreted protein gene No. 8.  
 PN WO9935158-A1.  
 PD 15-JUL-1999.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.7%; Score 133; DB 2; Length 936;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-34;

RESULT 977  
ID AAD07722 standard; cDNA; 938 BP.  
DE Human secreted protein-encoding gene 18 cDNA clone HLYDU43, SEQ ID NO:28.  
PN WO200134800-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 938;  
Best Local Similarity 100.0%; Pred. No. 4.5e-34;  
RESULT 978  
ID AD062833 standard; RNA; 1000 BP.  
DE Homopoly-A contaminant for RNaseH activity assay.  
PN WO2004059012-A1.  
PD 15-JUL-2004.  
PA (AMHP) WYETH.  
Query Match 4.7%; Score 133; DB 12; Length 1000;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
RESULT 979  
ID ADQ62832 standard; RNA; 1000 BP.  
DE Homopoly-U contaminant for RNaseH activity assay.  
PN WO2004059012-A1.  
PD 15-JUL-2004.  
PA (AMHP) WYETH.  
Query Match 4.7%; Score 133; DB 12; Length 1000;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
RESULT 980  
ID ADE40468 standard; DNA; 1047 BP.  
DE Human granzyme H (gene ID 1793) DNA.  
PN WO2003070883-A2.  
PD 28-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.7%; Score 133; DB 10; Length 1047;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
RESULT 981  
ID ABV78042 standard; DNA; 1071 BP.  
DE Hypoxia-regulated protein coding sequence #62.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 4.7%; Score 133; DB 6; Length 1071;  
Best Local Similarity 100.0%; Pred. No. 4.4e-34;  
RESULT 982  
ID ADM19286 standard; cDNA; 1167 BP.  
DE Novel human channel/transporter gene #83.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 5; Length 1167;  
Best Local Similarity 100.0%; Pred. No. 4.3e-34;  
RESULT 983  
ID AAF91902 standard; cDNA; 1198 BP.  
DE Human secreted protein-encoding gene 45 cDNA clone HRACI26, SEQ ID NO:55.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 4.2e-34;  
RESULT 984  
ID AD22434 standard; DNA; 1215 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5254.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 133; DB 12; Length 1215;  
Best Local Similarity 100.0%; Pred. No. 4.2e-34;  
RESULT 985  
ID ADP85917 standard; DNA; 1300 BP.  
DE Synthetic construct #1.  
PN US2004110205-A1.  
PD 10-JUN-2004.  
PA (WANG/) WANG H.  
Query Match 4.7%; Score 133; DB 12; Length 1300;  
Best Local Similarity 100.0%; Pred. No. 4.2e-34;  
RESULT 986

ID ADD9623 standard; cDNA; 1343 BP.  
DE Human REMAP cDNA - SEQ ID 52.  
PN WO2003048305-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.7%; Score 133; DB 10; Length 1343;  
Best Local Similarity 100.0%; Pred. No. 4.1e-34;  
RESULT 987  
ID ADM47812 standard; DNA; 1383 BP.  
DE Polynucleotide sequence #230 useful in producing transgenic plants.  
PN US2003233670-A1.  
PD 18-DEC-2003.  
PA (EDGE/) EDGERTON M D.  
PA (CHOM/) CHOMET P S.  
PA (LACC/) LACCETTI L B.  
Query Match 4.7%; Score 133; DB 12; Length 1383;  
Best Local Similarity 100.0%; Pred. No. 4.1e-34;  
RESULT 988  
ID ADN39370 standard; cDNA; 1416 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B54.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.7%; Score 133; DB 11; Length 1416;  
Best Local Similarity 100.0%; Pred. No. 4.1e-34;  
RESULT 989  
ID ACN41008 standard; cDNA; 1416 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA327030, SEQ ID NO:6163.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 133; DB 13; Length 1416;  
Best Local Similarity 100.0%; Pred. No. 4.1e-34;  
RESULT 990  
ID ADR62569 standard; cDNA; 1423 BP.  
DE Cotton cDNA sequence, SEQ ID 3350.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 4.7%; Score 133; DB 13; Length 1423;  
Best Local Similarity 100.0%; Pred. No. 4.1e-34;  
RESULT 991  
ID ADD9624 standard; cDNA; 1464 BP.  
DE Human REMAP cDNA - SEQ ID 53.  
PN WO2003048305-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.7%; Score 133; DB 10; Length 1464;  
Best Local Similarity 100.0%; Pred. No. 4e-34;  
RESULT 992  
ID AD50017 standard; cDNA; 1696 BP.  
DE Human secreted protein cDNA.  
PN WO200283914-A2.  
PD 24-OCT-2002.  
PA (PEKE) PE CORP NY.  
Query Match 4.7%; Score 133; DB 8; Length 1696;  
Best Local Similarity 100.0%; Pred. No. 3.9e-34;  
RESULT 993  
ID AAS20587 standard; cDNA; 1798 BP.  
DE Human methionine aminopeptidase protease cDNA.  
PN US6329188-B1.  
PD 11-DEC-2001.  
PA (PEKE) PE CORP NY.  
Query Match 4.7%; Score 133; DB 6; Length 1798;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 994  
ID ABX92004 standard; cDNA; 1808 BP.  
DE Lung specific nucleic acid (LSNA) #46.  
PN WO200268633-A2.  
PD 06-SEP-2002.  
PA (DIAD-) DIADEXUS INC.

Query Match 4.7%; Score 133; DB 6; Length 1808;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 995  
ID AAQ04690 standard; cDNA; 1834 BP.  
DE Encodes Mammalian amino acid dehydrogenase activating factor-eta.  
PN JP02111796-A.  
PD 24-APR-1990.  
PA (TOFU) TOA NENRYO KOGYO KK.  
Query Match 4.7%; Score 133; DB 2; Length 1834;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 996  
ID AD143478 standard; DNA; 1875 BP.  
DE Plant transcription factor polynucleotide #1329.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER) SHERMAN B K.  
PA (RIEC) RIECHMANN J L.  
PA (JIAN) JIANG C.  
PA (HEAR) HEARD J E.  
PA (HAAK) HAAKE V.  
PA (CREE) CREELMAN R A.  
PA (RATC) RATCLIFFE O.  
PA (ADAM) ADAM L J.  
PA (REUB) REUBER T L.  
PA (KEDD) KEDDIE J.  
PA (BROU) BROUN P E.  
PA (PILG) PILGRIM M L.  
PA (DUBE) DUBELL A N.  
PA (PINE) PINEDA O.  
PA (YUGG) YU G.  
Query Match 4.7%; Score 133; DB 12; Length 1875;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 997  
ID ADN05367 standard; cDNA; 1913 BP.  
DE Antiporiatric cDNA sequence #906.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.7%; Score 133; DB 12; Length 1913;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 998  
ID AA23442 standard; cDNA; 1933 BP.  
DE cDNA encoding human secreted protein vc52\_1, SEQ ID NO:39.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 4.7%; Score 133; DB 3; Length 1933;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 999  
ID AAA23441 standard; cDNA; 1954 BP.  
DE cDNA encoding human secreted protein vc51\_1, SEQ ID NO:37.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 4.7%; Score 133; DB 3; Length 1954;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 1000  
ID AB159287 standard; cDNA; 1957 BP.  
DE Nucleotide sequence of AA233368 protein (from first ORF).  
PN WO200246362-A2.  
PD 13-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISB) JAPAN TOBACCO INC.  
Query Match 4.7%; Score 133; DB 6; Length 1957;  
Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 1001  
ID ABL59288 standard; cDNA; 1957 BP.  
DE Nucleotide sequence of AA233368 protein (from second ORF).  
PN WO200246362-A2.  
PD 13-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISB) JAPAN TOBACCO INC.  
Query Match 4.7%; Score 133; DB 6; Length 1957;

Best Local Similarity 100.0%; Pred. No. 3.8e-34;  
RESULT 1002  
ID AAF72803 standard; DNA; 2057 BP.  
DE Secreted protein gene #5.  
PN WO200107459-A1.  
PD 01-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 4; Length 2057;  
Best Local Similarity 100.0%; Pred. No. 3.7e-34;  
RESULT 1003  
ID AA252560 standard; cDNA; 2262 BP.  
DE Human secreted protein clone ye7\_1 nucleotide sequence SEQ ID NO:171.  
PN WO9598642-A2.  
PD 18-NOV-1999.  
PA (GEMY) GENETICS INST INC.  
Query Match 4.7%; Score 133; DB 3; Length 2262;  
Best Local Similarity 100.0%; Pred. No. 3.6e-34;  
RESULT 1004  
ID AAV54587 standard; cDNA; 2447 BP.  
DE Human secretory protein encoding cDNA clone CO1020-1.  
PN WO9833916-A2.  
PD 06-AUG-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match 4.7%; Score 133; DB 2; Length 2447;  
Best Local Similarity 100.0%; Pred. No. 3.6e-34;  
RESULT 1005  
ID AA225607 standard; cDNA; 2447 BP.  
DE Human secreted protein clone CO1020\_1 nucleotide sequence.  
PN US9565397-A.  
PD 12-OCT-1999.  
PA (GEMY) GENETICS INST INC.  
Query Match 4.7%; Score 133; DB 8; Length 2501;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1007  
ID AB210078 standard; DNA; 2501 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #218.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 2501;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1007  
ID AB210224 standard; DNA; 2501 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #364.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 2501;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1008  
ID ADQ29621 standard; DNA; 2566 BP.  
DE Human colorectal cancer-associated protein coding sequence #43.  
PN EPI439393-A2.  
PD 21-JUN-2004.  
PA (FARB) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 4.7%; Score 133; DB 12; Length 2566;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1009  
ID ADQ24863 standard; DNA; 2575 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7683.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 133; DB 12; Length 2575;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1010  
ID AAA48576 standard; cDNA; 2604 BP.  
DE cDNA encoding wheat protein phosphatase 2A regulatory subunit A.  
PN WO200036121-A2.  
PD 22-JUN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 4.7%; Score 133; DB 3; Length 2604;

Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1011  
ID AAZ43781 standard; cDNA; 2685 BP.  
DE Human fetal brain cDNA clone v06\_1.  
PN WO9955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 4.7%; Score 133; DB 3; Length 2685;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1012  
ID ADQ22306 standard; DNA; 2700 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5126.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 133; DB 12; Length 2700;  
Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
RESULT 1013  
ID AAC77829 standard; cDNA; 2921 BP.  
DE Human cancer associated gene sequence SEQ ID NO:223.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.7%; Score 133; DB 3; Length 2921;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
RESULT 1014  
ID ABV23160 standard; cDNA; 2922 BP.  
DE Human prostate expression marker cDNA 23151.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.7%; Score 133; DB 5; Length 2922;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
RESULT 1015  
ID ADQ08601 standard; DNA; 3030 BP.  
DE Ciona intestinalis nervous system associated gene SeqID3.  
PN JP2004057127-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match 4.7%; Score 133; DB 12; Length 3030;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
RESULT 1016  
ID ADK00688 standard; DNA; 3226 BP.  
DE HOMO protein encoding sequence #33.  
PN WO2004014946-A1.  
PD 19-FEB-2004.  
PA (NEWO-) NEWORGEN LTD.  
Query Match 4.7%; Score 133; DB 12; Length 3226;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
RESULT 1017  
ID ADI18906 standard; DNA; 3232 BP.  
DE Human disease related protein DNA sequence SeqID238.  
PN WO2003018621-A2.  
PD 06-MAR-2003.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 4.7%; Score 133; DB 10; Length 3232;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
RESULT 1018  
ID ADQ23592 standard; DNA; 3454 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6412.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.7%; Score 133; DB 12; Length 3454;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
RESULT 1019  
ID ADJ48200 standard; DNA; 3505 BP.  
DE Maize oil-associated gene #18.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR-) LAURIE C C.  
PA (RAVA-) RAVANELLO M.  
PA (SAVA-) SAVAGE T.

PA (LEDE-) LEDEAUX J R.  
PA (ROGE-) ROGERS J A.  
Query Match 4.7%; Score 133; DB 12; Length 3505;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
RESULT 1020  
ID ABL32171 standard; DNA; 3973 BP.  
DE Human immune system associated gene SEQ ID NO: 144.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 3973;  
Best Local Similarity 100.0%; Pred. No. 3.2e-34;  
RESULT 1021  
ID ABK33928 standard; DNA; 4001 BP.  
DE Human DNA for staging of Astrocytomas, complement, #5.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 4001;  
Best Local Similarity 100.0%; Pred. No. 3.1e-34;  
RESULT 1022  
ID ADA20431 standard; DNA; 4001 BP.  
DE Prostate tumour related genomic DNA complement sample #48.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 4001;  
Best Local Similarity 100.0%; Pred. No. 3.1e-34;  
RESULT 1023  
ID ADA84238 standard; DNA; 4001 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:96.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 4001;  
Best Local Similarity 100.0%; Pred. No. 3.1e-34;  
RESULT 1024  
ID ABO92014 standard; cDNA; 4236 BP.  
DE Human polynucleotide SEQ ID NO 11.  
PN US2002065394-A1.  
PD 30-MAY-2002.  
PA (JACO-) JACOBS K.  
PA (MCCO-) MCCOY J M.  
PA (LAVA-) LAVALLIE E R.  
PA (COLL-) COLLINS-RACIE L A.  
PA (EVAN-) EVANS C.  
PA (MERB-) MERBERG D.  
PA (TREA-) TREACY M.  
PA (SPAU-) SPAULDING V.  
Query Match 4.7%; Score 133; DB 6; Length 4236;  
Best Local Similarity 100.0%; Pred. No. 3.1e-34;  
RESULT 1025  
ID AAV61487 standard; cDNA; 4237 BP.  
DE Human secreted protein fe366\_1 cDNA.  
PN WO9841539-A2.  
PD 24-SEP-1998.  
PA (GEMV-) GENETICS INST INC.  
Query Match 4.7%; Score 133; DB 2; Length 4237;  
Best Local Similarity 100.0%; Pred. No. 3.1e-34;  
RESULT 1026  
ID ABK40004 standard; DNA; 5586 BP.  
DE Human chemically pretreated gene sequence #43 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 5586;  
Best Local Similarity 100.0%; Pred. No. 2.9e-34;  
RESULT 1027  
ID ABQ67140 standard; DNA; 6134 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 170.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.



Query Match 4.7%; Score 133; DB 6; Length 6134;  
Best Local Similarity 100.0%; Pred. No. 2.8e-34;  
RESULT 1028  
ID ABL32411 standard; DNA; 6161 BP.  
DE Human immune system associated gene SEQ ID NO: 384.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 6161;  
Best Local Similarity 100.0%; Pred. No. 2.8e-34;  
RESULT 1029  
ID AC622785 standard; DNA; 7369 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:34.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 7369;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
RESULT 1030  
ID AB209991 standard; DNA; 7369 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #131.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 7369;  
Best Local Similarity 100.0%; Pred. No. 2.7e-34;  
RESULT 1031  
ID ABL92313 standard; DNA; 8079 BP.  
DE Chemically treated DNA repair gene fragment complementary to #61.  
PN WO2003181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 8079;  
Best Local Similarity 100.0%; Pred. No. 2.6e-34;  
RESULT 1032  
ID AAS46303 standard; DNA; 10369 BP.  
DE Tumour suppressor gene derived chemically modified sequence #25.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 4; Length 10369;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 1033  
ID ABL32392 standard; DNA; 10369 BP.  
DE Human immune system associated gene SEQ ID NO: 365.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 10369;  
Best Local Similarity 100.0%; Pred. No. 2.5e-34;  
RESULT 1034  
ID ABL32118 standard; DNA; 11416 BP.  
DE Human immune system associated gene SEQ ID NO: 91.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 11416;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 1035  
ID ABL70335 standard; DNA; 11416 BP.  
DE Chemically treated cell signalling DNA sequence #13.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 11416;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 1036  
ID AAS61063 standard; DNA; 11416 BP.  
DE Human gene regulation-associated gene oligonucleotide #18.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 11416;

Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 1037  
ID ABL32895 standard; DNA; 11729 BP.  
DE Human immune system associated gene SEQ ID NO: 868.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 11729;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 1038  
ID ABL32717 standard; DNA; 12007 BP.  
DE Human immune system associated gene SEQ ID NO: 690.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 12007;  
Best Local Similarity 100.0%; Pred. No. 2.4e-34;  
RESULT 1039  
ID ABL33032 standard; DNA; 14798 BP.  
DE Human immune system associated gene SEQ ID NO: 1005.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 14798;  
Best Local Similarity 100.0%; Pred. No. 2.3e-34;  
RESULT 1040  
ID ABL33404 standard; DNA; 16033 BP.  
DE Human immune system associated gene SEQ ID NO: 1377.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 16033;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
RESULT 1041  
ID ABN79984 standard; DNA; 16633 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 1.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 6; Length 16633;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
RESULT 1042  
ID AAS46815 standard; DNA; 21354 BP.  
DE Tumour suppressor gene derived chemically modified sequence #512.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 4; Length 21354;  
Best Local Similarity 100.0%; Pred. No. 2.1e-34;  
RESULT 1043  
ID AB209958 standard; DNA; 35962 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #98.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 35962;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 1044  
ID AB210104 standard; DNA; 35962 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #244.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.7%; Score 133; DB 8; Length 35962;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
RESULT 1045  
ID ACN59858 standard; cDNA; 531 BP.  
DE Cotton gynoecium tissue EST Clone ID: LFB3829-035-Q1-K6-D8, SEQ:14639.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E. 4.6%; Score 132; DB 13; Length 531;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-33;  
RESULT 1046  
ID ABV5662 standard; cDNA; 549 BP.  
DE Human prostate expression marker cDNA 56653.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-33;  
RESULT 1047  
ID ACN53254 standard; cDNA; 578 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-004-Q1-N6-F11, SEQ:8035.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-33;  
RESULT 1048  
ID ADG79210 standard; cDNA; 896 BP.  
DE Human secreted protein cDNA of the invention SEQ ID NO:16.  
PN WO200268638-A1.  
PD 06-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-33;  
RESULT 1049  
ID ABQ54211 standard; cDNA; 970 BP.  
DE Human ovarian antigen HHFBV53 cDNA, SEQ ID NO:91.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 9.7e-34;  
RESULT 1050  
ID ADP04748 standard; cDNA; 1352 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 343.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.7e-34;  
RESULT 1051  
ID ADQ22502 standard; DNA; 1389 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5322.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.7e-34;  
RESULT 1052  
ID ACC50413 standard; cDNA; 1663 BP.  
DE Human secreted protein coding sequence, SEQ ID 80.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.3e-34;  
RESULT 1053  
ID AB271230 standard; cDNA; 1663 BP.  
DE Human secreted protein-encoding gene 41 cDNA clone HDP5H53, SEQ ID NO:51.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.3e-34;  
RESULT 1054  
ID ADP91122 standard; cDNA; 1663 BP.  
DE Human secreted protein cDNA #SEQ ID 68.

PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.3e-34;  
RESULT 1055  
ID ADC73466 standard; DNA; 1663 BP.  
DE Human secreted protein-related DNA - SEQ ID 99.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 8.3e-34;  
RESULT 1056  
ID ADN04959 standard; cDNA; 1999 BP.  
DE Antipsoriatic cDNA sequence #694.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.9e-34;  
RESULT 1057  
ID AAF97906 standard; cDNA; 2394 BP.  
DE Human secreted protein cDNA, SEQ ID NO: 33.  
PN WO200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.6e-34;  
RESULT 1058  
ID ADH61306 standard; DNA; 3420 BP.  
DE INTSIG encoding DNA 7512389CBI, SEQ ID 23.  
PN WO2004001005-A2.  
PD 31-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.9e-34;  
RESULT 1059  
ID ABO67159 standard; DNA; 6775 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 189.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.9e-34;  
RESULT 1060  
ID ADS89685 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO:701.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 1061  
ID ADS89411 standard; DNA; 8900 BP.  
DE Oligonucleotide of the invention SEQ ID NO:427.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.5e-34;  
RESULT 1062  
ID ADG33178 standard; DNA; 1381 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID502.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e-33;  
RESULT 1063  
ID ADR44025 standard; DNA; 1806 BP.  
DE Human colon tumour associated gene clone-36 SEQ ID NO:35.  
PN WO2004074506-A2.

PD 02-SEP-2004.  
PA (MERG-) MERGEN LTD.  
Query Match 4.6%; Score 131; DB 13; Length 1806;  
Best Local Similarity 100.0%; Pred. No. 1.7e-33;  
RESULT 1064  
ID ABV23003 standard; cDNA; 2827 BP.  
DE Human prostate expression marker cDNA 22994.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.6%; Score 131; DB 5; Length 2827;  
Best Local Similarity 100.0%; Pred. No. 1.5e-33;  
RESULT 1065  
ID ABV28839 standard; cDNA; 2827 BP.  
DE Human prostate expression marker cDNA 28830.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.6%; Score 131; DB 5; Length 2827;  
Best Local Similarity 100.0%; Pred. No. 1.5e-33;  
RESULT 1066  
ID ADG32917 standard; DNA; 4670 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID241.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 4.6%; Score 131; DB 10; Length 4670;  
Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
RESULT 1067  
ID ADQ19630 standard; DNA; 4670 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2449.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.6%; Score 131; DB 12; Length 4670;  
Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
RESULT 1068  
ID ADQ23804 standard; DNA; 4672 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6624.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.6%; Score 131; DB 12; Length 4672;  
Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
RESULT 1069  
ID ABN80102 standard; DNA; 8712 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 119.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.6%; Score 131; DB 6; Length 8712;  
Best Local Similarity 100.0%; Pred. No. 1.2e-33;  
RESULT 1070  
ID ACN53490 standard; cDNA; 468 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-008-Q1-K6-D3, SEQ:8271.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.6%; Score 130; DB 13; Length 468;  
Best Local Similarity 100.0%; Pred. No. 5.1e-33;  
RESULT 1071  
ID ACN56061 standard; cDNA; 474 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-031-Q6-N6-P7, SEQ:10842.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.6%; Score 130; DB 13; Length 474;

Best Local Similarity 100.0%; Pred. No. 5.1e-33;  
RESULT 1072  
ID ACN56273 standard; cDNA; 517 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.6%; Score 130; DB 13; Length 517;  
Best Local Similarity 100.0%; Pred. No. 5e-33;  
RESULT 1073  
ID ACN51185 standard; cDNA; 603 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-011-Q1-N6-B6, SEQ:5966.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.6%; Score 130; DB 13; Length 603;  
Best Local Similarity 100.0%; Pred. No. 4.8e-33;  
RESULT 1074  
ID AAC74364 standard; cDNA; 639 BP.  
DE Human secreted protein gene 28 SEQ ID NO:38.  
PN WO200058340-A2.  
PD 05-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.6%; Score 130; DB 3; Length 639;  
Best Local Similarity 100.0%; Pred. No. 4.7e-33;  
RESULT 1075  
ID ABX15834 standard; cDNA; 1447 BP.  
DE cDNA encoding soybean sterol C5 desaturase protein #2.  
PN US6465717-B1.  
PD 15-OCT-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 4.6%; Score 130; DB 8; Length 1447;  
Best Local Similarity 100.0%; Pred. No. 3.9e-33;  
RESULT 1076  
ID ADI19006 standard; cDNA; 1447 BP.  
DE Soybean sterol-C5-desaturase cDNA #2.  
PN US200322914-A1.  
PD 11-DEC-2003.  
PA (FAMO/) FAMODU O O.  
PA (OROZ/) OROZCO E M.  
PA (RAFA/) RAFALSKI J A.  
PA (SHEN/) SHEN J B.  
Query Match 4.6%; Score 130; DB 12; Length 1447;  
Best Local Similarity 100.0%; Pred. No. 3.9e-33;  
RESULT 1077  
ID AAF91859 standard; cDNA; 3436 BP.  
DE Human secreted protein-encoding gene 2 cDNA clone HDPFB02, SEQ ID NO:12.  
PN WO200118022-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.6%; Score 130; DB 4; Length 3436;  
Best Local Similarity 100.0%; Pred. No. 3.1e-33;  
RESULT 1078  
ID AAS00767 standard; cDNA; 3436 BP.  
DE Human B7-H3 cDNA clone.  
PN WO200118021-A1.  
PD 15-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MAYO-) MAYO CLINIC.  
Query Match 4.6%; Score 130; DB 4; Length 3436;  
Best Local Similarity 100.0%; Pred. No. 3.1e-33;  
RESULT 1079  
ID ADA39737 standard; cDNA; 3436 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 4.6%; Score 130; DB 8; Length 3436;  
Best Local Similarity 100.0%; Pred. No. 3.1e-33;  
RESULT 1080  
ID ADC73453 standard; DNA; 3436 BP.  
DE Human secreted protein-related DNA - SEQ ID 86.  
FN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.6%; Score 130; DB 10; Length 3436;  
Best Local Similarity 100.0%; Pred. No. 3.1e-33;  
RESULT 1081  
ID ABX45893 standard; cDNA; 160 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11058.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.5%; Score 129; DB 8; Length 160;  
Best Local Similarity 100.0%; Pred. No. 1.4e-32;  
RESULT 1082  
ID ABX38052 standard; cDNA; 242 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #3217.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.5%; Score 129; DB 8; Length 242;  
Best Local Similarity 100.0%; Pred. No. 1.3e-32;  
RESULT 1083  
ID ACN48604 standard; cDNA; 249 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-023-Q6-K6-G7, SEQ:3385.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.5%; Score 129; DB 13; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.3e-32;  
RESULT 1084  
ID ACN50243 standard; cDNA; 368 BP.  
DE Cotton non-primed seed EST Clone ID: LIB3826-002-Q1-K6-B12, SEQ:5024.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.5%; Score 129; DB 13; Length 368;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
RESULT 1085  
ID ABX39555 standard; cDNA; 383 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4720.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.5%; Score 129; DB 8; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
RESULT 1086  
ID ABX43354 standard; cDNA; 395 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #8519.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.

PA (WARR/) WARREN W C.  
Query Match 4.5%; Score 129; DB 8; Length 395;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
RESULT 1087  
ID ADG37731 standard; DNA; 408 BP.  
DE Aspergillus solid-culture DNA #442.  
FN JP2003180365-A.  
PD 02-JUL-2003.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN SHURUI SOGO KENKY.  
Query Match 4.5%; Score 129; DB 10; Length 408;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
RESULT 1088  
ID ABX44057 standard; cDNA; 421 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #9222.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.5%; Score 129; DB 8; Length 421;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
RESULT 1089  
ID ABX39788 standard; cDNA; 460 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4953.  
FN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 4.5%; Score 129; DB 8; Length 460;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
RESULT 1090  
ID ABV57765 standard; cDNA; 502 BP.  
DE Human prostate expression marker cDNA 57756.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.5%; Score 129; DB 5; Length 502;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
RESULT 1091  
ID ACN61238 standard; cDNA; 548 BP.  
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-034-Q1-N6-C12, SEQ:16019.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.5%; Score 129; DB 13; Length 548;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
RESULT 1092  
ID ACN57821 standard; cDNA; 560 BP.  
DE Cotton gynoeicum tissue EST Clone ID: LIB3829-006-Q6-K6-C12, SEQ:12602.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.5%; Score 129; DB 13; Length 560;  
Best Local Similarity 100.0%; Pred. No. 1e-32;  
RESULT 1093  
ID ACN53147 standard; cDNA; 578 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-022-Q1-N6-E3, SEQ:7928.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.5%; Score 129; DB 13; Length 578;

Best Local Similarity 100.0%; Pred. No. 1e-32;  
 RESULT 1094  
 ID ADR59449 standard; cDNA; 639 BP.  
 DE Cotton cDNA sequence, SEQ ID 230.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA//) KOVALIC D K.  
 PA (ZHOU//) ZHOU Y.  
 PA (CAOY//) CAO Y.  
 Query Match 4.5%; Score 129; DB 13; Length 639;  
 Best Local Similarity 100.0%; Pred. No. 1e-32;  
 RESULT 1095  
 ID AA291918 standard; cDNA; 1051 BP.  
 DE Murine mahogany protein coding sequence akml004.  
 PN WO200005373-A2.  
 PD 03-FEB-2000.  
 PA (MILL-) MILLENIUM PHARM INC.  
 Query Match 4.5%; Score 129; DB 3; Length 1051;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-33;  
 RESULT 1096  
 ID ADF94940 standard; cDNA; 1311 BP.  
 DE Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.  
 PN WO2003031586-A2.  
 PD 17-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (BLON//) BLONDEL O.  
 PA (RUBE//) RUBEN S M.  
 Query Match 4.5%; Score 129; DB 10; Length 1311;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-33;  
 RESULT 1097  
 ID ABL39587 standard; cDNA; 1615 BP.  
 DE Human cancer suppressing gene PP432 encoding cDNA SEQ ID NO:12.  
 PN CN133318-A.  
 PD 19-SEP-2001.  
 PA (SHAN-) SHANGHAI INST ONCOLOGY.  
 Query Match 4.5%; Score 129; DB 6; Length 1615;  
 Best Local Similarity 100.0%; Pred. No. 8e-33;  
 RESULT 1098  
 ID ADM67116 standard; DNA; 2090 BP.  
 DE Human homologue of murine adipocyte specific DNA SeqID 252.  
 PN WO2004011618-A2.  
 PD 05-FEB-2004.  
 PA (HNGE-) HNGENE INC.  
 Query Match 4.5%; Score 129; DB 12; Length 2090;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-33;  
 RESULT 1099  
 ID AAQ04107 standard; cDNA; 2427 BP.  
 DE Human pro-urokinase cDNA of clone pcuk176.  
 PN EP365894-A.  
 PD 02-MAY-1990.  
 PA (FARM ) FARMITALIA ERBA SPA CARLO.  
 Query Match 4.5%; Score 129; DB 2; Length 2427;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-33;  
 RESULT 1100  
 ID ABN80138 standard; DNA; 6484 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 155.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.5%; Score 129; DB 6; Length 6484;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-33;  
 RESULT 1101  
 ID ABL33356 standard; DNA; 6577 BP.  
 DE Human immune system associated gene SEQ ID NO: 1329.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.5%; Score 129; DB 6; Length 6577;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-33;  
 RESULT 1102  
 ID ABL70561 standard; DNA; 6577 BP.  
 DE Chemically treated cell signalling DNA sequence#226.  
 PN WO200202807-A2.

PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.5%; Score 129; DB 6; Length 6577;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-33;  
 RESULT 1103  
 ID AAS61221 standard; DNA; 6577 BP.  
 DE Human gene regulation-associated gene oligonucleotide #176.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.5%; Score 129; DB 6; Length 6577;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-33;  
 RESULT 1104  
 ID ABX41830 standard; cDNA; 152 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #6995.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 4.5%; Score 128; DB 8; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 3e-32;  
 RESULT 1105  
 ID ABX40291 standard; cDNA; 365 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #5456.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 4.5%; Score 128; DB 8; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-32;  
 RESULT 1106  
 ID AAI84786 standard; cDNA; 414 BP.  
 DE Human polynucleotide SEQ ID NO 4846.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.5%; Score 128; DB 4; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-32;  
 RESULT 1107  
 ID ABX45932 standard; cDNA; 429 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #11097.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT//) BYATT J C.  
 PA (MATH//) MATHIALAGAN N.  
 PA (TAON//) TAO N.  
 PA (WARR//) WARREN W C.  
 Query Match 4.5%; Score 128; DB 8; Length 429;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-32;  
 RESULT 1108  
 ID ACN60066 standard; cDNA; 556 BP.  
 DE Cotton gynoeium tissue EST Clone ID: LIB3825-017-Q6-K6-E3, SEQ:14847.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK//) DEIKMAN J.  
 PA (FENG//) FENG P C C.  
 PA (FINC//) FINCHER K L.  
 PA (ZIEG//) ZIEGLER T E.  
 Query Match 4.5%; Score 128; DB 13; Length 556;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-32;  
 RESULT 1109  
 ID ACN45381 standard; cDNA; 577 BP.  
 DE Cotton primed seed EST Clone ID: LIB3825-001-Q1-N6-C7, SEQ:162.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK//) DEIKMAN J.  
 PA (FENG//) FENG P C C.  
 PA (FINC//) FINCHER K L.  
 PA (ZIEG//) ZIEGLER T E.

Query Match 4.5%; Score 128; DB 13; Length 577;  
Best Local Similarity 100.0%; Pred. No. 2.2e-32;  
RESULT 1110  
ID ABV58690 standard; cDNA; 579 BP.  
DE Human prostate expression marker cDNA 58681.  
FN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.5%; Score 128; DB 5; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e-32;  
RESULT 1111  
ID ACN51614 standard; cDNA; 584 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-005-Q1-N6-C5, SEQ:6395.  
FN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 4.5%; Score 128; DB 13; Length 584;  
Best Local Similarity 100.0%; Pred. No. 2.2e-32;  
RESULT 1112  
ID ACC60574 standard; cDNA; 878 BP.  
DE Polynucleotide relating to the invention SEQ ID NO: 151.  
FN WO200257460-A2.  
PD 25-JUL-2002.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 4.5%; Score 128; DB 6; Length 878;  
Best Local Similarity 100.0%; Pred. No. 2e-32;  
RESULT 1113  
ID AA243798 standard; cDNA; 1936 BP.  
DE Human fetal brain cDNA clone vc26\_1.  
FN WO955721-A1.  
PD 04-NOV-1999.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 4.5%; Score 128; DB 3; Length 1936;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1114  
ID AAC59406 standard; cDNA; 1985 BP.  
DE Human secreted protein cDNA #15.  
FN WO200056765-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.5%; Score 128; DB 3; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1115  
ID AAF72410 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
FN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 4; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1116  
ID AA545938 standard; cDNA; 1985 BP.  
DE Human DNA encoding PRO polypeptide sequence #14.  
FN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 4; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1117  
ID ACA60174 standard; cDNA; 1985 BP.  
DE Human cDNA for secreted/transmembrane protein PRO271.  
FN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1118  
ID ACA89388 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003036141-A1.

PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1119  
ID ACA73398 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1120  
ID ACA05713 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1121  
ID ACA66547 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
FN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1122  
ID ACD07574 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH-) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1123  
ID ACF20122 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1124  
ID ACF19508 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1125  
ID ACD21796 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1126  
ID ACF12961 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1127  
ID ACD25064 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1128  
ID ACF00113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

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PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1129 100.0%; Pred. No. 1.6e-32;
ID ACA72170 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1130 100.0%; Pred. No. 1.6e-32;
ID AC004694 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1131 100.0%; Pred. No. 1.6e-32;
ID AC004694 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1132 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1133 100.0%; Pred. No. 1.6e-32;
ID ABX71622 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1134 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1135 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1136 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1137 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1138 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1139 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1140 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1141 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1142 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1143 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1144 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane polypeptide PRO271 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1145 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1146 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1147 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;
RESULT 1148 100.0%; Pred. No. 1.6e-32;
ID AC008162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027266-A1.
PD 06-FEB-2003.

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Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1149  
ID ACD21182 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1150  
ID ABX75354 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO271.  
FN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1151  
ID ABX97757 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1152  
ID ACA97233 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1153  
ID ACA57696 standard; cDNA; 1985 BP.  
DE Human PRO271 cDNA.  
FN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1154  
ID ACD14224 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1155  
ID ACC91007 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1156  
ID ACC88749 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1157  
ID ACD06946 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1158  
ID ACA67397 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003017542-A1.  
PD 23-JAN-2003.

Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1159  
ID ACC81452 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1160  
ID ACC89056 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1161  
ID ACC86412 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1162  
ID ACC89670 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1163  
ID ACC92849 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1164  
ID ACA72477 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1165  
ID ACA88995 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1166  
ID ACA69731 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1167  
ID ACA96874 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1168  
ID ACA90870 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 8; Length 1985;  
RESULT 1169  
ID ACA90870 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003032108-A1.  
PD 13-FEB-2003.

RESULT 1169  
ID ACA70652 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1170  
ID ACA95162 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1171  
ID ACC86105 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1172  
ID ACC89977 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1173  
ID ACD12585 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1174  
ID ACF19815 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1175  
ID ABX76759 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1176  
ID ABX96191 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #40.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1177  
ID ACA73091 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;  
RESULT 1178  
ID ACA05512 standard; cDNA; 1985 BP.  
DE cDNA encoding human secreted protein PRO271.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 8; Length 1985;

RESULT 1179  
ID ACA68634 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1180  
ID ACA74478 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1181  
ID ACA70345 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1182  
ID ACD14531 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1183  
ID ACD20179 standard; cDNA; 1985 BP.  
DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1184  
ID ACA68203 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1185  
ID ABX98668 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1186  
ID ACC81145 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1187  
ID ACA95469 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1188  
ID ACD04387 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1189  
ID ACC87828 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1190  
ID ACF12490 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1191  
ID ACA96205 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1192  
ID ACA64979 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1193  
ID ACA73705 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1194  
ID ACA74117 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1195  
ID ACA96512 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1196  
ID ACD10618 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1197  
ID ACC91314 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1198  
ID ACD02649 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1199  
ID ACC87214 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036165-A1.

PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1200  
ID ACC85798 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1201  
ID ACA65286 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1202  
ID ACA94103 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1203  
ID ACA97847 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1204  
ID ACA91349 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1205  
ID ACA90563 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
FN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1206  
ID ACD16110 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1207  
ID ACD17271 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1208  
ID ACC91928 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1209  
ID ACA74785 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;

Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1210  
ID ACA91656 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1211  
ID ACA71300 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1212  
ID ACC90700 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1213  
ID ACA65710 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO protein #14.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1214  
ID ACA54982 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1215  
ID ACA94855 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1216  
ID ACD16417 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1217  
ID ACD15496 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1218  
ID ABX16599 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein #14.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 8; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1219  
ID ACA97540 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1220  
ID ACA98989 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1221  
ID ACC91621 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1222  
ID ACD11032 standard; cDNA; 1985 BP.  
DE Novel human secreted and transmembrane protein PRO271 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1223  
ID ACD14882 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1224  
ID ACD19817 standard; cDNA; 1985 BP.  
DE Human secreted / transmembrane polypeptide PRO271 cDNA.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1225  
ID ACD11646 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1226  
ID ACC95775 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1227  
ID ACF16338 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1228  
ID ACF02456 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1229  
ID ACF02763 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049743-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1230  
 ID ADA77779 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003073180-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1231  
 ID ACF10034 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068743-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1232  
 ID ACF7927 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054479-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1233  
 ID ACD46632 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068685-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1234  
 ID ACD49395 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068725-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1235  
 ID ACF28162 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003068752-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1236  
 ID ACD88852 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003068682-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1237  
 ID ACD84247 standard; cDNA; 1985 BP.  
 DE Human PRO polynucleotide #14.  
 PN US2003068701-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1238  
 ID ACD99021 standard; cDNA; 1985 BP.  
 DE cDNA encoding human PRO polypeptide #14.  
 PN US2003068755-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1239  
 ID ADA77779 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003073180-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1240  
 ID ACF48763 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003104539-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1241  
 ID ADB29417 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein cDNA, #42.  
 PN US2003092002-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1242  
 ID ACD09083 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003036131-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1243  
 ID ACF11876 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040075-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1244  
 ID ACF41110 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003054459-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1245  
 ID ACF15724 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003044930-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1246  
 ID ACF16031 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
 PN US2003040071-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1247  
 ID ACD31858 standard; cDNA; 1985 BP.  
 DE Human secreted/transmembrane protein (PRO) cDNA #14.  
 PN US2003054471-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.5%; Score 128; DB 9; Length 1985;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
 RESULT 1248  
 ID ACF18666 standard; cDNA; 1985 BP.  
 DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1249  
ID ACF09113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1250  
ID ACF78234 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1251  
ID ACF51833 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1252  
ID ACF26320 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1253  
ID ACF24113 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1254  
ID ACF63424 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1255  
ID ACF50298 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1256  
ID ACH07769 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1257  
ID ACF13575 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064462-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1258  
ID ACD41501 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1259  
ID ACF31914 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1260  
ID ACF23192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1261  
ID ACF39882 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1262  
ID ACD45404 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1263  
ID ACF53061 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1264  
ID ACF27241 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1265  
ID ACF45079 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1266  
ID ACF29697 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1267  
ID ACD89773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1268  
ID ACD84554 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1269  
ID ACD98714 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1270  
ID ACF77006 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1271  
ID ACF76699 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1272  
ID ACF49684 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1273  
ID ACF49991 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1274  
ID ACD09390 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1275  
ID ACD08469 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1276  
ID ACF12183 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036130-A1.

PD 20-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1277  
ID ACC94691 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1278  
ID ACD22410 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1279  
ID ACF15110 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1280  
ID ACC97205 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1281  
ID ADA18273 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
FN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1282  
ID ACD66964 standard; cDNA; 1985 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO271.  
FN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1283  
ID ACC92235 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1284  
ID ACF13882 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1285  
ID ACF14189 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
RESULT 1286  
ID ACF12183 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036130-A1.



RESULT 1286  
ID ACF09420 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN' US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1287  
ID ACF32221 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1288  
ID ACF47860 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1289  
ID ACF67591 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1290  
ID ACF25399 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1291  
ID ACF29083 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1292  
ID ACF84861 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1293  
ID ACF83940 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
FN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1294  
ID ACF87931 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1295

ID ACF30618 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1296  
ID ACF32221 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1297  
ID ACF11881 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1298  
ID ACF12188 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1299  
ID ACF40580 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1300  
ID ACF18052 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1301  
ID ACF08499 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1302  
ID ACF31300 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1303  
ID ACF52140 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1304  
ID ACF50009 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.

PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1305  
ID ACF38712 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1306  
ID ACF26627 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1307  
ID ACF24727 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1308  
ID ACF46307 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1309  
ID ACF27855 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1310  
ID ACF89159 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1311  
ID ACF63731 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1312  
ID ACF60371 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003083734-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1313  
ID ACF12495 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049773-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1314  
ID ACF09918 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1315  
ID ACF03773 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1316  
ID ACD10311 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1317  
ID ACD11953 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1318  
ID ACF83125 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1319  
ID ACF42338 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1320  
ID ADA16248 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1321  
ID ACF18359 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1322  
ID ACF02149 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1323

ID ACP21657 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1324  
ID ACP10341 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1325  
ID ACP33793 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1326  
ID ACP44755 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1327  
ID ACP91000 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1328  
ID ACP91000 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1329  
ID ACP30311 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1330  
ID ACP87010 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1331  
ID ACP60064 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1332  
ID ACP46614 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1333  
ID ACP75471 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1334  
ID ADA79571 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1335  
ID ACF17131 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1336  
ID ACF22885 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1337  
ID ACF07885 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1338  
ID ACP08192 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1339  
ID ACF40496 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1340  
ID ACF53675 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1341  
ID ACD46939 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1342  
ID ACF47842 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1343  
ID ACF47228 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1344  
ID ACF46000 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1345  
ID ACD86089 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1346  
ID ACF52447 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1347  
ID ACF52754 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1348  
ID ACF64747 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1349  
ID ACF76392 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1350  
ID ACF61292 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1351  
ID ACF61599 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1352  
ID ACD30630 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1353  
ID ACD31551 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1354  
ID ACD32472 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1355  
ID ACF17438 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1356  
ID ACF07271 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1357  
ID ACF20429 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1358  
ID ACF21043 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1359  
ID ACF20736 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1360  
ID ACD47553 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1361  
ID ACF47535 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1362  
ID ACF53368 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1363  
ID ACD86703 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1364  
ID ACH04951 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1365  
ID ACF4448 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1366  
ID ADA42393 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1367  
ID ADA81298 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1368  
ID ACD22103 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1369  
ID ACD24450 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1370  
ID ACD39653 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.

PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1371  
ID ACD39960 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1372  
ID ACF13268 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1373  
ID ACF03070 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1374  
ID ACD23303 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #38.  
PN US2003064367-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1375  
ID ACF78541 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1376  
ID ACF11262 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1377  
ID ACF50605 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1378  
ID ACF34100 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1379  
ID ACD46325 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1380  
ID ACD48167 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1381  
ID ACF27548 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1382  
ID ACF24420 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1383  
ID ACD85475 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1384  
ID ACD90080 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1385  
ID ACD83633 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1386  
ID ACF49070 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1387  
ID ACH07155 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1388  
ID ACH07462 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1389

ID ACH08076 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1390  
ID ACH11267 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1391  
ID ACH11574 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1392  
ID ACH10225 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1393  
ID ACF01228 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1394  
ID ACF40803 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1395  
ID ACD24143 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1396  
ID ACD31244 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1397  
ID ACF17745 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 128; DB 9; Length 1985;  
RESULT 1398  
ID ACF32528 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064445-A1.  
PD 03-APR-2003.

PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1399  
ID ACF40189 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1400  
ID ACF48149 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1401  
ID ACF38098 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1402  
ID ACF25034 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1403  
ID ACF26934 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1404  
ID ACF29390 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1405  
ID ACD87624 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1406  
ID ACF76085 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1407  
ID ACF49377 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1408

ID ACF43834 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1409  
ID ACH06179 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1410  
ID ACH06486 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1411  
ID ADA83096 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1412  
ID ACC92542 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1413  
ID ACC93156 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1414  
ID ACF19201 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1415  
ID ACD12892 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1416  
ID ACF06350 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1417  
ID ACC94384 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;



Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1418  
ID ACC97812 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1419  
ID AC94077 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1420  
ID ACF42031 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1421  
ID ACD30937 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1422  
ID ACD42966 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1423  
ID ACD43273 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1424  
ID ACF14803 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1425  
ID ACF01535 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1426  
ID ACF31607 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1427  
ID ACD67284 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
FN US2003064453-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1428  
ID ACD48474 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1429  
ID ACD48781 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1430  
ID ACF51219 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1431  
ID ACF53982 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1432  
ID ACF25706 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1433  
ID ACF39019 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1434  
ID ACF28776 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
FN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1435  
ID ACD90693 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 4.5%; Score 128; DB 9; Length 1985;  
PD 100.0%; Pred. No. 1.6e-32;  
RESULT 1436  
ID ACD86396 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
FN US2003068765-A1.  
PD 10-APR-2003.

PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1437  
ID ACH05258 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1438  
ID ACF65054 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1439  
ID ADB20139 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1440  
ID ACF43527 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1441  
ID ACH08997 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1442  
ID ACH09304 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1443  
ID ADA78391 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1444  
ID ACF09727 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1445  
ID ACF50912 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC. 4.5%; Score 128; DB 9; Length 1985;  
Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1446  
ID ACF23806 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1447  
ID ACD88238 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1448  
ID ACH09611 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1449  
ID ACH10532 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1450  
ID ACD11339 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1451  
ID ACC96389 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1452  
ID ACC98419 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1453  
ID ADA16672 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1454  
ID ACF41724 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1455  
ID ACF16645 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040073-A1.

PD 27-FEB-2003.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1456  
ID ADAL1301 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1457  
ID ACD32165 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1458  
ID ACD30323 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1459  
ID ACD41194 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1460  
ID ACF07578 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1461  
ID ACF30993 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1462  
ID ACF77313 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1463  
ID ACF10955 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1464  
ID ACF32835 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

RESULT 1465  
ID ACF26013 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1466  
ID ACD83326 standard; cDNA; 1985 BP.  
DE Human PRO polynucleotide #14.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1467  
ID ACF23499 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1468  
ID ACF42913 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1469  
ID ACF43320 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1470  
ID ACH05872 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1471  
ID ACH08690 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1472  
ID ADA41969 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1473  
ID ACC90284 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1474  
ID ACF10648 standard; cDNA; 1985 BP.



RESULT 1493  
ID ADA42819 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein cDNA, #42.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1494  
ID ACD10004 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1495  
ID ACD16729 standard; cDNA; 1985 BP.  
DE cDNA encoding human PRO polypeptide #14.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1496  
ID ACC99026 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1497  
ID ACF00420 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1498  
ID ACD40887 standard; cDNA; 1985 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #14.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1499  
ID ACF14496 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
RESULT 1500  
ID ACF22271 standard; cDNA; 1985 BP.  
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.5%; Score 128; DB 9; Length 1985;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 5970 Seconds  
(without alignments)  
18145.881 Million cell updates/sec

Title: US-10-063-692-37  
Perfect score: 2846  
Sequence: 1 cgtcgggaccagccggc.....aaaaaaaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsl1:\*

9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2468	86.7	3165	3	HSM806734
2	2394	84.1	2650	3	AF370388
3	1130	39.7	2214	9	AY406074
C 4	889	31.2	1100	5	BX337780
C 5	786	27.6	897	5	BX434191
6	724	25.4	795	6	CD653367
7	706	24.8	1049	5	BX399905
C 8	691	24.3	1008	5	BX399904
9	685	24.1	879	6	CD514783
C 10	677	23.8	952	5	BX439313
11	672	23.6	723	5	BQ014545
C 12	647	22.7	886	5	BX337781
13	640	22.5	645	4	BM728083
C 14	640	22.5	645	5	BM930545
C 15	640	22.5	722	5	BU742056
C 16	638	22.4	740	5	BQ009840
C 17	636	22.3	645	4	BM683392
C 18	636	22.3	650	4	BM684138
C 19	636	22.1	722	5	BQ014522
C 20	589	20.7	633	2	AW957662
21	589	20.7	645	5	BM929554
22	578	20.3	626	5	BF381335
23	566	19.9	566	5	BP289572
C 24	560	19.7	649	4	BM680642
					BM640676 Homo sapi
					AF370388 Homo sapi
					AY406074 Homo sapi
					BX337780 Homo sapi
					BX434191 Homo sapi
					CD653367 AGENCOURT
					BX399905 AGENCOURT
					BX399904 AGENCOURT
					CD514783 AGENCOURT
					BX439313 AGENCOURT
					BQ014545 UI-H-ED1-
					BX337781 BX337781
					BM728083 UI-E-EJ1-
					BM930545 UI-E-EJ1-
					BU742056 UI-E-EJ1-
					BQ009840 UI-E-EJ1-
					BM683392 UI-E-EJ1-
					BM684138 UI-E-EJ1-
					BQ014522 UI-H-ED1-
					AW957662 EST369732
					BM929554 UI-E-EJ1-
					BF381335 BP381335
					BP289572 BP289572
					BM680642 UI-E-EJ0-

557	19.6	557	1	AI954161	AI954161 wx80e03.x
555	19.5	555	5	EX350293	EX350293 BX350293
544	19.1	551	7	CO394970	CO394970 AGENCOURT
C 28	521	586	5	BM998737	BM998737 UI-H-DT1-
C 29	514	584	5	BP205877	BP205877 BP205877
C 30	507	574	1	AI671186	AI671186 wb14d04.x
C 31	491	574	7	CF125161	CF125161 UI-HF-EL0
32	476	574	7	CF125161	CF125161 UI-HF-EL0
33	452	452	2	BE048236	BE048236 tz48g03.y
C 34	444	449	1	AI990243	AI990243 ws20c03.x
C 35	425	449	1	AI823626	AI823626 w185e01.x
C 36	424	449	1	AI088620	AI088620 qb14f03.x
C 37	418	428	2	BF197805	BF197805 7p92f09.x
C 38	410	415	1	AI624892	AI624892 c872f03.x
C 39	409	442	2	AW340294	AW340294 hc95d04.x
C 40	397	630	4	BM724013	BM724013 UI-E-EJ1-
C 41	397	630	4	BM724013	BM724013 UI-E-EJ1-
C 42	386	557	1	AA460698	AA460698 xz69c08.g
C 43	385	715	1	AL048495	AL048495 DKF2p586L
C 44	382	433	1	AI432522	AI432522 th38b12.x
C 45	370	419	1	AA708420	AA708420 z157a04.s
C 46	367	367	1	AI057206	AI057206 oz11a09.x
C 47	364	545	1	AA045104	AA045104 zk63b08.g
C 48	356	382	6	CD707019	CD707019 EST23546
C 49	348	348	7	CN334668	CN334668 170005999
C 50	345	442	2	AW028008	AW028008 wv61b05.x
C 51	340	400	5	BM929450	BM929450 UI-E-EJ1-
C 52	340	401	5	BU742789	BU742789 UI-E-EJ1-
C 53	337	337	1	AA433935	AA433935 zw52f05.g
C 54	332	404	2	AW206753	AW206753 UI-H-B11-
C 55	325	325	2	AI420902	AI420902 tf03g11.x
C 56	319	584	5	BP312143	BP312143 BP312143
C 57	315	315	1	AI579963	AI579963 tq35g05.x
C 58	307	773	4	BG403264	BG403264 602419419
C 59	295	492	7	CN296855	CN296855 170004250
C 60	283	756	7	CN334669	CN334669 170006000
61	277	277	9	AY408075	AY408075 Pan trogl
C 62	274	330	1	AI583699	AI583699 tco1n09.x
C 63	263	411	7	CN296856	CN296856 170005326
C 64	255	274	1	AI824672	AI824672 zw48c08.x
C 65	253	436	1	AA430705	AA430705 zw52f06.x
C 66	252	258	1	AL701986	AL701986 DKF2p686M
C 67	252	406	2	AW511691	AW511691 xus3b03.x
C 68	237	8.3	237	1	AA989716
C 69	231	8.1	333	7	T52085
70	194	6.8	583	5	BP216550
71	187	6.6	491	1	AA460872
72	183	6.4	381	7	CF772910
C 73	178	6.3	359	2	AW340199
C 74	163	5.7	163	7	CN334667
C 75	150	5.3	356	7	N94393
C 76	150	5.3	410	5	EX473159
C 77	141	5.0	228	6	CA819677
C 78	139	4.9	674	1	AV711924
C 79	137	4.8	409	7	CR623263
C 80	137	4.8	194	5	EX489675
C 81	137	4.8	378	5	EX499601
C 82	137	4.8	393	5	EX507033
C 83	137	4.8	418	4	BF981774
C 84	137	4.8	738	6	CD641072
C 85	137	4.8	850	6	CD108244
C 86	137	4.8	865	5	BU555370
C 87	137	4.8	870	5	BU529694
C 88	137	4.8	2417	3	BC021396
C 89	136	4.8	164	4	BJ704049
C 90	136	4.8	243	7	CO193787
C 91	136	4.8	245	7	CF212786
C 92	136	4.8	273	7	CO416891
C 93	136	4.8	276	4	CK341777
C 94	136	4.8	276	7	CK385496
C 95	136	4.8	286	1	AL589270
C 96	136	4.8	291	7	CO417291
C 97	136	4.8	331	7	CO183642

98 136 4.8 346 7 CV525623 Mdlv4012b  
c 100 136 4.8 353 6 CD678777 hp13d03.y  
101 136 4.8 388 9 CNS02086 AL175479 Tetraodon  
102 136 4.8 425 7 CN831880 AGENCOURT  
103 136 4.8 472 7 CK241530 rx30f12.y  
104 136 4.8 474 2 BF726322 by04h07.y  
105 136 4.8 556 7 CK791071 AGENCOURT  
106 136 4.8 614 1 AV717179 AV717179  
107 136 4.8 705 5 BU554894 AGENCOURT  
108 136 4.8 820 7 CD403732 AGENCOURT  
109 136 4.8 854 5 BU555510 AGENCOURT  
110 136 4.8 953 5 BU159214 AGENCOURT  
111 136 4.8 1026 8 AZ546693 ENTPR96TF  
112 135 4.7 160 5 BU761067 sa62e05.y  
113 135 4.7 167 7 CR557934  
114 135 4.7 170 7 CR559085  
115 135 4.7 172 1 AA638754 vm94b12.r  
116 135 4.7 172 9 CNS020RQ AL175967 Tetraodon  
117 135 4.7 178 7 CO180729 EC03492.5  
118 135 4.7 180 7 CO192489 EC033879.5  
119 135 4.7 183 1 AJ796704 AJ796704  
120 135 4.7 188 4 BF971016 BF971016 602270336  
121 135 4.7 188 6 CA935203 CA935203 sau50c03.y  
122 135 4.7 190 7 CR539079 DKF2p459A CR559081 DKF2p468C  
123 135 4.7 192 7 CR559081 DKF2p468C  
124 135 4.7 195 5 BQ389262 NISC mc06  
125 135 4.7 196 6 CA819430 sau78c12.  
126 135 4.7 197 2 AW100960 ed63906.y  
127 135 4.7 198 7 CR766521 DKF2p469L  
128 135 4.7 208 4 BJ901084 BJ901084 lb84g08.y  
129 135 4.7 216 4 BJ311098 BJ311098  
130 135 4.7 216 6 CB073167 taa29c09.  
131 135 4.7 217 7 CR545913 CR545913 DKF2p470D  
132 135 4.7 226 6 CA819138 sau69f11.  
133 135 4.7 228 7 CF216003 CF216003 CAST0002  
134 135 4.7 230 7 CO180224 CO180224 EC01250.5  
135 135 4.7 234 7 CK430621 CK430621 oj51g01.y  
136 135 4.7 257 5 BX476287 BX476287 DKF2p686F  
137 135 4.7 259 2 AW100693 AW100693 sd58909.y  
138 135 4.7 259 5 BX250050 BX250050  
139 135 4.7 262 7 CF804520 lad74e09.  
140 135 4.7 263 7 CO989546 UMC-pd3en  
141 135 4.7 265 4 BI674494 sah96g05.  
142 135 4.7 267 7 CO184366 CO184366 EC27977.5  
143 135 4.7 269 6 CD638413 CD638413 AGENCOURT  
144 135 4.7 270 2 AW101788 AW101788 sd70d09.y  
145 135 4.7 272 7 CR655115 CR655115 AGENCOURT  
146 135 4.7 278 7 CO192919 CO192919 EC34778.5  
147 135 4.7 289 7 CK429678 CK429678 oj39g11.y  
148 135 4.7 290 7 CR771988 CR771988 DKF2p4680  
149 135 4.7 295 2 BF883916 BF883916 IL3-Et011  
150 135 4.7 297 7 CO180424 CO180424 EC01537.5  
151 135 4.7 298 7 CO184759 CO184759 EC28526.5  
152 135 4.7 301 7 CV042729 CV042729 dba10g08.  
153 135 4.7 302 2 AW100887 ad62f09.y  
154 135 4.7 303 7 CO752990 CO752990 Mdf3022e  
155 135 4.7 307 7 CV525614 Mdlv40120  
156 135 4.7 308 5 BX506616 BX506616 DKF2p779D  
157 135 4.7 310 4 BJ703028 BJ703028  
158 135 4.7 312 7 CK900688 CK900688 TSL9 Taiw  
159 135 4.7 313 5 BM897446 BM897446 pha1e09.y  
160 135 4.7 315 9 CNS022R1 AL178534 Tetraodon  
161 135 4.7 317 5 BQ599878 BQ599878 MI-P-E6-a  
162 135 4.7 319 1 AL121270 AL121270 DKF2p7621  
163 135 4.7 320 5 BQ261271 BQ261271 fz72a05.y  
164 135 4.7 323 4 BI709353 BI709353 fs63e06.y  
165 135 4.7 324 5 BU588095 BU588095 AGENCOURT  
166 135 4.7 339 7 CO192197 CO192197 EC33332.5  
167 135 4.7 351 7 CK378884 CK378884 la127f04.  
168 135 4.7 356 6 CB722234 jnn609B07  
169 135 4.7 361 7 CK005157 CK005157 AGENCOURT  
170 135 4.7 364 7 CK430797 CK430797 oj54a08.y

171 135 4.7 370 4 BG610096 BG610096  
172 135 4.7 373 7 CK429577 CK429577 oj38e03.y  
173 135 4.7 388 7 CV524829 CV524829 Mdlv2 402  
174 135 4.7 389 7 CK430907 CK430907  
175 135 4.7 395 7 CO184785 CO184785 EC28572.5  
176 135 4.7 409 6 CD052287 CD052287 EST1546 Z  
177 135 4.7 409 9 CNS02V5X AL215358 Tetraodon  
178 135 4.7 411 2 BF781925 BF781925 602105876  
179 135 4.7 422 6 CD679816 CD679816 lab08f08.  
180 135 4.7 462 6 CA334925 CA334925 NISC\_lt03  
181 135 4.7 462 9 CNS04PPQ AL301607 Tetraodon  
182 135 4.7 463 6 CB445238 CB445238 696490 MA  
183 135 4.7 466 7 CO168381 CO168381 Mdf3021m  
184 135 4.7 469 7 CK429230 CK429230 oj33h02.y  
185 135 4.7 481 7 CN838053 CN838053 AGENCOURT  
186 135 4.7 485 7 CR767537 CR767537 DKF2p468C  
187 135 4.7 487 1 AV755581 AV755581 AV755581  
188 135 4.7 494 9 CR128493 CR128493 Forward s  
189 135 4.7 509 6 CA374148 CA374148 648459 NC  
190 135 4.7 533 1 AV756477 AV756477  
191 135 4.7 536 9 CNS037X4 AL231889 Tetraodon  
192 135 4.7 551 4 BG926438 BG926438 HNC62-1-B  
193 135 4.7 593 5 BP743369 BP743369 BP743369  
194 135 4.7 606 7 CO898232 CO898232 Mdf3021m  
195 135 4.7 611 7 CV064412 CV064412 WNEL10f4  
196 135 4.7 613 7 CK005475 CK005475 AGENCOURT  
197 135 4.7 623 6 CD770235 CD770235 AGENCOURT  
198 135 4.7 635 6 CD773201 CD773201 AGENCOURT  
199 135 4.7 650 6 CD773004 CD773004 AGENCOURT  
200 135 4.7 651 6 CD433621 CD433621 EL01N0313  
201 135 4.7 661 6 CD641297 CD641297 AGENCOURT  
202 135 4.7 671 4 BG029399 BG029399 602296828  
203 135 4.7 730 2 BE513622 BE513622 601504411  
204 135 4.7 738 7 CF285052 CF285052 AGENCOURT  
205 135 4.7 756 7 CF290080 CF290080 AGENCOURT  
206 135 4.7 782 2 BE967113 BE967113 601660642  
207 135 4.7 793 5 BU555575 BU555575 AGENCOURT  
208 135 4.7 793 5 BU844017 BU844017 AGENCOURT  
209 135 4.7 832 5 BU529282 BU529282 AGENCOURT  
210 135 4.7 837 9 CNS060EL AL407971 T3 end of  
211 135 4.7 844 5 BU603787 BU603787 AGENCOURT  
212 135 4.7 847 5 BU954608 BU954608 AGENCOURT  
213 135 4.7 847 5 CK196959 CK196959 FGAS00542  
214 135 4.7 848 7 CV064704 CV064704 WNEL14b12  
215 135 4.7 863 2 BE964633 BE964633 601658560  
216 135 4.7 863 5 BU842140 BU842140 AGENCOURT  
217 135 4.7 868 5 BU955256 BU955256 AGENCOURT  
218 135 4.7 868 7 CN385261 CN385261 LE2FR03C0  
219 135 4.7 877 6 CD517184 CD517184 AGENCOURT  
220 135 4.7 898 6 CD251269 CD251269 AGENCOURT  
221 135 4.7 913 5 BU563702 BU563702 AGENCOURT  
222 135 4.7 916 5 BU588527 BU588527 AGENCOURT  
223 135 4.7 918 7 CV069762 CV069762 WPAEhuk15  
224 135 4.7 924 5 BQ960177 BQ960177 AGENCOURT  
225 135 4.7 924 5 BU555708 BU555708 AGENCOURT  
226 135 4.7 941 8 AZ539217 AZ539217 ENTRJ48TF  
227 135 4.7 941 8 BF968041 BF968041 602269570  
228 135 4.7 943 4 BF968041 BF968041 602269570  
229 135 4.7 945 6 CB202961 CB202961 AGENCOURT  
230 135 4.7 948 6 CA476817 CA476817 AGENCOURT  
231 135 4.7 975 5 BU555889 BU555889 AGENCOURT  
232 135 4.7 983 6 CD386907 CD386907 AGENCOURT  
233 135 4.7 989 4 BM415116 BM415116 OP20188 M  
234 135 4.7 995 6 CA476250 CA476250 AGENCOURT  
235 135 4.7 1016 5 BQ718364 BQ718364 AGENCOURT  
236 135 4.7 1022 3 BC050966 BC050966 Mus musecu  
237 135 4.7 1065 6 CA476982 CA476982 AGENCOURT  
238 135 4.7 1071 6 CD050614 CD050614 AGENCOURT  
239 135 4.7 1079 9 CNS035IX AL228786 Tetraodon  
240 135 4.7 1101 9 CNS0021U AL061936 Drosophil  
241 135 4.7 1134 4 BM804069 BM804069 AGENCOURT  
242 135 4.7 1165 9 CL082700 CL082700 CH216-169  
243 135 4.7 1189 5 BQ049769 BQ049769 AGENCOURT



C 244	135	4.7	1211	5	BQ929879	BQ929879	AGENCYCOURT	C 317	134	4.7	212	4	BM638146	BM638146	170006875
245	135	4.7	1213	5	BQ718626	BQ718626	AGENCYCOURT	318	134	4.7	214	5	BU760607	BU760607	sauss509.
246	135	4.7	1214	5	BU167807	BU167807	AGENCYCOURT	319	134	4.7	215	6	CA819195	CA819195	sauss509.
247	135	4.7	1225	9	CL078581	CL078581	CH216-151	320	134	4.7	216	2	BR048071	BR048071	tz47f01.y
C 248	135	4.7	1226	9	AG365340	AG365340	Mus muscu	321	134	4.7	217	7	CR765974	CR765974	DKF2p468N
C 249	135	4.7	1280	9	AG347131	AG347131	Mus muscu	322	134	4.7	218	5	BK645556	BK645556	DKF2p781P
C 250	135	4.7	1316	9	AG381842	AG381842	Mus muscu	323	134	4.7	219	1	AI945904	AI945904	b618b09.y
C 251	135	4.7	1324	9	CL078591	CL078591	CH216-151	324	134	4.7	219	4	BG361185	BG361185	SG62b04.y
C 252	135	4.7	1324	9	CL078591	CL078591	CH216-151	325	134	4.7	219	5	BK255540	BK255540	EX255540
C 253	135	4.7	1390	9	CL647502	CL647502	CH213-139	326	134	4.7	221	7	CR290189	CR290189	170006000
C 254	135	4.7	1409	6	CD049654	CD049654	AGENCYCOURT	327	134	4.7	221	1	AI868831	AI868831	wc58h03.x
255	135	4.7	1430	4	BM805984	BM805984	AGENCYCOURT	328	134	4.7	222	1	AI868831	AI868831	BJ047503
256	135	4.7	1550	3	BC049704	BC049704	Mus muscu	329	134	4.7	222	4	BM186176	BM186176	fv98h07.y
257	135	4.7	1596	8	CC293489	CC293489	CH261-62N	330	134	4.7	222	5	BQ085944	BQ085944	1112b02.y
258	135	4.7	1654	9	CL118709	CL118709	ISB1-7211	331	134	4.7	222	6	CA935086	CA935086	sauss4b10.
259	135	4.7	1761	8	CC188336	CC188336	CH261-70H	332	134	4.7	223	1	AL697974	AL697974	DKF2p686J
260	135	4.7	1899	3	BC061196	BC061196	Mus muscu	333	134	4.7	223	4	BU927029	BU927029	sauss4g09.
261	135	4.7	2007	3	HSB807665	HSB807665	Mus muscu	334	134	4.7	224	5	BU927029	BU927029	sauss4g09.
262	135	4.7	2596	3	BC053452	BC053452	Mus muscu	335	134	4.7	224	6	CA935085	CA935085	sauss4b08.
263	135	4.7	3028	3	HSB801560	HSB801560	Mus muscu	336	134	4.7	224	6	CD721912	CD721912	0j03a11.y
264	135	4.7	3145	3	BC027896	BC027896	Homo sapi	337	134	4.7	225	4	BM155365	BM155365	fw03e12.y
265	135	4.7	3226	3	CR627326	CR627326	Homo sapi	338	134	4.7	225	4	BM186096	BM186096	fv97h07.y
266	135	4.7	3270	3	CR749650	CR749650	Homo sapi	339	134	4.7	225	4	BM811854	BM811854	fx11c08.y
267	135	4.7	4643	3	CR749348	CR749348	Homo sapi	340	134	4.7	226	7	CR547597	CR547597	DKF2p459M
268	135	4.7	4793	3	CR749666	CR749666	Homo sapi	341	134	4.7	226	4	BM533163	BM533163	fx68f08.y
C 269	134	4.7	8296	3	CR749511	CR749511	Homo sapi	342	134	4.7	229	4	BM532465	BM532465	fy08e01.y
270	134	4.7	150	2	BE964700	BE964700	CGF100428	343	134	4.7	230	5	BQ075932	BQ075932	fz10e11.y
271	134	4.7	152	7	CK933635	CK933635	CGF100428	344	134	4.7	230	2	AW101750	AW101750	sd69g09.y
272	134	4.7	156	6	CA335198	CA335198	NISC 1c07	345	134	4.7	230	4	BJ697384	BJ697384	BJ697384
273	134	4.7	157	5	BK475990	BK475990	NISC 1c07	346	134	4.7	231	2	AW733931	AW733931	8k85c03.y
274	134	4.7	160	5	BK645532	BK645532	NISC 1c07	347	134	4.7	232	2	BE190203	BE190203	sc08h07.y
C 275	134	4.7	161	7	CR557780	CR557780	DKF2p468B	348	134	4.7	232	4	BM155357	BM155357	fw03c02.y
276	134	4.7	162	4	BY745065	BY745065	rkx9508.y	349	134	4.7	232	4	BM155357	BM155357	fw03c02.y
277	134	4.7	163	1	CLN01762	CLN01762	Tetraodon	350	134	4.7	233	7	CK376983	CK376983	lah7ze12.
C 278	134	4.7	164	4	BM539426	BM539426	hb09c07.y	351	134	4.7	233	1	AI443075	AI443075	sa47a11.y
C 279	134	4.7	167	6	CR045764	CR045764	NISC 1c07	352	134	4.7	233	2	AW101785	AW101785	sd70d01.y
C 280	134	4.7	169	7	CR791760	CR791760	DKF2p468F	353	134	4.7	238	5	BK476126	BK476126	DKF2p686H
C 281	134	4.7	177	2	BE964812	BE964812	601658467	354	134	4.7	238	6	CB079729	CB079729	hp75f10.b
282	134	4.7	178	5	BM888959	BM888959	bm03c03.y	355	134	4.7	239	7	BE013300	BE013300	1230009.NA
283	134	4.7	179	5	BK956705	BK956705	DKF2p781M	356	134	4.7	239	7	CK376983	CK376983	lah7ze12.
284	134	4.7	182	1	BM697655	BM697655	DKF2p686A	357	134	4.7	240	7	CR046048	CR046048	DKF2p468P
C 285	134	4.7	183	7	CO893077	CO893077	Bovsen.21	358	134	4.7	241	6	CR046048	CR046048	DKF2p468P
286	134	4.7	184	6	CA935285	CA935285	sauss1f03.	359	134	4.7	242	2	BE059705	BE059705	NISC 9c05
287	134	4.7	185	6	CA935579	CA935579	sauss1f03.	360	134	4.7	242	7	CR629082	CR629082	DKF2p468K
C 288	134	4.7	187	6	CA674774	CA674774	w1eu2.pk0	361	134	4.7	243	7	CO747844	CO747844	ShESTbaas
C 289	134	4.7	187	6	CB099929	CB099929	py18h06.y	362	134	4.7	244	4	BM573234	BM573234	fy01d08.y
290	134	4.7	187	7	CR771877	CR771877	DKF2p468C	363	134	4.7	244	6	CB938710	CB938710	IdCGJx13
291	134	4.7	188	6	CA819358	CA819358	sauss7b11.	364	134	4.7	244	7	CO182898	CO182898	EC24236.5
C 292	134	4.7	189	1	AJ798430	AJ798430	sauss7b11.	365	134	4.7	245	4	BI840174	BI840174	fw70d09.y
293	134	4.7	189	6	CA935078	CA935078	sauss4a10.	366	134	4.7	245	4	BM342819	BM342819	fw48d03.y
294	134	4.7	190	4	BG036846	BG036846	602326790	367	134	4.7	245	5	BK951835	BK951835	DKF2p781A
295	134	4.7	192	4	BM093800	BM093800	sauss20h11.	368	134	4.7	245	4	BJ745342	BJ745342	BJ745342
296	134	4.7	192	7	CF3227002	CF3227002	NACL--01-	369	134	4.7	248	1	AJ768204	AJ768204	sauss4a10.
297	134	4.7	193	4	BG156523	BG156523	sauss10e12.	370	134	4.7	248	4	BM154574	BM154574	fv86g03.y
298	134	4.7	193	5	BK955696	BK955696	DKF2p781C	371	134	4.7	249	6	BM187301	BM187301	sauss4b05.y
299	134	4.7	193	6	CA819599	CA819599	sauss7b02.	372	134	4.7	249	6	CA935136	CA935136	sauss4b05.y
300	134	4.7	195	4	BM186912	BM186912	fv79e10.y	373	134	4.7	251	4	BM573771	BM573771	fv03e10.y
301	134	4.7	196	2	BR795712	BR795712	602259590	374	134	4.7	252	7	CF212181	CF212181	CGF100066
302	134	4.7	198	5	BK667440	BK667440	pb61e09.y	375	134	4.7	252	7	CR525101	CR525101	DKF2p453L
C 303	134	4.7	201	6	CB045621	CB045621	NISC 1c07	376	134	4.7	255	7	CR525101	CR525101	DKF2p453L
304	134	4.7	201	7	CF613757	CF613757	CESS008061	377	134	4.7	256	7	CO168373	CO168373	Mdf3003o
305	134	4.7	203	2	AW100931	AW100931	sd63d04.y	378	134	4.7	257	4	BM582842	BM582842	170006872
306	134	4.7	203	5	BK470454	BK470454	DKF2p686A	379	134	4.7	257	7	CF804375	CF804375	lad7f112.
307	134	4.7	206	7	CO938248	CO938248	UMC-pd14c	380	134	4.7	261	2	BF724691	BF724691	bx07f11.x
C 308	134	4.7	207	1	AI433376	AI433376	tl12c12.x	381	134	4.7	261	4	BM154485	BM154485	fv85g02.y
309	134	4.7	207	6	CB721787	CB721787	op01e04.f	382	134	4.7	261	6	CF071153	CF071153	FE1.15.F1
310	134	4.7	208	1	AL697778	AL697778	DKF2p686P	383	134	4.7	261	7	CK937009	CK937009	CGF100451
311	134	4.7	208	6	CA802715	CA802715	sauss4a12.	384	134	4.7	263	5	BM900884	BM900884	rc42f02.y
312	134	4.7	209	7	CP804603	CP804603	lad76b09.	385	134	4.7	263	6	CB722227	CB722227	170006000
313	134	4.7	209	7	CO417475	CO417475	Mdf+3012j	386	134	4.7	265	7	CM275140	CM275140	fv87e09.y
314	134	4.7	211	7	CM549956	CM549956	Q00244.B3	387	134	4.7	266	4	BM154640	BM154640	fv90d09.y
315	134	4.7	212	2	AW101775	AW101775	sd70b04.y	388	134	4.7	268	4	BM154858	BM154858	DKF2p468H
C 316	134	4.7	212	4	BM599268	BM599268	170006690	389	134	4.7	269	7	CR766078	CR766078	DKF2p468H

330	134	4.7	271	7	CF755569	lae43all.	463	134	4.7	333	7	CO184639	CO184639	EC28357.5
331	134	4.7	272	1	AJ799419	AJ799419	464	134	4.7	334	2	BE806983	BE806983	se0e10.y
332	134	4.7	272	7	CF510988	CABud0001	C 465	134	4.7	334	4	BM496453	BM496453	IPcGBx2.1
333	134	4.7	272	7	CK428530	laJ28d05.	C 466	134	4.7	339	5	EX551395	EX551395	EX551395
334	134	4.7	272	7	COL84738	EC28495.5	467	134	4.7	339	7	CO182353	CO182353	EC22486.5
335	134	4.7	272	7	CR630238	DKF2p4690	468	134	4.7	341	5	EX953635	EX953635	DKF2p781M
336	134	4.7	272	2	BE0133212	123085 MA	C 469	134	4.7	342	6	CB080456	CB080456	hp86h08.b
337	134	4.7	273	7	CF635575	zmrw00.0	470	134	4.7	343	7	CV525143	MD1v4010m	CV525143
338	134	4.7	274	5	BQ298677	sa049a05	471	134	4.7	344	6	CB721972	jnn603C04	CB721972
339	134	4.7	277	7	CO185085	EC29302.5	472	134	4.7	346	7	CO416889	MDf30119	CO416889
400	134	4.7	279	4	B1671444	fs48d07.y	473	134	4.7	347	2	BE785905	601477905	BE785905
401	134	4.7	279	5	BQ242916	TaeE15021F	474	134	4.7	347	5	EX506028	DKF2p686P	EX506028
402	134	4.7	280	4	BM532335	fy05f11.y	475	134	4.7	348	4	BJ696950	BJ696950	BJ696950
403	134	4.7	280	6	CA802930	sau44d08.	476	134	4.7	348	6	CB704555	AMGNNUC.N	CB704555
404	134	4.7	280	7	CK975391	4106215.B	477	134	4.7	348	7	CO191264	EC30590.5	CO191264
405	134	4.7	281	6	CA934992	sau62C06.	478	134	4.7	352	5	BU760774	sas58c11.	BU760774
406	134	4.7	282	1	AJ774701	AJ774701	479	134	4.7	353	5	BU081852	sar01d06.	BU081852
407	134	4.7	282	7	CR559176	DKF2p468F	480	134	4.7	358	5	EX505899	DKF2p686P	EX505899
408	134	4.7	285	6	CA334895	NISC 1102	481	134	4.7	363	6	CA468702	734551 MA	CA468702
409	134	4.7	285	7	CR791521	DKF2p468L	C 482	134	4.7	364	6	CB409286	NISC nc04	CB409286
410	134	4.7	287	5	EX503626	DKF2p686G	483	134	4.7	364	7	CK375041	lai44b01.	CK375041
411	134	4.7	287	7	CO748478	SnESTbaa7	484	134	4.7	364	7	CR789952	DKF2p459L	CR789952
412	134	4.7	289	7	CR559200	DKF2p468F	485	134	4.7	365	5	BM966550	ko09a03.y	BM966550
413	134	4.7	291	2	AW459750	sh91f03.y	C 486	134	4.7	368	1	AI500553	AGENCOURT	AI500553
414	134	4.7	291	4	BJ697356	BJ697356	487	134	4.7	369	6	CD638357	AGENCOURT	CD638357
415	134	4.7	292	5	BU760770	sas58c07.	488	134	4.7	369	7	CF644109	K17 A10 F	CF644109
416	134	4.7	292	7	CO191848	EC32243.5	489	134	4.7	373	2	BE057180	sm97f06.y	BE057180
417	134	4.7	293	2	BE023554	BE023554	C 490	134	4.7	376	6	CB084484	hq16a10.b	CB084484
418	134	4.7	294	1	AL706899	DKF2p686A	491	134	4.7	376	7	CK004038	AGENCOURT	CK004038
419	134	4.7	294	1	AL725181	AL725181	C 492	134	4.7	377	1	AI863014	wm45c09.x	AI863014
420	134	4.7	294	2	AW101221	sd75f11.y	493	134	4.7	378	1	AV762488	AV762488	AV762488
421	134	4.7	294	6	CB045066	NISC 9C08	494	134	4.7	379	2	AW117882	xe38c06.x	AW117882
422	134	4.7	295	2	BE013898	125413 MA	495	134	4.7	379	7	CK937918	QGF100448	CK937918
423	134	4.7	295	6	CB641171	AGENCOURT	496	134	4.7	380	6	CD243157	AGENCOURT	CD243157
424	134	4.7	299	1	AJ7988370	AJ7988370	497	134	4.7	380	7	CK933848	CGF100427	CK933848
425	134	4.7	299	5	BU760890	sas60a07.	498	134	4.7	386	6	CB939082	IPcGJx13	CB939082
426	134	4.7	300	7	CK429583	oj38e10.y	500	134	4.7	387	7	CF426295	lad22b03.	CF426295
427	134	4.7	301	6	CA802821	sau42902.	501	134	4.7	388	6	CA345950	676724 NC	CA345950
428	134	4.7	302	7	CF253048	mdv004_e0	502	134	4.7	389	3	EC022358	Homo sapi	EC022358
429	134	4.7	302	7	CB831978	AGENCOURT	C 503	134	4.7	389	6	CB044164	NISC 9C02	CB044164
430	134	4.7	305	6	CD672586	fg13h02.x	504	134	4.7	389	7	CR537555	DKF2p459J	CR537555
431	134	4.7	306	4	BI945447	sbj86j12.y	505	134	4.7	390	4	AG896775	HOA50-1-A	AG896775
432	134	4.7	307	6	CD722153	oj06b12.y	C 506	134	4.7	391	1	AI690751	tx88h11.x	AI690751
433	134	4.7	307	6	CD722153	oj06b12.y	C 507	134	4.7	391	5	BQ527112	NISC nc20	BQ527112
434	134	4.7	309	4	BM874527	laai1h09	C 508	134	4.7	391	6	CB721942	jnn602H03	CB721942
435	134	4.7	309	7	CA414161	170005339	509	134	4.7	392	7	CO370974	taH67904.	CO370974
436	134	4.7	310	7	CR559169	DKF2p468L	C 510	134	4.7	396	5	EX473239	AV711509	EX473239
437	134	4.7	310	7	CR752937	DKF2p468F	511	134	4.7	396	1	AV711509	AV711509	AV711509
438	134	4.7	311	4	BM154732	fv88f10.y	512	134	4.7	398	2	BE048081	tz47g03.y	BE048081
439	134	4.7	311	4	BM154818	fv89h02.y	513	134	4.7	398	6	CB722395	jnn612A04	CB722395
440	134	4.7	311	7	CF321259	HD--12-H0	514	134	4.7	398	7	CK375940	lah76h05.	CK375940
441	134	4.7	311	7	CO182176	EC22214.5	C 515	134	4.7	399	1	AI226246	ue8h04.y	AI226246
442	134	4.7	314	1	AL697923	DKF2p686D	516	134	4.7	399	6	CD673835	fs05b06.x	CD673835
443	134	4.7	314	2	BE047863	tz43c10.y	C 517	134	4.7	400	4	BG553256	DAF23h02.	BG553256
444	134	4.7	316	6	CD639207	AGENCOURT	518	134	4.7	402	1	AL698015	DKF2p686N	AL698015
445	134	4.7	318	5	EX500893	DKF2p779B	519	134	4.7	402	7	BF726297	by04e10.y	BF726297
446	134	4.7	319	5	EX489110	DKF2p686J	520	134	4.7	402	7	CR791705	DKF2p468P	CR791705
447	134	4.7	320	2	AW509353	s122a03.y	521	134	4.7	403	6	CB768447	AMGNNUC:M	CB768447
448	134	4.7	320	9	CNS01E1H	Anopheles	522	134	4.7	403	7	CK626362	mj21a12.y	CK626362
449	134	4.7	321	7	CO417155	MDf30111	C 523	134	4.7	405	1	AI567632	tp62c08.x	AI567632
450	134	4.7	323	4	BG237484	sab07b11.	C 524	134	4.7	406	5	BQ526114	NISC no14	BQ526114
451	134	4.7	323	6	CB410191	NISC nc10	C 525	134	4.7	408	7	CR770942	DKF2p469G	CR770942
452	134	4.7	323	6	CB430419	606310 MA	C 526	134	4.7	409	6	CB054205	NISC_gm03	CB054205
453	134	4.7	326	4	BM154967	fv91h04.y	527	134	4.7	410	4	CK983358	re24a04.y	CK983358
454	134	4.7	327	6	CD723900	oj27g11.y	528	134	4.7	411	7	BM532515	fy09b01.y	BM532515
455	134	4.7	327	6	CB721391	jnn606F09	529	134	4.7	413	5	EX953260	DKF2p781H	EX953260
456	134	4.7	328	7	CR767432	DKF2p468H	530	134	4.7	414	7	CO871032	rt66g04.y	CO871032
457	134	4.7	329	7	CO183457	EC25753.5	531	134	4.7	415	7	CO192413	EC31671.5	CO192413
458	134	4.7	330	7	CK623571	mi11b03.y	532	134	4.7	416	7	CB834026	AGENCOURT	CB834026
459	134	4.7	331	4	BG155453	sab44d04.	C 533	134	4.7	417	6	CB053341	NISC_g113	CB053341
460	134	4.7	331	5	BU860679	AGENCOURT	534	134	4.7	419	7	CF511730	CABud0002	CF511730
461	134	4.7	332	7	CO185234	EC39979.5	C 535	134	4.7	421	5	BQ396582	NISC_ng21	BQ396582
462	134	4.7	332	7	CV122318	MD1v4003e								

536	134	4.7	424	1	AV682809	AV682809	AV682809	134	4.7	535	5	BQ527144	BQ527144	NISC_no20
c 537	134	4.7	426	6	CD678845	CD678845	hq01b011.x	134	4.7	538	7	CO752656	CO752656	Mdf3025c
c 538	134	4.7	429	7	CK997642	CK997642	ip21c10.1.b	134	4.7	540	7	CF123120	CF123120	UI-HF-CH0
c 539	134	4.7	431	6	CB410125	NISC_nc09	CB410125	134	4.7	542	6	CD796549	EST667910	EST667910
c 540	134	4.7	431	6	CO191531	EC31328.5	CO191531	134	4.7	545	7	CV223275	taj59h05	taj59h05
c 541	134	4.7	433	7	CR835159	AGENCOURT	CR835159	134	4.7	546	7	CF370112	kg48c10.y	kg48c10.y
c 542	134	4.7	435	7	CR753204	DXFzp480	CR753204	134	4.7	549	6	CB523098	CB523098	UI-M-GK0
c 543	134	4.7	436	6	CB817673	d3o23pz.f	CB817673	134	4.7	549	7	CF754275	EST-77-2-	EST-77-2-
c 544	134	4.7	437	7	CF358365	rm89f08.y	CF358365	134	4.7	550	7	CK426429	rx15c08.y	rx15c08.y
c 545	134	4.7	437	7	CV525154	MD1v4010a	CV525154	134	4.7	552	7	CK426429	rx15c08.y	rx15c08.y
c 546	134	4.7	438	6	CB075288	hz42a10.b	CB075288	134	4.7	557	6	CB089052	if09c01.b	if09c01.b
c 547	134	4.7	441	7	CK428352	la1j4906	CK428352	134	4.7	557	6	CB089052	if09c01.b	if09c01.b
c 548	134	4.7	443	5	BQ637878	hd15f11.y	BQ637878	134	4.7	558	7	CK118076	218d01.pl	218d01.pl
c 549	134	4.7	447	6	CB723709	UI-M-GK0-	CB723709	134	4.7	559	6	CB376949	HB02A03.L	HB02A03.L
c 550	134	4.7	451	7	CV525442	Mdlv4011d	CV525442	134	4.7	564	7	CO722540	Mdf30171	Mdf30171
c 551	134	4.7	452	3	BC050981	Mus muscu	BC050981	134	4.7	565	5	BX549733	BX549733	BX549733
c 552	134	4.7	453	7	CK005374	AGENCOURT	CK005374	134	4.7	565	7	CF612717	lae95q12	lae95q12
c 553	134	4.7	459	5	BX953619	DKF2p781K	BX953619	134	4.7	568	4	BG929104	HNC33-1-H	HNC33-1-H
c 554	134	4.7	461	5	BX472677	DKF2p686I	BX472677	134	4.7	569	7	CV222905	taj54d02	taj54d02
c 555	134	4.7	462	6	CA394496	cs2b212.y	CA394496	134	4.7	575	6	CB054849	NISC_gm06	NISC_gm06
c 556	134	4.7	463	7	CR790920	DKF2p4691	CR790920	134	4.7	577	6	CB044223	NISC_gc03	NISC_gc03
c 557	134	4.7	464	6	CF041960	CF041960	CF041960	134	4.7	578	6	CB051669	NISC_g102	NISC_g102
c 558	134	4.7	466	6	CB044446	NISC_gc04	CB044446	134	4.7	580	6	CB088637	if03f11.b	if03f11.b
c 559	134	4.7	468	6	CB721944	jnm502H05	CB721944	134	4.7	580	7	CV223330	taj50g10	taj50g10
c 560	134	4.7	470	5	BX554535	NISC_n121	BX554535	134	4.7	581	7	CO067712	Mdf3014p	Mdf3014p
c 561	134	4.7	471	5	BQ523226	NISC_n121	BQ523226	134	4.7	582	4	BG925169	HNC39-1-G	HNC39-1-G
c 562	134	4.7	475	6	CB089293	qs07d05.b	CB089293	134	4.7	582	7	CV222884	taj54b02	taj54b02
c 563	134	4.7	476	5	BQ399811	NISC_mp05	BQ399811	134	4.7	585	2	BF673434	602136211	602136211
c 564	134	4.7	477	6	CD677843	ho23b03.y	CD677843	134	4.7	585	7	CO403863	AGENCOURT	AGENCOURT
c 565	134	4.7	478	7	CO722515	Mdf3017c	CO722515	134	4.7	587	3	AF116639	Homo_sapi	Homo_sapi
c 566	134	4.7	479	6	CA335089	NISC_l106	CA335089	134	4.7	589	1	A1207510	HA2865_Hu	HA2865_Hu
c 567	134	4.7	480	7	CO191784	EC31982.5	CO191784	134	4.7	590	6	CB937830	IPCGJX13	IPCGJX13
c 568	134	4.7	482	6	CV122300	Mdlv4003a	CV122300	134	4.7	594	7	CV065309	WNE120H4	WNE120H4
c 569	134	4.7	486	6	CB044432	NISC_gc04	CB044432	134	4.7	594	7	CV0507247	klc13cl1.y	klc13cl1.y
c 570	134	4.7	486	7	CK379180	lai1j906	CK379180	134	4.7	596	7	CV199662	km18b02.y	km18b02.y
c 571	134	4.7	488	7	CF755040	lae51g03	CF755040	134	4.7	600	5	BQ391797	NISC_mq20	NISC_mq20
c 572	134	4.7	489	7	CO417069	CO417069	CO417069	134	4.7	602	7	CO415672	Mdf3007b	Mdf3007b
c 573	134	4.7	491	5	BQ525482	NISC_no10	BQ525482	134	4.7	606	7	CK619769	mk28b09.y	mk28b09.y
c 574	134	4.7	491	6	CD722238	oj07b10.y	CD722238	134	4.7	608	4	BG678047	602625771	602625771
c 575	134	4.7	491	7	CF123999	UI-HF-CH0	CF123999	134	4.7	613	7	CV121985	MD1v4002b	MD1v4002b
c 576	134	4.7	491	7	CO866143	Mdf3020c	CO866143	134	4.7	618	6	CD676511	ho01h07.x	ho01h07.x
c 577	134	4.7	491	9	CNS0359Q	Tetraodon	AL228455	134	4.7	620	5	BQ393958	NISC_ng06	NISC_ng06
c 578	134	4.7	494	7	CV525345	MD1v40111	CV525345	134	4.7	626	6	CD771746	AGENCOURT	AGENCOURT
c 579	134	4.7	495	5	BX504818	DKF2p686K	BX504818	134	4.7	626	7	CO069285	Mdf3015g	Mdf3015g
c 580	134	4.7	495	6	CD236950	FNPAEG11	CD236950	134	4.7	627	7	CK837813	4063204.B	4063204.B
c 581	134	4.7	495	7	CO752765	Mdf3025b	CO752765	134	4.7	630	4	BI651834	603299838	603299838
c 582	134	4.7	499	1	AL119748	DKF2p761C	AL119748	134	4.7	631	7	CF330508	NACL--06-	NACL--06-
c 583	134	4.7	501	5	BF742677	BP742677	BP742677	134	4.7	634	7	CK120520	207911.pl	207911.pl
c 584	134	4.7	501	5	BQ392601	NISC_mq25	BQ392601	134	4.7	634	7	CK120520	207911.pl	207911.pl
c 585	134	4.7	501	5	BQ396639	NISC_pg22	BQ396639	134	4.7	635	6	CD638395	AGENCOURT	AGENCOURT
c 586	134	4.7	503	6	CA376868	655327_NC	CA376868	134	4.7	637	6	CD766445	AGENCOURT	AGENCOURT
c 587	134	4.7	503	6	CB350381	ACHG165.H	CB350381	134	4.7	637	7	CK005551	AGENCOURT	AGENCOURT
c 588	134	4.7	503	7	CO417413	Mdf30121	CO417413	134	4.7	639	1	A1969601	wz69b11.x	wz69b11.x
c 589	134	4.7	504	5	BQ524016	NISC_no02	BQ524016	134	4.7	639	7	CK459607	929814.MA	929814.MA
c 590	134	4.7	504	5	BQ526248	NISC_no15	BQ526248	134	4.7	640	7	CV065863	WNE127f11	WNE127f11
c 591	134	4.7	504	7	CF513671	CABud0007	CF513671	134	4.7	645	6	CD773631	AGENCOURT	AGENCOURT
c 592	134	4.7	506	7	CK430668	oj52c07.y	CK430668	134	4.7	647	7	CV222879	taj54a03	taj54a03
c 593	134	4.7	507	4	BI437760	ic83d10.y	BI437760	134	4.7	656	7	CV064567	WNE12e4	WNE12e4
c 594	134	4.7	510	5	BQ748115	UI-M-FA0-	BQ748115	134	4.7	659	6	CD640691	AGENCOURT	AGENCOURT
c 595	134	4.7	510	5	CV057219	BNEL25c9	CV057219	134	4.7	659	6	CD640691	AGENCOURT	AGENCOURT
c 596	134	4.7	512	5	BQ266641	NISC_ff14	BQ266641	134	4.7	661	6	CD640938	AGENCOURT	AGENCOURT
c 597	134	4.7	512	5	BQ523234	NISC_n121	BQ523234	134	4.7	663	7	CK242290	rx08a11.y	rx08a11.y
c 598	134	4.7	512	5	BX568557	BX568557	BX568557	134	4.7	667	6	CD638527	AGENCOURT	AGENCOURT
c 599	134	4.7	512	6	CB095854	ie95e09.b	CB095854	134	4.7	669	6	CD638433	AGENCOURT	AGENCOURT
c 600	134	4.7	513	7	CO417018	Mdf3011b	CO417018	134	4.7	670	6	CD642160	AGENCOURT	AGENCOURT
c 601	134	4.7	516	1	AV757012	AV757012	AV757012	134	4.7	671	7	CO898117	Mdf3020d	Mdf3020d
c 602	134	4.7	523	6	CB083179	hm67f10.b	CB083179	134	4.7	673	4	BG259801	602371947	602371947
c 603	134	4.7	523	7	CV525558	MD1v4012k	CV525558	134	4.7	674	4	BG259801	602371947	602371947
c 604	134	4.7	527	7	CV072206	EST4367.Z	CV072206	134	4.7	679	7	CB843802	AGENCOURT	AGENCOURT
c 605	134	4.7	529	1	AV758217	AV758217	AV758217	134	4.7	680	7	CO074617	GR_Ea34N	GR_Ea34N
c 606	134	4.7	532	1	AJ658998	AJ658998	AJ658998	134	4.7	680	7	CO095071	GR_Ea171	GR_Ea171
c 607	134	4.7	534	6	CA336360	NISC_lu12	CA336360	134	4.7	683	1	AV682672	AV682672	AV682672
c 608	134	4.7	535	1	AV757455	AV757455	AV757455	134	4.7	688	7	CO074646	GR_Ea34N	GR_Ea34N

682	134	4.7	689	7	CK003202	CK003202	AGENCOURT	755	134	4.7	871	5	BU529398	BU529398	AGENCOURT
683	134	4.7	690	7	CV065814	WNEI27a11		756	134	4.7	872	5	BU529249	BU529249	AGENCOURT
684	134	4.7	691	7	CV005554	CK005554	AGENCOURT	757	134	4.7	875	5	BU587868	BU587868	AGENCOURT
685	134	4.7	693	6	CD641480	CD641480	AGENCOURT	758	134	4.7	872	5	BU588646	BU588646	AGENCOURT
686	134	4.7	701	7	CV520583	CV520583	0089P0047	759	134	4.7	873	6	CD520987	CD520987	AGENCOURT
687	134	4.7	702	7	CV065824	CV065824	WNEI27b1	760	134	4.7	873	7	CN385475	LE2TR03L1	
688	134	4.7	707	6	CD640765	CD640765	AGENCOURT	761	134	4.7	874	5	BU590078	BU590078	AGENCOURT
689	134	4.7	708	6	CD237931	CD237931	FNPARF04	c 762	134	4.7	874	7	CF783995	CF783995	AGENCOURT
690	134	4.7	710	2	AK349204	AK349204	GM210004A	c 763	134	4.7	875	7	CV068606	f2_new_ch	
691	134	4.7	712	4	BG733805	BG733805	603630530	764	134	4.7	875	7	BU555372	AGENCOURT	
692	134	4.7	713	1	AV733819	AV733819		765	134	4.7	878	7	CK790722	AGENCOURT	
693	134	4.7	713	7	CO870545	CO870545	rt60b09.Y	766	134	4.7	878	7	BU936542	AGENCOURT	
694	134	4.7	714	6	CB339355	CB339355	CA23EI03I	767	134	4.7	884	5	BU850517	AGENCOURT	
695	134	4.7	714	7	CV064496	CV064496	WNEI11f11	768	134	4.7	885	5	BU565751	AGENCOURT	
696	134	4.7	712	6	CD639592	CD639592	AGENCOURT	769	134	4.7	888	5	BU955497	AGENCOURT	
697	134	4.7	724	7	CK460466	CK460466	930744 MA	770	134	4.7	889	5	BU850913	AGENCOURT	
698	134	4.7	726	6	CD639437	CD639437	AGENCOURT	771	134	4.7	889	5	BU963271	AGENCOURT	
699	134	4.7	728	5	BU803096	BU803096	SJFARA03	772	134	4.7	890	5	BU603755	AGENCOURT	
700	134	4.7	729	6	CD640222	CD640222	AGENCOURT	773	134	4.7	893	5	BU851134	AGENCOURT	
701	134	4.7	731	4	BM367453	BM367453	NXLV 049	774	134	4.7	894	5	BQ441805	AGENCOURT	
702	134	4.7	738	4	BG284611	BG284611	602408778	775	134	4.7	894	5	BU588228	AGENCOURT	
703	134	4.7	739	1	AV726951	AV726951		776	134	4.7	895	5	BQ342584	AGENCOURT	
704	134	4.7	748	5	BU942149	BU942149	AGENCOURT	c 777	134	4.7	895	7	CV068617	f2_new_ch	
705	134	4.7	754	7	CO395166	CO395166	AGENCOURT	c 778	134	4.7	897	4	BM415645	BM415645	OP20723 M
706	134	4.7	769	5	BU537812	BU537812	AGENCOURT	779	134	4.7	899	5	BQ218921	AGENCOURT	
707	134	4.7	769	7	CF547327	CF547327	AGENCOURT	780	134	4.7	899	5	BU588232	AGENCOURT	
708	134	4.7	769	7	CV064941	CV064941	WNEI17c10	781	134	4.7	905	6	CB946345	AGENCOURT	
709	134	4.7	770	5	BU537695	BU537695	AGENCOURT	782	134	4.7	907	6	CA977049	AGENCOURT	
710	134	4.7	771	5	BU943072	BU943072	AGENCOURT	783	134	4.7	909	5	BU587993	AGENCOURT	
711	134	4.7	773	7	CV064559	CV064559	WNEI12d8	784	134	4.7	913	5	BQ952206	AGENCOURT	
712	134	4.7	776	5	BU555076	BU555076	AGENCOURT	785	134	4.7	914	5	BU851349	AGENCOURT	
713	134	4.7	778	7	CV066825	CV066825	f2_new_ch	786	134	4.7	921	6	CB844970	M2PN-0536	
714	134	4.7	782	4	B1861670	B1861670	603389343	787	134	4.7	923	5	BU960730	AGENCOURT	
715	134	4.7	785	7	CK790726	CK790726	AGENCOURT	788	134	4.7	924	5	BU960730	OP20389 M	
716	134	4.7	793	6	CD298877	CD298877	AGENCOURT	c 789	134	4.7	926	7	CV068623	f2_new_ch	
717	134	4.7	801	5	BU940225	BU940225	AGENCOURT	790	134	4.7	927	6	CA455489	AGENCOURT	
718	134	4.7	802	5	BU851163	BU851163	AGENCOURT	791	134	4.7	930	5	BU958002	AGENCOURT	
719	134	4.7	804	7	CV066336	CV066336	WNEI32f2	792	134	4.7	931	5	BU960826	AGENCOURT	
720	134	4.7	805	5	BU944935	BU944935	AGENCOURT	c 793	134	4.7	932	4	BG033403	602301577	
721	134	4.7	809	5	BU958264	BU958264	AGENCOURT	c 794	134	4.7	933	7	CV070185	WPAEhux15	
722	134	4.7	809	6	CD559362	CD559362	AGENCOURT	795	134	4.7	937	5	BU193300	AGENCOURT	
723	134	4.7	811	3	BC050987	BC050987	Mus muscu	796	134	4.7	939	5	BQ434577	AGENCOURT	
724	134	4.7	811	6	CD523425	CD523425	AGENCOURT	c 797	134	4.7	939	7	CV068729	f2_new_ch	
725	134	4.7	813	5	BU563257	BU563257	AGENCOURT	798	134	4.7	942	5	BU941184	AGENCOURT	
726	134	4.7	813	7	CK794968	CK794968	AGENCOURT	799	134	4.7	946	6	CA454659	AGENCOURT	
727	134	4.7	814	5	BU530990	BU530990	AGENCOURT	c 800	134	4.7	947	5	CV068644	f2_new_ch	
728	134	4.7	815	5	BU564423	BU564423	AGENCOURT	801	134	4.7	947	5	BQ921561	AGENCOURT	
729	134	4.7	816	5	BU955315	BU955315	AGENCOURT	c 802	134	4.7	952	7	CK151506	FGAS03407	
730	134	4.7	816	5	BU564811	BU564811	AGENCOURT	803	134	4.7	955	5	BU148296	AGENCOURT	
731	134	4.7	817	8	BH156712	BH156712	ENTSM49TF	c 804	134	4.7	961	4	BM416179	OP21266 M	
732	134	4.7	819	5	BU564488	BU564488	AGENCOURT	805	134	4.7	965	5	BQ233225	AGENCOURT	
733	134	4.7	821	5	BU945039	BU945039	AGENCOURT	c 806	134	4.7	966	4	BM415421	OP20495 M	
734	134	4.7	826	5	BU958181	BU958181	AGENCOURT	807	134	4.7	969	5	BQ337042	AGENCOURT	
735	134	4.7	830	5	BU842943	BU842943	AGENCOURT	808	134	4.7	971	5	BQ880542	AGENCOURT	
736	134	4.7	830	5	BU843607	BU843607	AGENCOURT	c 809	134	4.7	972	7	CV068750	f2_new_ch	
737	134	4.7	831	7	CV490005	CV490005	AGENCOURT	810	134	4.7	977	2	BE777769	601463009	
738	134	4.7	832	5	BU540111	BU540111	AGENCOURT	811	134	4.7	979	5	BU176137	AGENCOURT	
739	134	4.7	835	7	CK799632	CK799632	AGENCOURT	c 812	134	4.7	981	6	CD513655	AGENCOURT	
740	134	4.7	837	5	BU536801	BU536801	AGENCOURT	813	134	4.7	995	6	CB756884	AGENCOURT	
741	134	4.7	840	5	BU935967	BU935967	AGENCOURT	814	134	4.7	996	6	CD050659	AGENCOURT	
742	134	4.7	841	5	BU962609	BU962609	AGENCOURT	815	134	4.7	1008	6	CD246480	AGENCOURT	
743	134	4.7	842	1	AV757327	AV757327		816	134	4.7	1012	4	BG121222	602350980	
744	134	4.7	842	5	BU587831	BU587831	AGENCOURT	817	134	4.7	1017	4	BG108324	602280329	
745	134	4.7	845	5	BU844149	BU844149	AGENCOURT	818	134	4.7	1020	6	CD050222	AGENCOURT	
746	134	4.7	846	5	BU537024	BU537024	AGENCOURT	819	134	4.7	1024	5	BU907570	AGENCOURT	
747	134	4.7	846	5	BU851167	BU851167	AGENCOURT	820	134	4.7	1025	3	BC027804	Mus muscu	
748	134	4.7	847	7	CK196235	CK196235	FGAS00468	821	134	4.7	1026	5	BU556025	AGENCOURT	
749	134	4.7	848	7	CV068583	CV068583	f2_new_ch	822	134	4.7	1027	5	BU559878	AGENCOURT	
750	134	4.7	850	5	BU589468	BU589468	AGENCOURT	823	134	4.7	1036	9	CNS03LWJ	AL250012 Tetraodon	
751	134	4.7	856	5	BU934849	BU934849	AGENCOURT	824	134	4.7	1037	4	BG104782	602311731	
752	134	4.7	856	7	CV480269	CV480269	AGENCOURT	825	134	4.7	1041	6	CD051043	AGENCOURT	
753	134	4.7	863	6	CD107497	CD107497	AGENCOURT	826	134	4.7	1052	5	BU560001	AGENCOURT	
754	134	4.7	868	5	BU529631	BU529631	AGENCOURT	827	134	4.7	1057	6	CD387510	AGENCOURT	

828	134	4.7	1061	4	BM803249	AGENCOURT	901	133	4.7	142	4	BM014138	BM014138	603639815
829	134	4.7	1063	4	BM469499	AGENCOURT	902	133	4.7	142	5	BU066696	BU066696	1609_H09
830	134	4.7	1066	5	BU540067	AGENCOURT	C 903	133	4.7	143	7	CK615751	CK615751	ou03c06.y
831	134	4.7	1067	6	CD386564	AGENCOURT	C 904	133	4.7	143	7	CK616902	CK616902	ou29b11.y
C 832	134	4.7	1068	5	BU908068	AGENCOURT	C 905	133	4.7	143	7	CO478890	CO478890	Q00177_B7
833	134	4.7	1077	5	BU540030	AGENCOURT	C 906	133	4.7	144	7	CF329001	CF329001	NACL--04-
834	134	4.7	1081	6	CB182058	AGENCOURT	C 907	133	4.7	144	7	CK120535	CK120535	207420.p1
835	134	4.7	1086	5	BU960798	AGENCOURT	C 908	133	4.7	145	7	CF308439	CF308439	ABF--02-E
C 836	134	4.7	1097	4	BM464212	AGENCOURT	C 909	133	4.7	145	7	CF320486	CF320486	HD--11-G0
837	134	4.7	1099	4	BM457274	AGENCOURT	C 910	133	4.7	145	7	CK118018	CK118018	207921.p1
838	134	4.7	1109	5	BU530365	AGENCOURT	C 911	133	4.7	145	7	CK616841	CK616841	ou27f08.y
839	134	4.7	1116	6	CA475599	AGENCOURT	C 912	133	4.7	148	7	CK616682	CK616682	ou24a08.y
C 840	134	4.7	1139	4	BM476544	AGENCOURT	C 913	133	4.7	148	7	CO474093	CO474093	Q0046.TB
841	134	4.7	1141	5	BM905793	AGENCOURT	C 914	133	4.7	149	5	BP454965	BP454965	BP454965
C 842	134	4.7	1150	4	BM477385	AGENCOURT	C 915	133	4.7	149	6	CB089104	CB089104	1f09h09.b
843	134	4.7	1150	5	BO902080	AGENCOURT	C 916	133	4.7	149	7	CK616434	CK616434	ou18h11.y
844	134	4.7	1152	5	BO956600	AGENCOURT	C 917	133	4.7	150	7	CK616925	CK616925	ou29g08.y
C 845	134	4.7	1188	4	BM458180	AGENCOURT	C 918	133	4.7	150	8	BZ239557	BZ239557	CH230-507
846	134	4.7	1200	5	BU508078	AGENCOURT	C 919	133	4.7	151	7	CK615670	CK615670	ou01c04.y
C 847	134	4.7	1202	4	BM450025	AGENCOURT	C 920	133	4.7	152	7	BE877769	BE877769	601486336
848	134	4.7	1213	3	BC029635	Mus muscu	C 921	133	4.7	152	7	CR557690	CR557690	DKF2p4681
849	134	4.7	1234	4	BM460327	AGENCOURT	C 922	133	4.7	153	1	AL036396	AL036396	DKF2p564H
850	134	4.7	1235	4	BM470058	AGENCOURT	C 923	133	4.7	153	4	BM033066	BM033066	kh62g03.y
851	134	4.7	1251	4	BM453439	AGENCOURT	C 924	133	4.7	153	4	BM033228	BM033228	kh64g07.y
852	134	4.7	1297	5	BU840145	AGENCOURT	C 925	133	4.7	153	5	BQ134995	BQ134995	IN1r1_2_H
853	134	4.7	1304	5	BQ719553	AGENCOURT	C 926	133	4.7	153	6	CB409976	CB409976	NISC.nc08
854	134	4.7	1329	2	BF342709	AGENCOURT	C 927	133	4.7	153	7	CK120779	CK120779	206b23.p1
855	134	4.7	1334	4	BM555708	AGENCOURT	C 928	133	4.7	153	7	CR546234	CR546234	DKF2p459B
856	134	4.7	1422	3	AF118064	Homo sapi	C 929	133	4.7	154	2	BF422215	BF422215	FM1_13_D1
857	134	4.7	1511	3	BC030320	Mus muscu	C 930	133	4.7	155	4	BM155493	BM155493	fw06e02.y
858	134	4.7	1521	3	AF118070	Homo sapi	C 931	133	4.7	155	4	BM187047	BM187047	fv81d02.y
859	134	4.7	1534	3	CR749559	Homo sapi	C 932	133	4.7	155	5	BM896646	BM896646	ph54a07.y
860	134	4.7	1611	4	BM466171	AGENCOURT	C 933	133	4.7	155	5	BM897043	BM897043	ph55f05.y
861	134	4.7	1699	3	HSMB01509	Homo sapi	C 934	133	4.7	155	5	BQ134923	BQ134923	IN1r1_1_H
862	134	4.7	1708	3	BC027831	Mus muscu	C 935	133	4.7	155	7	CR772376	CR772376	DKF2p4680
863	134	4.7	1762	3	BC050651	Homo sapi	C 936	133	4.7	157	6	CR084762	CR084762	hg22d11.b
864	134	4.7	1782	3	CR749618	Homo sapi	C 937	133	4.7	158	5	EX493591	EX493591	DKF2p781P
865	134	4.7	1800	3	BC030213	Homo sapi	C 938	133	4.7	158	6	CB099755	CB099755	py16e12.y
866	134	4.7	1842	3	BC036564	Mus muscu	C 939	133	4.7	158	7	CF572034	CF572034	MCSA032D0
867	134	4.7	1977	3	BC044307	Homo sapi	C 940	133	4.7	159	4	BI783190	BI783190	kh48a07.y
868	134	4.7	1999	3	BC027914	Homo sapi	C 941	133	4.7	159	6	CB045580	CB045580	NISC.9e11
869	134	4.7	2001	3	BC032428	Homo sapi	C 942	133	4.7	159	6	CB046652	CB046652	NISC_9f05
870	134	4.7	2080	3	CR749502	Homo sapi	C 943	133	4.7	160	4	BI500352	BI500352	rs71a10.y
871	134	4.7	2084	3	BC025705	Homo sapi	C 944	133	4.7	160	5	BM896912	BM896912	ph49f06.y
872	134	4.7	2105	3	HSMB03705	Homo sapi	C 945	133	4.7	160	6	CB970716	CB970716	CAB10004
873	134	4.7	2286	3	AF116646	Homo sapi	C 946	133	4.7	160	7	CK615771	CK615771	ou03g05.y
874	134	4.7	2401	3	AF130075	Homo sapi	C 947	133	4.7	161	4	BM155043	BM155043	fv92g09.y
875	134	4.7	2500	3	BC026293	Homo sapi	C 948	133	4.7	162	1	AL696159	AL696159	DKF2p686B
876	134	4.7	2623	3	HSMB08057	Homo sapi	C 949	133	4.7	162	4	BG252929	BG252929	602365530
877	134	4.7	2700	3	BC036824	Homo sapi	C 950	133	4.7	162	5	EX475911	EX475911	DKF2p686E
878	134	4.7	2949	3	BC075812	Homo sapi	C 951	133	4.7	162	7	CK616920	CK616920	ou29f10.y
879	134	4.7	3250	3	BC035530	Mus muscu	C 952	133	4.7	162	8	BH579624	BH579624	BOGFV03TF
880	134	4.7	3645	3	HSMB07326	Homo sapi	C 953	133	4.7	163	7	CR557869	CR557869	DKF2p468H
881	134	4.7	4195	3	HSMB03410	Homo sapi	C 954	133	4.7	163	4	BM154953	BM154953	fv91f07.y
882	134	4.7	4712	3	CR749443	Homo sapi	C 955	133	4.7	164	7	CK615828	CK615828	ou03b09.y
883	134	4.7	5152	3	HSMB03128	Homo sapi	C 956	133	4.7	164	7	CR545142	CR545142	DKF2p470P
884	134	4.7	5239	3	CR749475	Homo sapi	C 957	133	4.7	165	4	BI498656	BI498656	sai16h09.y
885	134	4.7	5940	3	CB627133	Homo sapi	C 958	133	4.7	165	5	EX644947	EX644947	DKF2p781M
886	134	4.7	7420	3	CR749364	Homo sapi	C 959	133	4.7	165	6	CA675110	CA675110	wluu2.pk0
C 887	133	4.7	133	2	BE965556	601659488	C 960	133	4.7	165	7	CK616281	CK616281	ou1se08.y
C 888	133	4.7	133	7	CK616244	ou14g02.y	C 961	133	4.7	165	7	CK765941	CK765941	DKF2p469D
C 889	133	4.7	133	7	CK616732	ou25b09.y	C 962	133	4.7	165	7	CV308657	CV308657	tj53f112.b
C 890	133	4.7	133	7	CK617018	ou31h08.y	C 963	133	4.7	166	5	BM966627	BM966627	ko10b04.y
C 891	133	4.7	135	6	CB817288	d3e09p2.f	C 964	133	4.7	166	6	CA335025	CA335025	NISC.lt04
C 892	133	4.7	135	7	CK120739	206g18.p1	C 965	133	4.7	166	6	CA670213	CA670213	wluu1.pk0
893	133	4.7	137	8	AZ062854	RPCI-23-4	C 966	133	4.7	166	6	CK543887	CK543887	DKF2p470B
C 894	133	4.7	139	7	CK615954	ou08b08.y	C 967	133	4.7	166	7	CR791520	CR791520	DKF2p468L
C 895	133	4.7	139	7	CK616580	ou22a11.y	C 968	133	4.7	166	7	CR791545	CR791545	DKF2p468P
C 896	133	4.7	140	2	AW632765	92893.MAR	C 969	133	4.7	167	1	AI433157	AI433157	t132b12.x
897	133	4.7	140	2	BE358901	DG1_32.B0	C 970	133	4.7	167	4	BM130014	BM130014	pb25b06.y
898	133	4.7	141	6	CA334915	NISC_1C03	C 971	133	4.7	167	7	CK120239	CK120239	208b19.p1
899	133	4.7	141	6	CB409169	NISC.nc02	C 972	133	4.7	167	7	CK616891	CK616891	ou29a04.y
C 900	133	4.7	141	8	BH700897	BOGSL41TR	C 973	133	4.7	167	9	DR38A1T	DR38A1T	Danio rer

974	133	4.7	168	7	CO194577	1047	133	4.7	186	2	BF343172	602015819
975	133	4.7	169	7	CR555269	1048	133	4.7	186	6	CA802489	sau37b06.
c 976	133	4.7	168	1	AL045500	1049	133	4.7	186	6	CA819169	sau70c02.
977	133	4.7	169	4	BI781645	1050	133	4.7	186	7	CK120313	208b05.pl
978	133	4.7	169	4	BI784430	c1051	133	4.7	186	7	CR753497	KR753497 DKF2p469K
979	133	4.7	169	4	BI863663	1052	133	4.7	187	4	BI468624	sai01d03.
980	133	4.7	169	5	BM898046	1053	133	4.7	187	4	BI468624	sai01d03.
c 981	133	4.7	169	6	BM898046	1054	133	4.7	187	4	BI749319	ro76f11.y
c 982	133	4.7	169	6	CS118899	1055	133	4.7	187	6	CA802526	sau37g01.
c 983	133	4.7	170	7	CS136079	1056	133	4.7	187	7	CO191674	EC31648.5
c 984	133	4.7	170	2	AW268253	c1056	133	4.7	188	5	EX479066	KDF2p686L
985	133	4.7	170	4	BJ701151	c1057	133	4.7	188	5	CA819174	sau70c07.
986	133	4.7	170	5	BS033607	c1058	133	4.7	188	6	CA819174	sau70c07.
987	133	4.7	170	6	CS072967	1059	133	4.7	189	1	AA590777	vm21b06.r
988	133	4.7	171	4	BI863546	1060	133	4.7	189	4	BM178937	SAJ61c09.
989	133	4.7	171	5	BM889202	1061	133	4.7	189	5	BM400307	NISC mp08
990	133	4.7	171	5	BU926898	1062	133	4.7	189	7	CO182475	EC22756.5
991	133	4.7	171	7	CR555329	c1063	133	4.7	189	7	CA747073	wri2a.pk0
992	133	4.7	172	1	AL697684	1064	133	4.7	190	6	CA802078	sau29g04.
993	133	4.7	172	4	BM874768	1065	133	4.7	191	1	AL696149	AL696149 DKF2p686B
994	133	4.7	172	6	CS075586	1066	133	4.7	191	5	BM965865	ko18c09.y
c 995	133	4.7	173	6	CB084519	1067	133	4.7	191	5	BS033634	KDF2p686L
c 996	133	4.7	174	1	AJ654741	1068	133	4.7	191	6	CA819538	sau80a11.
c 997	133	4.7	174	4	BM186145	c1069	133	4.7	191	7	CF214566	GGF100081
c 998	133	4.7	174	5	BM896563	c1070	133	4.7	191	7	CR789784	KDF2p459E
c 999	133	4.7	174	7	CR616865	1071	133	4.7	192	1	AI856699	sb43f11.y
1000	133	4.7	174	9	CNS023TP	1072	133	4.7	192	4	BM154409	fv84g05.y
c1001	133	4.7	175	4	BM318082	1073	133	4.7	192	6	CD570788	kb76f12.y
c1002	133	4.7	175	5	BM896455	1074	133	4.7	192	7	CR557731	KDF2p468K
1003	133	4.7	175	7	CF215776	1075	133	4.7	193	6	CA819381	sau77f02.
1004	133	4.7	175	7	CR7119906	1076	133	4.7	193	7	CO192922	EC34787.5
1005	133	4.7	176	4	BM155475	1077	133	4.7	194	4	BI783226	sk48f02.y
1006	133	4.7	176	5	BS033619	1078	133	4.7	194	4	BM308918	sk48f02.y
c1007	133	4.7	176	6	CR645509	c1079	133	4.7	195	1	AU060359	AU060359
c1008	133	4.7	176	6	BS045579	1080	133	4.7	195	4	BJ021877	BJ021877
1009	133	4.7	176	7	CR765894	1081	133	4.7	195	4	BJ251931	BJ251931
1010	133	4.7	177	1	AL697773	1082	133	4.7	195	5	BS045579	BS045579
1011	133	4.7	177	4	BG464649	1083	133	4.7	195	6	CB817512	d3k21p2.f
c1012	133	4.7	177	4	BM155200	1084	133	4.7	195	7	CK120094	208p09.pl
c1013	133	4.7	177	6	CR045548	1085	133	4.7	195	9	CNS02TGO	Tetraodon
1014	133	4.7	177	7	CR121639	1086	133	4.7	196	1	AL712417	KDF2p686P
1015	133	4.7	177	7	CR771835	1087	133	4.7	196	6	CA339374	NISC_ly02
1016	133	4.7	178	4	BJ696903	c1088	133	4.7	196	6	CB045738	NISC_gcl2
1017	133	4.7	178	5	BM965687	1089	133	4.7	196	6	CB073175	taa39d07.
c1018	133	4.7	178	5	BM965687	c1090	133	4.7	196	7	CR537792	KDF2p459E
c1019	133	4.7	178	6	CR192208	1091	133	4.7	197	4	BG179993	602329538
c1020	133	4.7	179	6	CR670281	1092	133	4.7	197	5	BO666607	pb44e06.y
c1021	133	4.7	179	6	CB216118	c1093	133	4.7	197	5	EX484617	KDF2p686L
1022	133	4.7	180	1	AV184931	c1094	133	4.7	197	6	CA670214	wlsul.pk0
c1023	133	4.7	180	1	AV200626	1095	133	4.7	197	6	CA802643	sau39h03.
1024	133	4.7	180	6	CA819701	1096	133	4.7	197	6	CA935345	sau52d04.
c1025	133	4.7	180	7	CK120267	c1097	133	4.7	198	5	BQ392333	NISC mg23
1026	133	4.7	181	4	BS069304	1098	133	4.7	198	6	CA819320	sau72f08.
c1027	133	4.7	181	5	BM899727	1099	133	4.7	198	7	CO181348	EC14089.5
c1028	133	4.7	181	6	CR980398	1100	133	4.7	199	1	AU037638	AU037638
c1029	133	4.7	181	7	CR543183	1101	133	4.7	199	6	CB376865	CB376865
1030	133	4.7	181	8	CR791725	1102	133	4.7	200	5	BQ667387	pb60g04.y
c1031	133	4.7	182	2	AW062901	1103	133	4.7	200	5	BS033618	KDF2p686E
1032	133	4.7	182	2	AW101133	1104	133	4.7	200	6	CD724098	o3j0d06.y
1033	133	4.7	182	4	BM155169	1105	133	4.7	200	7	CK593192	lad41d04.
1034	133	4.7	182	4	BM155421	1106	133	4.7	200	7	CR559013	KDF2p468P
c1035	133	4.7	182	5	BU801954	c1107	133	4.7	201	5	BQ523741	NISC nl23
c1036	133	4.7	182	6	CA340216	1108	133	4.7	201	5	EX474221	KDF2p686D
c1037	133	4.7	182	6	CB101650	1109	133	4.7	201	6	CA802122	sau30e05.
1038	133	4.7	183	5	BQ740714	c1110	133	4.7	201	7	CR546762	KDF2p4700
1039	133	4.7	183	5	BS0508387	1111	133	4.7	201	7	CR765965	KDF2p468E
1040	133	4.7	183	7	CR766049	1112	133	4.7	202	4	BG736221	tk53d03.y
1041	133	4.7	183	7	CR791704	1113	133	4.7	202	4	BM154309	fv84e04.y
1042	133	4.7	184	4	BI705276	1114	133	4.7	202	5	BM965808	ko18e03.y
1043	133	4.7	184	6	CR721356	1115	133	4.7	202	7	CK118991	214p04.pl
1044	133	4.7	185	5	BQ077400	1116	133	4.7	202	7	CO168360	Mdf33001i
1045	133	4.7	185	5	BS014448	c1117	133	4.7	202	7	CO185210	EC29934.5
1046	133	4.7	185	7	CR772164	c1118	133	4.7	203	5	BQ399198	NISC mp02
					CR772164	1119	133	4.7	203	7	CK428917	1aj19b11.

1120	133	4.7	203	7	CR546261	DKF2p459D	CR546261	DKF2p459D	1193	133	4.7	220	7	CR630411	DKF2p469D
1121	133	4.7	204	1	AL712721	DKF2p686I	AL712721	DKF2p686I	1194	133	4.7	220	9	CNS0148D	AL103831
1122	133	4.7	204	4	BM064528	KS01068C0	BM064528	KS01068C0	1195	133	4.7	220	9	CNS037J	AL231400
1123	133	4.7	204	5	BA75691	DKF2p686J	BA75691	DKF2p686J	1196	133	4.7	221	4	BM532327	BM532327
1124	133	4.7	204	6	CA819112	CA819112	CA819112	CA819112	1197	133	4.7	221	5	BU764039	BU764039
1125	133	4.7	204	7	CK120836	205n01.p1	CK120836	205n01.p1	1198	133	4.7	221	7	CV168252	CV168252
1126	133	4.7	205	1	AA153231	mm31b12.r	AA153231	mm31b12.r	1199	133	4.7	221	7	CV192584	CV192584
1127	133	4.7	205	4	BM155383	fw04a12.y	BM155383	fw04a12.y	1200	133	4.7	221	7	CV193270	CV193270
1128	133	4.7	205	6	CA819594	CA819594	CA819594	CA819594	1201	133	4.7	222	1	AL696218	AL696218
1129	133	4.7	205	6	CA935286	CA935286	CA935286	CA935286	1202	133	4.7	222	4	BI863321	BI863321
1130	133	4.7	205	6	CA935286	CA935286	CA935286	CA935286	1203	133	4.7	222	4	CA802046	CA802046
1131	133	4.7	205	6	CA935286	CA935286	CA935286	CA935286	1204	133	4.7	222	8	B2043861	B2043861
1132	133	4.7	205	6	CA935286	CA935286	CA935286	CA935286	1205	133	4.7	223	6	CA819345	CA819345
1133	133	4.7	205	7	CR557702	DKF2p468I	CR557702	DKF2p468I	1206	133	4.7	223	7	CR791578	CR791578
1134	133	4.7	206	7	CF331225	NACL--07-	CF331225	NACL--07-	1207	133	4.7	223	9	CNS027EU	AL184575
1135	133	4.7	207	4	BI709283	f862e01.y	BI709283	f862e01.y	1208	133	4.7	224	5	EX503628	EX503628
1136	133	4.7	207	5	BO399361	BO399361	BO399361	BO399361	1209	133	4.7	224	6	CA935362	CA935362
1137	133	4.7	207	6	CR088898	CR088898	CR088898	CR088898	1210	133	4.7	224	7	CR544817	CR544817
1138	133	4.7	207	7	CK119802	210107.p1	CK119802	210107.p1	1211	133	4.7	224	7	CR768779	CR768779
1139	133	4.7	207	7	CR524509	DKF2p470B	CR524509	DKF2p470B	1212	133	4.7	225	2	AW100941	AW100941
1140	133	4.7	208	6	CB410192	NISC nc10	CB410192	NISC nc10	1213	133	4.7	225	6	CA819034	CA819034
1141	133	4.7	208	7	CO195491	CO195491	CO195491	CO195491	1214	133	4.7	226	6	CB093154	CB093154
1142	133	4.7	209	1	AA638753	vm93e12.r	AA638753	vm93e12.r	1215	133	4.7	226	7	CF572350	CF572350
1143	133	4.7	209	5	BQ825960	OK-YZ-B49	BQ825960	OK-YZ-B49	1216	133	4.7	226	9	CNS0486K	AL287957
1144	133	4.7	209	5	BA484868	BA484868	BA484868	BA484868	1217	133	4.7	227	5	BU764188	BU764188
1145	133	4.7	209	6	CA819818	CA819818	CA819818	CA819818	1218	133	4.7	227	6	CB285901	CB285901
1146	133	4.7	209	6	CB337509	CB337509	CB337509	CB337509	1219	133	4.7	228	7	CK119140	CK119140
1147	133	4.7	209	7	CK427762	CK427762	CK427762	CK427762	1220	133	4.7	228	9	CNS021AJ	AL176644
1148	133	4.7	209	7	CO732829	CO732829	CO732829	CO732829	1221	133	4.7	229	1	AA734226	AA734226
1149	133	4.7	210	4	BM873785	BM873785	BM873785	BM873785	1222	133	4.7	229	5	BQ075610	BQ075610
1150	133	4.7	210	6	CA935503	CA935503	CA935503	CA935503	1223	133	4.7	229	6	CA802763	CA802763
1151	133	4.7	210	7	CK121439	CK121439	CK121439	CK121439	1224	133	4.7	229	7	CF929107	CF929107
1152	133	4.7	211	4	B748687	B748687	B748687	B748687	1225	133	4.7	230	4	BI784178	BI784178
1153	133	4.7	211	4	B7680884	B7680884	B7680884	B7680884	1226	133	4.7	230	4	BM595688	BM595688
1154	133	4.7	211	6	CA935582	CA935582	CA935582	CA935582	1227	133	4.7	230	6	CA936756	CA936756
1155	133	4.7	211	6	CD722487	CD722487	CD722487	CD722487	1228	133	4.7	230	6	CB287035	CB287035
1156	133	4.7	211	7	CK120334	207m23.p1	CK120334	207m23.p1	1229	133	4.7	230	7	CF572716	CF572716
1157	133	4.7	212	5	BU760971	BU760971	BU760971	BU760971	1230	133	4.7	231	2	AW164838	AW164838
1158	133	4.7	212	7	CO195530	CO195530	CO195530	CO195530	1231	133	4.7	231	5	EX644880	EX644880
1159	133	4.7	213	4	BG168696	BG168696	BG168696	BG168696	1232	133	4.7	231	7	CO181733	CO181733
1160	133	4.7	213	6	CA935478	CA935478	CA935478	CA935478	1233	133	4.7	232	7	CR537572	CR537572
1161	133	4.7	214	1	AL703357	AL703357	AL703357	AL703357	1234	133	4.7	233	2	BE030380	BE030380
1162	133	4.7	214	7	CR630363	CR630363	CR630363	CR630363	1235	133	4.7	233	5	EX502988	EX502988
1163	133	4.7	215	4	BG731047	BG731047	BG731047	BG731047	1236	133	4.7	233	6	CB079472	CB079472
1164	133	4.7	215	4	BG893071	BG893071	BG893071	BG893071	1237	133	4.7	233	6	CF122270	CF122270
1165	133	4.7	215	6	CB100794	CB100794	CB100794	CB100794	1238	133	4.7	233	7	CF124181	CF124181
1166	133	4.7	215	7	CF207515	CF207515	CF207515	CF207515	1239	133	4.7	234	4	BM154438	BM154438
1167	133	4.7	215	7	CF214757	CF214757	CF214757	CF214757	1240	133	4.7	234	4	BM873724	BM873724
1168	133	4.7	215	7	CF425648	CF425648	CF425648	CF425648	1241	133	4.7	234	6	CD722669	CD722669
1169	133	4.7	216	6	CA935095	CA935095	CA935095	CA935095	1242	133	4.7	235	2	AW101589	AW101589
1170	133	4.7	216	6	CA935420	CA935420	CA935420	CA935420	1243	133	4.7	235	4	BI749483	BI749483
1171	133	4.7	216	7	CF970477	CF970477	CF970477	CF970477	1244	133	4.7	235	4	BJ081948	BJ081948
1172	133	4.7	217	1	AI500077	AI500077	AI500077	AI500077	1245	133	4.7	235	6	CB051841	CB051841
1173	133	4.7	217	1	BZ251664	BZ251664	BZ251664	BZ251664	1246	133	4.7	235	6	CD577826	CD577826
1174	133	4.7	217	7	CR524654	CR524654	CR524654	CR524654	1247	133	4.7	235	7	CF925885	CF925885
1175	133	4.7	217	7	AL666596	AL666596	AL666596	AL666596	1248	133	4.7	235	7	CO195635	CO195635
1176	133	4.7	218	4	BM154944	BM154944	BM154944	BM154944	1249	133	4.7	236	6	CA339334	CA339334
1177	133	4.7	218	6	CA935222	CA935222	CA935222	CA935222	1250	133	4.7	236	6	CB948928	CB948928
1178	133	4.7	218	7	CF426331	CF426331	CF426331	CF426331	1251	133	4.7	236	7	CO180970	CO180970
1179	133	4.7	218	7	CK377805	CK377805	CK377805	CK377805	1252	133	4.7	237	5	BQ128671	BQ128671
1180	133	4.7	218	7	CO727269	CO727269	CO727269	CO727269	1253	133	4.7	237	7	CK616649	CK616649
1181	133	4.7	219	4	BI791181	BI791181	BI791181	BI791181	1254	133	4.7	237	7	CR791203	CR791203
1182	133	4.7	219	4	BM587451	BM587451	BM587451	BM587451	1255	133	4.7	237	7	CR543081	CR543081
1183	133	4.7	219	6	CA818936	CA818936	CA818936	CA818936	1256	133	4.7	238	7	CO184969	CO184969
1184	133	4.7	219	6	CA818959	CA818959	CA818959	CA818959	1257	133	4.7	238	7	CO983126	CO983126
1185	133	4.7	219	6	CR875278	CR875278	CR875278	CR875278	1258	133	4.7	239	5	BQ094174	BQ094174
1186	133	4.7	219	7	BI705030	BI705030	BI705030	BI705030	1259	133	4.7	239	5	EX503636	EX503636
1187	133	4.7	220	4	BM764212	BM764212	BM764212	BM764212	1260	133	4.7	239	6	CA782245	CA782245
1188	133	4.7	220	4	BM764212	BM764212	BM764212	BM764212	1261	133	4.7	239	6	CA802785	CA802785
1189	133	4.7	220	5	BU764212	BU764212	BU764212	BU764212	1262	133	4.7	239	7	CO184329	CO184329
1190	133	4.7	220	6	CA819276	CA819276	CA819276	CA819276	1263	133	4.7	240	1	AV184850	AV184850
1191	133	4.7	220	7	CF424575	CF424575	CF424575	CF424575	1264	133	4.7	240	2	BE417917	BE417917
1192	133	4.7	220	7	CK429243	CK429243	CK429243	CK429243	1265	133	4.7	240	6	CH020904	CH020904



c1266	133	4.7	240	6	CB0433994	CB0433994	NISC gc01	1339	133	4.7	257	7	CV193143	CV193143	SnESTbab2
1267	133	4.7	240	6	CD520495	AGENCOURT	CD520495	1340	133	4.7	258	4	BG735588	BG735588	rk41c01.y
1268	133	4.7	240	7	CR774358	KFP2p459P	CR774358	1341	133	4.7	259	1	AL697721	AL697721	KFP2p686I
1269	133	4.7	241	4	B1863365		B1863365	1342	133	4.7	259	1	AL707050	AL707050	KFP2p686M
1270	133	4.7	241	4	B1863432		B1863432	1343	133	4.7	259	7	CK624985	CK624985	mi27905.y
1271	133	4.7	242	1	AL036146	KFP2p564D	AL036146	1344	133	4.7	259	7	CO159753	CO159753	FLD1_15.D
1272	133	4.7	242	1	AL697724	KFP2p686I	AL697724	1345	133	4.7	260	4	BN307865	BN307865	sak39a09.
1273	133	4.7	242	6	CA802129	sau30f01.	CA802129	1346	133	4.7	260	7	CK377340	CK377340	lai02e06.
1274	133	4.7	243	2	B8057234	sm9sc12.y	BE057234	1347	133	4.7	260	7	CO988045	CO988045	Mdf13020e
1275	133	4.7	243	4	BG237165	sab04d10.	BG237165	1348	133	4.7	260	7	CR772316	CR772316	KFP2p468L
1276	133	4.7	243	4	B1142830	rk74f05.y	B1142830	1349	133	4.7	260	9	CNS02QNR	AL209520	Tetraodon
1277	133	4.7	243	6	CD578259	21_H11_21	CD578259	1350	133	4.7	261	4	BJ469921	BJ469921	BJ469921
1278	133	4.7	243	7	CO752945	Mdf13022i	CO752945	1351	133	4.7	261	6	CA802634	CA802634	sau39g05.
1279	133	4.7	243	7	CO905671	SnESTbaa4	CO905671	1352	133	4.7	261	7	CV280938	CV280938	WS0138.B2
1280	133	4.7	244	6	CB721659	jnn613D09	CB721659	1353	133	4.7	262	7	CK593385	CK593385	tad39f12.
1281	133	4.7	244	7	CK430436	oj49d02.y	CK430436	1354	133	4.7	262	7	CR791700	CR791700	KFP2p468P
1282	133	4.7	245	2	AW100988	sd64b09.y	AW100988	c1355	133	4.7	263	6	CF040070	CF040070	QCH8d09.y
1283	133	4.7	245	5	BX476550	KFP2p686O	BX476550	1356	133	4.7	263	7	CO982740	CO982740	GM89016B1
1284	133	4.7	246	1	AL696192	AL696192	AL696192	1357	133	4.7	264	7	CF317367	CF317367	HD--07-A1
1285	133	4.7	246	4	BG237816	sab08e11.	BG237816	1358	133	4.7	265	2	AW185173	AW185173	se87h05.y
c1286	133	4.7	246	5	BQ394140		BQ394140	1359	133	4.7	265	6	CA935083	CA935083	sau64b05.
1287	133	4.7	246	6	CA802566		CA802566	1360	133	4.7	265	7	CN411756	CN411756	170005322
1288	133	4.7	246	6	CA802581	sau38g01.	CA802581	c1361	133	4.7	265	7	CR766084	CR766084	KFP2p468I
1289	133	4.7	246	6	CB092960		CB092960	1362	133	4.7	266	5	BQ842918	BQ842918	ID_269_Su
c1290	133	4.7	246	7	CF214774	CGF100082	CF214774	1363	133	4.7	266	5	BX504760	BX504760	KFP2p686E
1291	133	4.7	246	7	CR559419	KFP2p468I	CR559419	1364	133	4.7	266	6	CD640467	CD640467	AGENCOURT
c1292	133	4.7	246	9	CNS013NL	Drosophi1	AL103083	1365	133	4.7	266	6	CD678505	CD678505	hp08g11.y
1293	133	4.7	247	4	BJ701295		BJ701295	1366	133	4.7	267	5	BU703468	BU703468	UI-N-F00
1294	133	4.7	247	4	BM187242	fw13902.y	BM187242	1367	133	4.7	267	7	CO982402	CO982402	GM89014A2
1295	133	4.7	248	1	AL712394	KFP2p686M	AL712394	1368	133	4.7	268	1	AL135661	AL135661	KFP2p762M
1296	133	4.7	248	4	BM521849	sak76g12.	BM521849	1369	133	4.7	268	4	BG058208	BG058208	nah22b05.
c1297	133	4.7	248	5	BQ265006	NISC ff02	BQ265006	1370	133	4.7	268	6	CD640467	CD640467	AGENCOURT
1298	133	4.7	248	5	BU721072	SJM2BJD06	BU721072	1371	133	4.7	268	7	CK430337	CK430337	oj48b09.y
1299	133	4.7	248	5	BX507072		BX507072	1372	133	4.7	269	1	AL708133	AL708133	KFP2p686D
1300	133	4.7	248	6	CA935253	sau51b05.	CA935253	1373	133	4.7	269	5	EX474011	EX474011	KFP2p686L
c1301	133	4.7	248	6	CB977176	CAB40003	CB977176	1374	133	4.7	269	7	CO416572	CO416572	Mdf130081
1302	133	4.7	248	7	CO878154	BovGen_06	CO878154	1375	133	4.7	270	1	AV836739	AV836739	AV836739
1303	133	4.7	249	2	CR772335	KFP2p468M	CR772335	1376	133	4.7	270	4	BG737252	BG737252	rk68h06.y
1304	133	4.7	249	2	BQ059724	sn36a12.y	BE059724	1377	133	4.7	270	4	BJ686519	BJ686519	BJ686519
1305	133	4.7	249	4	BM493181		BM493181	1378	133	4.7	270	4	BJ696724	BJ696724	BJ696724
1306	133	4.7	249	5	BQ785446	saq77h12.y	BQ785446	1379	133	4.7	270	5	BM881117	BM881117	ki09f12.y
1307	133	4.7	249	7	CR559477	KFP2p468J	CR559477	1380	133	4.7	270	5	BM882656	BM882656	rb28b09.y
c1308	133	4.7	250	5	BQ395199	NISC ng13	BQ395199	1381	133	4.7	270	5	BU503644	BU503644	SJM2CBF02
1309	133	4.7	250	7	CA429184	oj33c07.y	CA429184	1382	133	4.7	270	5	BX503644	BX503644	KFP2p686N
1310	133	4.7	251	5	BX503645		BX503645	c1383	133	4.7	270	7	CN266212	CN266212	170004251
1311	133	4.7	251	7	CK121775		CK121775	1384	133	4.7	270	7	CO979289	CO979289	GM89004A2
1312	133	4.7	251	7	COL80942		COL80942	1385	133	4.7	271	6	CA802092	CA802092	sau30a04.
1313	133	4.7	252	6	CA336435		CA336435	1386	133	4.7	271	6	CA802549	CA802549	sau38b03.
c1314	133	4.7	252	6	CB0433981	NISC gc01	CB0433981	1387	133	4.7	271	7	CR629027	CR629027	KFP2p468O
1315	133	4.7	252	6	CB409398	NISC nc05	CB409398	1388	133	4.7	272	4	B1142828	B1142828	rk74e10.y
1316	133	4.7	252	7	CO415260	Mdf13006k	CO415260	1389	133	4.7	272	5	BX507023	BX507023	KFP2p779A
c1317	133	4.7	252	7	CR545848		CR545848	1390	133	4.7	272	6	CA935343	CA935343	sau52d02.
1318	133	4.7	252	7	CR771899		CR771899	1391	133	4.7	272	6	CD520705	CD520705	AGENCOURT
1319	133	4.7	252	7	CD241885		CD241885	1392	133	4.7	272	7	CO069398	CO069398	Mdf13015k
1320	133	4.7	253	9	CNS0149M	Drosophi1	AL103876	1393	133	4.7	273	7	CR763153	CR763153	KFP2p470L
1321	133	4.7	254	2	BQ057342	sn01h03.y	BE057342	1394	133	4.7	273	6	CB945895	CB945895	AGENCOURT
1322	133	4.7	254	4	B1705355	fr57g11.y	B1705355	1395	133	4.7	273	7	CN266183	CN266183	170004250
c1323	133	4.7	254	5	BX493069		BX493069	c1396	133	4.7	274	5	BQ385858	BQ385858	NISC ma14
1324	133	4.7	254	7	CR559205	KFP2p468M	CR559205	1397	133	4.7	274	6	CA934958	CA934958	sau61f10.
1325	133	4.7	254	7	CR559920		CR559920	1398	133	4.7	275	4	BN522686	BN522686	sam9eb08.
1326	133	4.7	255	4	BG879342	ib62g05.y	BG879342	1399	133	4.7	275	7	CF612545	CF612545	lae11h04.
1327	133	4.7	255	6	CA335171		CA335171	1400	133	4.7	275	9	CR767523	CR767523	KFP2p468K
1328	133	4.7	255	6	CA802891	sau43g09.	CA802891	c1401	133	4.7	275	9	CNS034C8	AL227249	Tetraodon
c1329	133	4.7	255	7	CF519323		CF519323	1402	133	4.7	276	4	BG736627	AGENCOURT	rk60b07.y
1330	133	4.7	256	7	CO066438	Mdf13004O	CO066438	1403	133	4.7	276	7	CN550423	CN550423	QO243.B3
1331	133	4.7	256	6	CB088964	if08a08.b	CB088964	c1404	133	4.7	277	4	BN644486	BN644486	170006873
1332	133	4.7	256	7	CO183275	EC25346.5	CO183275	1405	133	4.7	279	6	CD721804	CD721804	oj01f10.y
1333	133	4.7	256	7	CO195335	EC40072.5	CO195335	1406	133	4.7	279	7	CF400770	CF400770	RTW1_7.D
1334	133	4.7	257	1	AL731976		AL731976	1407	133	4.7	280	1	AJ769221	AJ769221	AJ769221
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ORIGIN

Query Match		86.7%;	Score 2468;	DB 3;	Length 3165;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 2718;		Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	CGCTCGGACACAGCGCGGCAAGATGAGCTGGGTTGCTGGACGCAAGTTGGGCTCAC	60		
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Db	662	GGAGAAATGAGTGTGATCTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAACCTGCAA	721		
Qy	301	GAGCTGCCGAATGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTCTTA	360		
Db	722	GAGCTGCCGAATGCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTCTTA	781		
Qy	361	CTGTGCAGATGTCGAGCAGGCTGTGTACGGAGGAGACTGCATGCGATGTGCGCAGGTTCT	420		
Db	782	CTGTGCAGATGTCGAGCAGGCTGTGTACGGAGGAGACTGCATGCGATGTGCGCAGGTTCT	841		
Qy	421	GGAGCCCCAAAGGTCAGATTTGTGTGAAAGCTATCCCTAAATGCTCACTGTGAATG	480		
Db	842	GGAGCCCCAAAGGTCAGATTTGTGTGAAAGCTATCCCTAAATGCTCACTGTGAATG	901		
Qy	481	GACCAATTCATGCTAAACCTGGGTTGTTCATCCAACTAAGATTTGTGAGTCTGGA	540		
Db	902	GACCAATTCATGCTAAACCTGGGTTGTTCATCCAACTAAGATTTGTGAGTCTGGA	961		
Qy	541	GTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTGATGAGACAACCGCGATGG	600		
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Qy	601	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTTATCCAGACATAGGATC	660		
Db	1022	CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCAGCTCTTATCCAGACATAGGATC	1081		
Qy	661	CTCACTCCACGTCCTCTTCCACTCCGATGGCTCCCAAGAAATTTGACGGTTTCCATGCCAT	720		
Db	1082	CTCACTCCACGTCCTCTTCCACTCCGATGGCTCCCAAGAAATTTGACGGTTTCCATGCCAT	1141		
Qy	721	TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGCGCAGTGGCTCT	780		
Db	1142	TTATGAGGAGATCACAGCATGCTCTCATCCCTTTGTTTCCATGACGCGCAGTGGCTCT	1201		
Qy	781	TGACGAGCTGGATCTTACAGATGTGCTGTGGCAGGCTATATCTGGGCGAGCGCTGTGA	840		
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Qy	1321	TGGGAAGTGGAGTGGGCGGCGACCATCTGTCATCCCTATCTGCGGGAATAATGAGAAAT	1380		
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Db	1982	CACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAAATTTCTACCGGGATGATGA	2041		
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DEFINITION Homo sapiens FP938 mRNA, complete cds.  
ACCESSION AF370388  
VERSION AF370388.1 GI:33341705  
KEYWORDS HTC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2650)  
AUTHORS Huang, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao, X.T.,  
Wan, D.P. and Gu, J.R.  
TITLE Novel human cDNA clones with function of inhibiting cancer cell  
growth  
JOURNAL Unpublished

2 (bases 1 to 2650)  
Qin, W.X., Wan, D.P., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Huang, Y.,  
Zhao, X.T. and Gu, J.R.  
Direct Submission  
Submitted (16-APR-2001) National Laboratory For Oncogenes & Related  
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai  
200032, P. R. China  
LOCATION/Qualifiers  
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Query Match 84.1%; Score 2394; DB 3; Length 2650;  
Best Local Similarity 99.9%; Pred. No. 0;  
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Qy 153 GGGAGTGTGATATGATCAGATTCAGTGGCTGCTGCCCGAAGAGGAGGAGCTGCG 212  
Db 62 GGGAGTGTGATATGATCAGATTCAGTGGCTGCTGCCCGAAGAGGAGGAGCTGCG 121  
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DEFINITION genomic survey sequence.  
ACCESSION AY406074  
VERSION AY406074.1 GI:39762048  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN	
Query Match	31.2%; Score 889; DB 5; Length 1100;
Best Local Similarity	99.9%; Pred. No. 0;
Matches	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1722 TCCTAGACAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCGCAGTCGGG 1781
DB	962 TCCTAGACAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCGCAGTCGGG 903
QY	1782 ATCTCAGACATCTCTCCAGGAGTCCACATCAGTGTGGCTGGTGAATGTCCTGGCAG 1841
DB	902 ATCTCAGACATCTCTCCAGGAGTCCACATCAGTGTGGCTGGTGAATGTCCTGGCAG 843
QY	1842 ACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGCTGCTCAGTGTGGTG 1901
DB	842 ACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGCTGCTCAGTGTGGTG 783
QY	1902 ACTGCTCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGCTACTGATA 1961
DB	782 ACTGCTCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGCTACTGATA 723
QY	1962 ACATGTTCTGTGCGAGCTGGGACCCACTGCCCCCTTCTGATATCTGCACTGAGAGAG 2021
DB	722 ACATGTTCTGTGCGAGCTGGGACCCACTGCCCCCTTCTGATATCTGCACTGAGAGAGAG 663
QY	2022 GAGGCATCGCGCTGTGCTTCCCGGAGCAGAGCATCTCCTGAGCCAGCTGGCATCTGA 2081
DB	662 GAGGCATCGCGCTGTGCTTCCCGGAGCAGAGCATCTCCTGAGCCAGCTGGCATCTGA 603
QY	2082 TGGGACTGCTGCTGAGCTGATGATAAAACATGAGCCACAGGCTCTCCACTGCTTCA 2141
DB	602 TGGGACTGCTGAGCTGATGATAAAACATGAGCCACAGGCTCTCCACTGCTTCA 543
QY	2142 CCAAGTCTGCTTTTAAAGCTGGATGAAAGAAATATGAATGAACCATGCTCATGC 2201
DB	542 CCAAGTCTGCTTTTAAAGCTGGATGAAAGAAATATGAATGAACCATGCTCATGC 483
QY	2202 ACTCCTCTGAGAAGTGTCTGTATATCCGTCTGTACGTGTGTCATTGGTGAAGCAGTGT 2261
DB	482 ACTCCTCTGAGAAGTGTCTGTATATCCGTCTGTACGTGTGTCATTGGTGAAGCAGTGT 423
QY	2262 GGGCTGGAAGTGTGATTTGGCTGTGAACTTGGCTGTGCCAGGGCTTCTGACTTCAGGGA 2321
DB	422 GGGCTGGAAGTGTGATTTGGCTGTGAACTTGGCTGTGCCAGGGCTTCTGACTTCAGGGA 363
QY	2322 CAAGACTCAGTGAAGGGTGAAGTGAACCTTCCATTGCTGTAGCTGATCCCGGTCCTCA 2381
DB	362 CAAGACTCAGTGAAGGGTGAAGTGAACCTTCCATTGCTGTAGCTGATCCCGGTCCTCA 303
QY	2382 CTAGGACAGCCAAATGGAAGATGCCAGGGCTTGCAGGAAGTAAAGTTCTTCAAAGAAGAC 2441
DB	302 CTAGGACAGCCAAATGGAAGATGCCAGGGCTTGCAGGAAGTAAAGTTCTTCAAAGAAGAC 243
QY	2442 CATATACAAAACCTTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTTCAAGTTATACG 2501
DB	242 CATATACAAAACCTTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTTCAAGTTATACG 183
QY	2502 AATGCCATCAGCTTGACAGGAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCA 2561
DB	182 AATGCCATCAGCTTGACAGGAGATCTGGGCTTCATGAGGCCCTTTTGGAGCTCTCA 123
QY	2562 AGTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGC 2621
DB	122 AGTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGC 63
QY	2622 CTTTGTGTACATGCCCACAGTACAGTCTGGTCTTTTCTT 2661

Db	62 CTTTGTGTACATGCGCCAGTACAGTCTGTGCTTTTCTT 23
RESULT 5	
LOCUS	BX434191/c
DEFINITION	BX434191 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DB009YD01
ACCESSION	BX434191
VERSION	BX434191.2
KEYWORDS	3-PRIME, mRNA sequence.
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	1 (bases 1 to 897)
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 15, 2003 this sequence version replaced gi:30775248. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5757.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAK025BH09NM1&c=5757.r. Location/Qualifiers 1. .897 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DB009YD01" /tissue_type="PLACENTA" /clone_lib="Homo sapiens PLACENTA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
FEATURES	
source	
ORIGIN	
Query Match	27.6%; Score 786; DB 5; Length 897;
Best Local Similarity	99.9%; Pred. No. 0;
Matches	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1861 CAAGAACACACACTGGGCTCTGGGCTGCTCAGTGTGGTGGACTCGCTGCTGTGAGGA 1920
DB	845 CAAGAACACACACTGGGCTCTGGGCTGCTCAGTGTGGTGGACTCGCTGCTGTGAGGA 786
QY	1921 CGAGCATGAGGACCATGGCATCCAGTGTGTCTGATTAACATGTTCTGTGCCAGCTG 1980
DB	785 CGAGCATGAGGACCATGGCATCCAGTGTGTCTGATTAACATGTTCTGTGCCAGCTG 726
QY	1981 GGAACCCCACTGCCCTTCTGATATCTGCACTGCGAGAGACAGGAGCATCGCGGCTGTGTC 2040
DB	725 GGAACCCCACTGCCCTTCTGATATCTGCACTGCGAGAGACAGGAGCATCGCGGCTGTGTC 666
QY	2041 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGAGCTGCTGAGCTGAG 2100
DB	665 CTTCCCGGAGCAGCATCTCTGAGCCACGCTGGCATCTGATGGAGCTGCTGAGCTGAG 606
QY	2101 CTATGATAAACAATGACAGCCACAGGCTCTCCACTGCGCTTCCACCAAGGTGCTGCTTTTAA 2160
DB	605 CTATGATAAACAATGACAGCCACAGGCTCTCCACTGCGCTTCCACCAAGGTGCTGCTTTTAA 546
QY	2161 AGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACTCTTGTGAGAGTGTTC 2220





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Db 492 GGAGACACATTACACGCTATATCTCAGCGCCTTCAGCAAGCAGAACTGCAGAGTGC 551
Qy 1186 CCCTACCAAGAGCCAGCCCTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCA 1245
Db 552 CCCTACCAAGAGCCAGCCCTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCA 611
Qy 1246 TACCAGCTCCAGTATGAGTGCATCTCACCCCTTTACCGCGCCCTGGGCGAGCAGCAGGAG 1305
Db 612 TACCAGCTCCAGTATGAGTGCATCTCACCCCTTTACCGCGCCCTGGGCGAGCAGCAGGAG 671
Qy 1306 GACATGCTGAGGACTCGGAAGTGGAGTGGCGGCGCACCATCTGTCATCTCCCTATCTCGG 1365
Db 672 GACATGCTGAGGACTCGGAAGTGGAGTGGCGGCGCACCATCTGTCATCTCCCTATCTCGG 731
Qy 1366 GAAA 1369
Db 732 GAAA 735

RESULT 7
BX399905
LOCUS BX399905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1086Y021 5-PRIME, mRNA sequence.
ACCESSION BX399905
VERSION BX399905.2 GI:46876619
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li W.B., Gruber C., Jessee J., and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622029.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen. This sequence belongs to sequence cluster
5757.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1086AH1QPI&c=5757.r.
FEATURES
source
1. 1049
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086Y021"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 24.8%; Score 706; DB 5; Length 1049;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 14 GCCGGGCAAGGATGAGCTGGTTCGCGAGCGAGTGGGGCTCACATTTTCTTCAGCTC 73
Db 1 GCCGGGCAAGGATGAGCTGGTTCGCGAGCGAGTGGGGCTCACATTTTCTTCAGCTC 60
Qy 74 CTTCTCATCTCGTCTGCCAAGAGATACACAGTCATTAAATGAAGCTGCCCTCGAGCA 133
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Db 61 CTTCTCATCTCGTCTGCCAAGAGATACACAGTCATTAAATGAAGCTGCCCTCGAGCA 120
Qy 134 GAGTGAATATCATCTGTCGGGAGTGTCTGTAATATGATCAGATTGAGTGGCTCTGCCCC 193
Db 121 GAGTGAATATCATCTGTCGGGAGTGTCTGTAATATGATCAGATTGAGTGGCTCTGCCCC 180
Qy 194 GGAAGAGGGGAAGTCTGGTGGTTATACCATCCCTTCTGTCAGGAAATGAGGAGAATGAGTGT 253
Db 181 GGAAGAGGGGAAGTCTGGTGGTTATACCATCCCTTCTGTCAGGAAATGAGGAGAATGAGTGT 240
Qy 254 GACTCTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAT 313
Db 241 GACTCTCTGCTGATCCACCCAGGTTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAT 300
Qy 314 GGCTCATGGGGGGTACCTTCGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGC 373
Db 301 GGCTCATGGGGGGTACCTTCGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGC 360
Qy 374 CGAGCAGGCTGGTACGGAGGAGACTGCAATGCGATGTGGCCAGGTTCTCGAGCCCCAAAG 433
Db 361 CGAGCAGGCTGGTACGGAGGAGACTGCAATGCGATGTGGCCAGGTTCTCGAGCCCCAAAG 420
Qy 434 GGTGAGATTTGTTGGAAAAGCTATCCCTAAATGCTCATCTGTAATGACCATTCATGCT 493
Db 421 GGTGAGATTTGTTGGAAAAGCTATCCCTAAATGCTCATCTGTAATGACCATTCATGCT 480
Qy 494 AAACCTGGTGTGTCATCCAACTAAGATTTCTGTCATGTTGAGTCTGGAGTTTGACTACATG 553
Db 481 AAACCTGGTGTGTCATCCAACTAAGATTTCTGTCATGTTGAGTCTGGAGTTTGACTACATG 540
Qy 554 TGCCAGTATGACTATGTTGAGTTCGTGATGGAGACAAACCCGATGGCCAGATCATCAAG 613
Db 541 TGCCAGTATGACTATGTTGAGTTCGTGATGGAGACAAACCCGATGGCCAGATCATCAAG 600
Qy 614 CGTGTCTGTGCAACAGCGCCAGCTCTTATCCAGAGCATAGATCTCTCACTCCACGTC 673
Db 601 CGTGTCTGTGCAACAGCGCCAGCTCTTATCCAGAGCATAGGATCTCTCACTCCACGTC 660
Qy 674 CTCCTTCCACTCCGATGGCTCCAAAGATTTTCACCGTTTCCATGCCATTTATGAGGAGATC 733
Db 661 CTCCTTCCACTCCGATGGCTCCAAAGATTTTCACCGTTTCCATGCCATTTATGAGGAGATC 720
Qy 734 ACAGCATGCTCTCTCATCCCTTGTGTTCCATGACGGCA 770
Db 721 ACAGCATGCTCTCTCATCCCTTGTGTTCCATGACGGCA 757

RESULT 8
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LOCUS BX399904 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1086Y021 3-PRIME, mRNA sequence.
ACCESSION BX399904
VERSION BX399904.2 GI:46874780
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li W.B., Gruber C., Jessee J., and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30622027.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen. This sequence belongs to sequence cluster
```

5757.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?S=CS0D1086AH11NP1&c=5757.r.

## FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086Y021"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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## ORIGIN

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Query Match      24.3%; Score 691; DB 5; Length 1008;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 791; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1869 ACACACTGGCTCTGGGGTGGTCACTGTGGTCACTCGCTGCTGTGTGAGGAGCAGCATG 1928
DB 1815 ACACACTGGCTCTGGGGTGGTCACTGTGGTCACTCGCTGCTGTGTGAGGAGCAGCATG 756
QY 1929 AGGACCATGGCATCCAGTGAAGTGTCACTGATPAACATGTTCTGTGCCAGCTGGGAACCCA 1988
DB 755 AGGACCATGGCATCCAGTGAAGTGTCACTGATPAACATGTTCTGTGCCAGCTGGGAACCCA 696
QY 1989 CTGCCCCCTTCTGATATCTGCACTGACAGACAGAGAGGCATCGCGCTGTGCTTCCCGG 2048
DB 695 CTGCCCCCTTCTGATATCTGCACTGACAGACAGAGAGGCATCGCGCTGTGCTTCCCGG 636
QY 2049 GACGAGCATCTCTGAGCCACGCTGGCATCTCATGGAGCTGTGAGTGGAGCTATGATA 2108
DB 635 GACGAGCATCTCTGAGCCACGCTGGCATCTCATGGAGCTGTGAGTGGAGCTATGATA 576
QY 2109 AAACATGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGA 2168
DB 575 AAACATGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTTAAAGACTGGA 516
QY 2169 TTGAAGAAATATGAATGAACCATCTCATGCTTCCACCAAGGTGCTGCTTTTAAAGACTG 2228
DB 515 TTGAAGAAATATGAATGAACCATCTCATGCTTCCACCAAGGTGCTGCTTTTAAAGACTG 456
QY 2229 CGTCTGTAGCTGTGTCATTGGCTGAAGCAGTGTGGGCTGGAAGTGTGATTTGGCCCTGTGA 2288
DB 455 CGTCTGTAGCTGTGTCATTGGCTGAAGCAGTGTGGGCTGGAAGTGTGATTTGGCCCTGTGA 396
QY 2289 ACTTGGCTGTGTCAGGGCTTCTGACTTTCAGGGACAAACTCAGTGAAGGGTGAAGTAGACC 2348
DB 395 ACTTGGCTGTGTCAGGGCTTCTGACTTTCAGGGACAAACTCAGTGAAGGGTGAAGTAGACC 336
QY 2349 TCCATTGTGTGATGCTGATGCGCGTCCACTACTAGAGACCCAAATGGGAAGATGCCAG 2408
DB 335 TCCATTGTGTGATGCTGATGCGCGTCCACTACTAGAGACCCAAATGGGAAGATGCCAG 276
QY 2409 GGCTTGAAGAGTAAAGTTCCTTCAAGAGACCATATACAAACCTCTCCACTCCACTG 2468
DB 275 GGCTTGAAGAGTAAAGTTCCTTCAAGAGACCATATACAAACCTCTCCACTCCACTG 216
QY 2469 ACCTGGTGGTCTTCCCAACTTTCAGTTATAGAAATGCGCATCAGCTTGACACAGGGAAGAT 2528
DB 215 ACCTGGTGGTCTTCCCAACTTTCAGTTATAGAAATGCGCATCAGCTTGACACAGGGAAGAT 156
QY 2529 CTGGGCTTCATGAGGCCCTTTTGAAGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACAG 2588
DB 155 CTGGGCTTCATGAGGCCCTTTTGAAGCTCTCAAGTCTTAGAGAGCTGCTGTGGGACAG 96
QY 2589 CCCAGGCGAGCAGAGCTGGAGTGTGGTGCATGCCCTTTGTGTACATGGCCACAGTACATC 2648
DB 95 CCCAGGCGAGCAGAGCTGGAGTGTGGTGCATGCCCTTTGTGTACATGGCCACAGTACATC 36
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QY 2649 TGGTCTCTTTTCT 2661

DB 35 TGGTCTCTTTTCT 23

## RESULT 9

CD514783

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 879)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgsbbs-re@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM477 row: m column: 24

High quality sequence stop: 613.

Location/Qualifiers

1..879

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:30396311"

/tissue\_type="White Matter"

/dev\_stage="Unknown"

/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"

/clone\_lib="NIH MGC 181"

/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV

(destroyed); Library is oligo-dT primed and directionally

cloned (EcoRV site is destroyed upon cloning). Average

insert size 1.42 kb. Library was constructed by

(Invitrogen). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match

Best Local Similarity

Matches 785; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

QY 952 CGTGTGTCTTTCTTTTGTAACTCTTCTAGTGGCAATGAGAAAGAACTTG 1011

DB 1 CGTGTGTCTTTCTTTTGTAACTCTTCTAGTGGCAATGAGAAAGAACTTG 60

QY 1012 CCAGCAGATGGAGAGTGGTCAGGAAACAGCCCATCTGCATATAAGCCTGCCGAGAAC 1071

DB 61 CCAGCAGATGGAGAGTGGTCAGGAAACAGCCCATCTGCATATAAGCCTGCCGAGAAC 120

QY 1072 AAAGATTTACACCTGGTGAAGAGAGTCTTCCGATGCAAGTTCAGTCAAGGAGAC 1131

DB 121 AAAGATTTACACCTGGTGAAGAGAGTCTTCCGATGCAAGTTCAGTCAAGGAGAC 180

QY 1132 ACCATTACACAGCTATATCTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGCCCTTAC 1191

DB 181 ACCATTACACAGCTATATCTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTGCCCTTAC 240

QY 1192 CAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCA 1251



ACCESSION B0014545  
VERSION B0014545.1 GI:19739446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 723)  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Dr. Jose Mercuende  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
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/mol\_type="mRNA"  
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/clone="IMAGE:5833419"  
/tissue\_type="Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP ED1"  
/note="Organ: Left Pubic Bone; Vector: p7T73-Pac  
(Pharmacia) with a modified polylinker; Site 1: Ecor I;  
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library  
containing the following tissue(s): Chondrosarcoma cell  
line C55. The library was constructed according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an Ecor I adaptor, digested with Not  
I, and cloned directionally into p7T73-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is GCTCAAGGCT.  
TAG TISSUE=chondrosarcoma  
TAG\_LIIB=UI-H-ED1  
TAG\_SEQ=CGTCAAGGCT"

ORIGIN  
Query Match 23.6%; Score 672; DB 5; Length 723;  
Best Local Similarity 99.9%; Pred. No. 1.8e-313;  
Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2007 GCATGCGAGACAGAGGACATCGCGGTGTGCTCTCCCGGACGAGCATCTCTGTAGC 2066  
DB 723 GCATGCGAGACAGAGGACATCGCGGTGTGCTCTCCCGGACGAGCATCTCTGTAGC 664  
QY 2067 CACGCTGCGATCTGATGGACTGTGTCAGCTGGAGCTATGATAAATGACGACGACGAC 2126  
DB 663 CACGCTGCGATCTGATGGAGCTGTGTCAGCTGGAGCTATGATAAATGACGACGACGAC 604  
QY 2127 TCTCCACTGCTTACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAT 2186  
DB 603 TCTCCACTGCTTACCAAGGTGCTGCTTTTAAAGACTGGATTGAAAGAAATATGAAT 544  
QY 2187 GAACCATGCTCATGCACTCTCTTGAGAGAGTGTTCGTATATCCGCTGTACGTGTGTCAT 2246  
DB 543 GAACCATGCTCATGCACTCTCTTGAGAGAGTGTTCGTATATCCGCTGTACGTGTGTCAT 484  
QY 2247 TCGGTGAAGCAGTGTGGGCGCTGAAGTGTGATTGGCCCTGTGAACCTTGGCTGTGCCAGGCG 2306

DB 483 TCGGTGAAGCAGTGTGGGCGCTGAAGTGTGATTGGCCCTGTGAACCTTGGCTGTGCCAGGCG 424  
QY 2307 TTCTCACTTCAGGGACAAAACCTCAGTGAAGGCTGAGTAGACCTCCATTCCTGGTAGGCTG 2366  
DB 423 TTCTCACTTCAGGGACAAAACCTCAGTGAAGGCTGAGTAGACCTCCATTCCTGGTAGGCTG 364  
QY 2367 ATGGCGGCTCCACTACTAGGACAGCCCAATTCGAAGATGCCAGGCTTCGAAGAAGTAAGT 2426  
DB 363 ATGGCGGCTCCACTACTAGGACAGCCCAATTCGAAGATGCCAGGCTTCGAAGAAGTAAGT 304  
QY 2427 TTCTTCAAGAGAACCATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCCA 2486  
DB 303 TTCTTCAAGAGAACCATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCCA 244  
QY 2487 ACTTTCAGTTATACGAATGCCATCAGCTTGACCGAGGAAGATCTGGGCTTCATGAGGCC 2546  
DB 243 ACTTTCAGTTATACGAATGCCATCAGCTTGACCGAGGAAGATCTGGGCTTCATGAGGCC 184  
QY 2547 CTTTGTAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGACAGCCCGAGGCGCAGAGCTG 2606  
DB 183 CTTTGTAGGCTCTCAAGTCTTAGAGAGCTGCTGTGGACAGCCCGAGGCGCAGAGCTG 124  
QY 2607 GGATGTGGTGCATGCTTTGTGTATCATGGCCACAGTACAGTCTGCTCTTTCTTCCCC 2666  
DB 123 GGATGTGGTGCATGCTTTGTGTATCATGGCCACAGTACAGTCTGCTCTTTCTTCCCC 64  
QY 2667 ATCTCTTGTACACATTTTAAATAAATAGGGTGTGGCTTCTGAACCTACAAAATAAAAAA 2726  
DB 63 ATCTCTTGTACACATTTTAAATAAATAGGGTGTGGCTTCTGAACCTACAAAATAAAAAA 4  
QY 2727 AAA 2729  
DB 3 AAA 1

RESULT 12  
BX337781 886 bp mRNA linear EST 07-APR-2004  
LOCUS BX337781 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CSODI051YA20 5-PRIME, mRNA sequence.  
ACCESSION BX337781  
VERSION BX337781.2 GI:46268407  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 2, 2003 this sequence version replaced gi:30333640.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5757.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CSODI051BA10QPI&c=5757.r.

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/note="1st strand cDNA was primed with a NotI-oligo(dT)





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QY 2274 TGATTTGGCTGTGAACCTTGGCTGTGTCAGGGCTTCTGACTTCAGGGACAAACCTCAGTG 2333
Db 181 TGATTTGGCTGTGAACCTTGGCTGTGTCAGGGCTTCTGACTTCAGGGACAAACCTCAGTG 240
QY 2334 AAGGGTGAGTAGACCTCCATTCGTGTAGGCTGATCCGCGTCCACTACTAGGACAGCCA 2393
Db 241 AAGGGTGAGTAGACCTCCATTCGTGTAGGCTGATCCGCGTCCACTACTAGGACAGCCA 300
QY 2394 ATTGAAGATGTCAGGGCTTGCAAGAAGTAAGTTCTTCAAGAAGAACCATATACAAAAC 2453
Db 301 ATTGAAGATGTCAGGGCTTGCAAGAAGTAAGTTCTTCAAGAAGAACCATATACAAAAC 360
QY 2454 CTCTCCACTCCACTGACCTGTGCTTCCCACTTCCTGATTTACGAATGCCATCAGC 2513
Db 361 CTCTCCACTCCACTGACCTGTGCTTCCCACTTCCTGATTTACGAATGCCATCAGC 420
QY 2514 TTGACCGGAGATCTGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 2573
Db 421 TTGACCGGAGATCTGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 480
QY 2574 CTGCTGTGGGACAGCCAGGCGCAGAGCTGGGATGTGTGCAATGCTTTGTGTACAT 2633
Db 481 CTGCTGTGGGACAGCCAGGCGCAGAGCTGGGATGTGTGCAATGCTTTGTGTACAT 540
QY 2634 GGCCACAGTACAGTCTGTGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 2693
Db 541 GGCCACAGTACAGTCTGTGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 600
QY 2694 AGGGTTGGCTTCTGAACTACAAAAAATAAAAAAAAAAAAAAAAAAAAA 2733
Db 601 AGGGTTGGCTTCTGAACTACAAAAAATAAAAAAAAAAAAAAAAAAAAA 640
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RESULT 14
BM930545
LOCUS BM930545 645 bp mRNA linear EST 13-MAR-2002
DEFINITION UI-E-EJ1-ajm-e-22-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajm-e-22-0-UI 5', mRNA sequence.
ACCESSION BM930545
VERSION BM930545.1 GI:19389718
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS Bonaldo,M.P., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
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/tissue_type="fetal eyes, lens, eye anterior segment,
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## ORIGIN

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Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2154 CTTTAAAGACTGGATTGAAAGAAATATGAATGAACCATGCTCATGCACCTCTTTGAGAA 2213
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QY 2214 GTGTTTCTGTATATCCGCTCTGTAGCTGTGTCAATTCGCTGAAGAGCATGTGGGCTGAAGTG 2273
Db 121 GTGTTTCTGTATATCCGCTCTGTAGCTGTGTCAATTCGCTGAAGAGCATGTGGGCTGAAGTG 180

QY 2274 TGATTTGGCTGTGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGACAAACCTCAGTG 2333
Db 181 TGATTTGGCTGTGAACCTTGGCTGTGCCAGGCTTCTGACTTCAGGGACAAACCTCAGTG 240

QY 2334 AAGGCTGAGTAGACCTCCATTCGTGTAGGCTGATCCGCGTCCACTACTAGGACAGCCA 2393
Db 241 AAGGCTGAGTAGACCTCCATTCGTGTAGGCTGATCCGCGTCCACTACTAGGACAGCCA 300

QY 2394 ATTGAAGATGCCAGGGCTTGCAAGAAGTAAGTTCTTCAAGAAGAACCATATACAAAAC 2453
Db 301 ATTGAAGATGCCAGGGCTTGCAAGAAGTAAGTTCTTCAAGAAGAACCATATACAAAAC 360

QY 2454 CTCTCCACTCCACTGACCTGTGCTTCCCACTTCCTGATTTACGAATGCCATCAGC 2513
Db 361 CTCTCCACTCCACTGACCTGTGCTTCCCACTTCCTGATTTACGAATGCCATCAGC 420

QY 2514 TTGACCGGAGATCTGGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 2573
Db 421 TTGACCGGAGATCTGGGCTTCATGAGGCCCTTTGAGGCTCTCAAGTTCTAGAGAG 480

QY 2574 CTGCTGTGGGACAGCCAGGCGCAGAGCTGGGATGTGTGCAATGCTTTGTGTACAT 2633
Db 481 CTGCTGTGGGACAGCCAGGCGCAGAGCTGGGATGTGTGCAATGCTTTGTGTACAT 540

QY 2634 GGCCACAGTACAGTCTGTGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 2693
Db 541 GGCCACAGTACAGTCTGTGCTCTTTTCCCTCCCATCTCTGTGACACATTTAATAAATA 600

QY 2694 AGGGTTGGCTTCTGAACTACAAAAAATAAAAAAAAAAAAAAAAAAAAA 2733
Db 601 AGGGTTGGCTTCTGAACTACAAAAAATAAAAAAAAAAAAAAAAAAAAA 640
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optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"

/dev stage="fetal and adult"

/lab host="DH10B (Life Technologies) (T1 phage resistant)"

/clone lib="UI-E-EJ1"

/note="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tags for this library are: fetal eyes, AGATCAGA; lens, CGATTAGCA; eye anterior segment, AATGCCGAT; optic nerve, CCAATAGTG; retina, CCGG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."



RESULT 15  
 BU742056/c  
 LOCUS  
 DEFINITION BU742056 722 bp mRNA linear EST 10-OCT-2002  
 UI-E-E01-aiy-g-09-0-UI.s1 UI-E-E01 Homo sapiens cDNA clone  
 UI-E-E01-aiy-g-09-0-UI 3', mRNA sequence.  
 ACCESSION  
 VERSION BU742056  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 722)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 FORWARD  
 POLYA=yes.

## FEATURES

Location/Qualifiers  
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 /clone\_lib="UI-E-E01"  
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 UI-E-E01 is a normalized cDNA library containing the  
 following tissue(s): fetal eye. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT7T3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 CGGTATACC. This library was created for the program, Gene  
 Discovery in the Visual System, supported by National Eye  
 Institute (NEI).  
 TAG\_TISSUE=human fetal eye  
 TAG\_LIB=UI-E-E01  
 TAG\_SEQ=CGGTATACC"

## ORIGIN

Query Match 22.5%; Score 640; DB 5; Length 722;  
 Best Local Similarity 99.9%; Pred. No. 4.7e-298;  
 Matches 690; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 DB 691 TCCTTCCCGGACGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGG 632

QY 2099 AGCTATGATAAAACATGACGAGCCACAGGCTCTCCACTGCTTCCACCAAGGTGCTGCTTTT 2158  
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Search completed: May 8, 2005, 13:11:45  
 Job time : 6103 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 8, 2005, 11:21:33 ; Search time 1081 Seconds  
(without alignments)  
16098.112 Million cell updates/sec

Perfect score: 2846

Sequence: 1 cgtcggccaccgacgcgg.....aaaaaaaaaaaaaaaaaa 2846

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 5654200 seqs, 3057283753 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Published Applications NA: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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739	2846	100.0	2846	15	US-10-972-317-37
740	2556	89.8	2845	15	US-10-101-510-644
741	2043	71.8	2306	14	US-10-004-551-3
742	2043	71.8	2306	16	US-10-098-871-25
743	1880	66.1	2144	15	US-10-037-270-969
744	1880	66.1	2144	17	US-10-117-722-969
745	1827	64.2	2142	15	US-10-037-270-1006
746	1827	64.2	2142	17	US-10-117-722-1006
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					Sequence 169, App
					Sequence 37, Appl
					Sequence 37, Appl
					Sequence 644, App
					Sequence 3, Appl
					Sequence 25, Appl
					Sequence 969, App
					Sequence 969, App
					Sequence 1006, App
					Sequence 1006, App
					Sequence 2, Appl

748	1672	58.7	2632	17	US-10-274-639-38	Sequence 38, Appl
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c 752	337	11.8	337	9	US-09-954-531-1223	Sequence 1223, App
c 753	337	11.8	337	19	US-10-843-641A-1856	Sequence 1856, App
c 754	337	11.8	337	19	US-10-843-641A-2290	Sequence 2290, App
c 755	314	11.0	548	15	US-10-101-510-29	Sequence 29, Appl
756	232	8.2	403	18	US-09-918-995-6744	Sequence 6744, App
757	202	7.1	286	18	US-10-723-860-4638	Sequence 4638, App
c 758	202	7.1	554	13	US-10-027-632-275184	Sequence 275184, App
c 759	202	7.1	554	17	US-10-027-632-275184	Sequence 275184, App
760	136	4.8	2226	17	US-10-374-780A-1714	Sequence 1714, App
761	136	4.8	11394	15	US-10-412-699B-1354	Sequence 1354, App
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c 763	135	4.7	165	9	US-09-764-846-344	Sequence 344, App
764	135	4.7	165	10	US-09-764-872-709	Sequence 709, App
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773	135	4.7	606	18	US-10-437-963-54715	Sequence 54715, A
774	135	4.7	685	18	US-10-425-115-131293	Sequence 131293, App
775	135	4.7	687	17	US-10-424-599-115631	Sequence 115631, App
776	135	4.7	716	19	US-10-764-420-422	Sequence 422, App
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779	135	4.7	2022	18	US-10-739-930-4367	Sequence 4367, App
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c 789	135	4.7	6944	15	US-10-172-086-112	Sequence 112, App
c 790	135	4.7	6944	18	US-10-311-507-114	Sequence 114, App
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801	134	4.7	368	18	US-10-425-115-138566	Sequence 138566, App
802	134	4.7	381	18	US-10-021-323-10489	Sequence 10489, A
803	134	4.7	381	18	US-10-357-930-58681	Sequence 58681, A
804	134	4.7	389	18	US-10-437-963-8873	Sequence 8873, App
805	134	4.7	396	18	US-10-357-930-57615	Sequence 57615, A
806	134	4.7	409	9	US-09-822-849A-37	Sequence 37, Appl
807	134	4.7	411	18	US-10-425-115-92368	Sequence 92368, A
808	134	4.7	416	17	US-10-424-599-71220	Sequence 71220, A
809	134	4.7	426	18	US-10-021-323-9484	Sequence 9484, App
810	134	4.7	431	18	US-10-021-323-15260	Sequence 15260, A
811	134	4.7	437	17	US-10-424-599-87401	Sequence 87401, A
812	134	4.7	457	18	US-10-425-115-95616	Sequence 95616, A
813	134	4.7	458	18	US-10-021-323-11004	Sequence 11004, A
814	134	4.7	479	18	US-10-425-115-158896	Sequence 158896, App
815	134	4.7	481	18	US-10-021-323-14917	Sequence 14917, A
816	134	4.7	483	18	US-10-021-323-16622	Sequence 16622, A
817	134	4.7	490	18	US-10-357-930-57078	Sequence 57078, A
818	134	4.7	496	18	US-10-021-323-4109	Sequence 4109, App
819	134	4.7	500	18	US-10-425-115-170711	Sequence 170711, App
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c 822	134	4.7	509	18	US-10-021-323-6707	Sequence 6707, Ap	134	4.7	1929	18	US-10-425-115-161709	Sequence 161709, A
c 823	134	4.7	510	18	US-10-437-963-1928	Sequence 1928, Ap	134	4.7	1958	17	US-10-424-599-60709	Sequence 60709, A
c 824	134	4.7	518	18	US-10-021-323-4634	Sequence 4634, Ap	134	4.7	1999	18	US-10-723-860-7767	Sequence 7767, Ap
c 825	134	4.7	524	18	US-10-425-115-109499	Sequence 109499, A	134	4.7	2094	18	US-10-425-115-51614	Sequence 51614, A
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c 827	134	4.7	528	18	US-10-425-115-137716	Sequence 137716, A	134	4.7	2235	19	US-10-887-553A-987	Sequence 987, App
c 828	134	4.7	536	18	US-10-021-323-14752	Sequence 14752, A	134	4.7	2270	17	US-10-424-599-44604	Sequence 44604, A
c 829	134	4.7	540	18	US-10-021-323-10245	Sequence 10245, A	134	4.7	2288	17	US-10-424-599-67031	Sequence 67031, A
c 830	134	4.7	544	18	US-10-425-115-162816	Sequence 162816, A	134	4.7	2322	17	US-10-424-599-1231	Sequence 1231, Ap
c 831	134	4.7	545	18	US-10-021-323-6099	Sequence 6099, Ap	134	4.7	2333	17	US-10-424-599-127867	Sequence 127867, A
c 832	134	4.7	547	18	US-10-437-963-20806	Sequence 20806, A	134	4.7	2499	18	US-10-723-860-5438	Sequence 5438, Ap
c 833	134	4.7	553	18	US-10-021-323-7987	Sequence 7987, Ap	134	4.7	2520	17	US-10-389-566-205	Sequence 205, App
c 834	134	4.7	554	18	US-10-425-115-882	Sequence 882, App	134	4.7	2617	18	US-10-425-115-151022	Sequence 151022, A
c 835	134	4.7	554	18	US-10-425-115-23306	Sequence 23306, A	134	4.7	2809	17	US-10-172-118-340	Sequence 340, App
c 836	134	4.7	557	18	US-10-425-115-148098	Sequence 148098, A	134	4.7	2809	17	US-10-342-887-340	Sequence 340, App
c 837	134	4.7	560	18	US-10-021-323-3016	Sequence 3016, Ap	134	4.7	2971	18	US-10-425-115-103107	Sequence 103107, A
c 838	134	4.7	568	17	US-10-424-599-117111	Sequence 117111, A	134	4.7	3275	9	US-09-738-973-151	Sequence 151, App
c 839	134	4.7	570	18	US-10-021-323-143	Sequence 143, App	134	4.7	3275	9	US-09-854-133-151	Sequence 151, App
c 840	134	4.7	578	18	US-10-021-323-7450	Sequence 7450, Ap	134	4.7	3275	15	US-10-144-649A-151	Sequence 151, App
c 841	134	4.7	583	18	US-10-767-795-134	Sequence 134, App	134	4.7	3758	18	US-10-437-963-81706	Sequence 81706, A
c 842	134	4.7	595	18	US-10-425-115-175716	Sequence 175716, A	134	4.7	4824	18	US-10-723-860-5191	Sequence 5191, Ap
c 843	134	4.7	596	17	US-10-424-599-18370	Sequence 18370, A	134	4.7	6171	15	US-10-311-455-761	Sequence 761, App
c 844	134	4.7	597	18	US-10-021-323-11423	Sequence 11423, A	134	4.7	6486	18	US-10-433-793-80	Sequence 80, Appl
c 845	134	4.7	606	17	US-10-424-599-54586	Sequence 54586, A	134	4.7	7115	18	US-10-723-860-7372	Sequence 7372, Ap
c 846	134	4.7	606	17	US-10-424-599-93300	Sequence 93300, A	134	4.7	7369	18	US-10-473-126-277	Sequence 277, App
c 847	134	4.7	608	18	US-10-021-323-636	Sequence 636, App	134	4.7	7369	19	US-10-486-319A-56	Sequence 56, Appl
c 848	134	4.7	616	18	US-10-021-323-5390	Sequence 5390, Ap	134	4.7	8899	15	US-10-311-455-810	Sequence 810, App
c 849	134	4.7	647	18	US-10-425-115-18397	Sequence 18397, A	134	4.7	8946	17	US-10-257-166-156	Sequence 156, App
c 850	134	4.7	684	18	US-10-425-115-168572	Sequence 168572, A	134	4.7	8946	15	US-10-311-455-884	Sequence 884, App
c 851	134	4.7	704	18	US-10-425-115-21405	Sequence 21405, A	134	4.7	15832	14	US-10-239-676-106	Sequence 106, App
c 852	134	4.7	704	18	US-10-425-115-21405	Sequence 21405, A	134	4.7	15832	15	US-10-311-455-1316	Sequence 1316, Ap
c 853	134	4.7	718	18	US-10-425-115-154975	Sequence 154975, A	134	4.7	15832	15	US-10-240-453-118	Sequence 118, App
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c 855	134	4.7	831	18	US-10-913-553-67	Sequence 67, Appl	133	4.7	148	9	US-09-764-869-1437	Sequence 1437, Ap
c 856	134	4.7	899	18	US-10-437-963-27088	Sequence 27088, A	133	4.7	148	9	US-09-764-846-272	Sequence 272, App
c 857	134	4.7	924	18	US-10-425-115-173094	Sequence 173094, A	133	4.7	148	9	US-09-764-846-285	Sequence 285, App
c 858	134	4.7	936	17	US-10-424-599-69990	Sequence 69990, A	133	4.7	148	9	US-09-764-846-295	Sequence 295, App
c 859	134	4.7	936	17	US-10-424-599-112681	Sequence 112681, A	133	4.7	148	9	US-09-764-846-337	Sequence 337, App
c 860	134	4.7	980	18	US-10-723-860-4894	Sequence 4894, Ap	133	4.7	148	10	US-09-764-891-7489	Sequence 7489, Ap
c 861	134	4.7	987	17	US-10-424-599-114407	Sequence 114407, A	133	4.7	148	10	US-09-764-891-7703	Sequence 7703, Ap
c 862	134	4.7	1068	18	US-10-437-963-86611	Sequence 86611, A	133	4.7	148	10	US-09-764-891-9406	Sequence 9406, Ap
c 863	134	4.7	1091	18	US-10-723-860-6015	Sequence 6015, Ap	133	4.7	148	10	US-09-764-891-9809	Sequence 9809, Ap
c 864	134	4.7	1093	18	US-10-425-115-68317	Sequence 68317, A	133	4.7	148	11	US-09-973-278-836	Sequence 836, App
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c 867	134	4.7	1133	18	US-10-425-115-159679	Sequence 159679, A	133	4.7	148	14	US-10-091-483-295	Sequence 295, App
c 868	134	4.7	1140	18	US-10-437-963-26438	Sequence 26438, A	133	4.7	148	14	US-10-091-483-337	Sequence 337, App
c 869	134	4.7	1233	17	US-10-424-599-44264	Sequence 44264, A	133	4.7	148	14	US-10-091-504-1437	Sequence 1437, Ap
c 870	134	4.7	1301	18	US-10-425-115-179473	Sequence 179473, A	133	4.7	148	15	US-10-205-428-950	Sequence 950, App
c 871	134	4.7	1306	18	US-10-425-115-83709	Sequence 83709, A	133	4.7	148	17	US-10-091-414-274	Sequence 274, App
c 872	134	4.7	1398	18	US-10-425-115-169951	Sequence 169951, A	133	4.7	148	17	US-10-227-577-1437	Sequence 1437, Ap
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c 874	134	4.7	1463	17	US-10-424-599-88284	Sequence 88284, A	133	4.7	196	18	US-10-668-749A-5	Sequence 5, Appl
c 875	134	4.7	1484	18	US-10-425-115-24588	Sequence 24588, A	133	4.7	212	17	US-10-242-535A-22243	Sequence 22243, A
c 876	134	4.7	1492	18	US-10-425-115-103271	Sequence 103271, A	133	4.7	212	17	US-10-085-783A-22243	Sequence 22243, A
c 877	134	4.7	1504	18	US-10-425-115-63627	Sequence 63627, A	133	4.7	220	9	US-09-960-352-14522	Sequence 14522, A
c 878	134	4.7	1512	18	US-10-425-115-131408	Sequence 131408, A	133	4.7	225	9	US-09-925-299-744	Sequence 744, App
c 879	134	4.7	1519	18	US-10-425-115-17631	Sequence 17631, A	133	4.7	225	10	US-09-925-299-744	Sequence 744, App
c 880	134	4.7	1521	17	US-10-172-118-1450	Sequence 1450, Ap	133	4.7	231	17	US-10-242-535A-30412	Sequence 30412, A
c 881	134	4.7	1521	17	US-10-342-887-1450	Sequence 1450, Ap	133	4.7	231	17	US-10-085-783A-30412	Sequence 30412, A
c 882	134	4.7	1576	18	US-10-723-860-5808	Sequence 5808, Ap	133	4.7	242	9	US-09-960-352-3873	Sequence 3873, Ap
c 883	134	4.7	1603	18	US-10-357-930-22091	Sequence 22091, A	133	4.7	260	17	US-10-242-535A-40371	Sequence 40371, A
c 884	134	4.7	1603	18	US-10-357-930-23103	Sequence 23103, A	133	4.7	260	17	US-10-085-783A-40371	Sequence 40371, A
c 885	134	4.7	1603	18	US-10-357-930-27953	Sequence 27953, A	133	4.7	286	9	US-09-960-352-13342	Sequence 13342, A
c 886	134	4.7	1603	18	US-10-357-930-28971	Sequence 28971, A	133	4.7	305	17	US-10-231-956A-85	Sequence 85, Appl
c 887	134	4.7	1617	18	US-10-425-115-164014	Sequence 164014, A	133	4.7	309	18	US-10-357-930-45013	Sequence 45013, A
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c 890	134	4.7	1678	18	US-10-437-963-95688	Sequence 95688, A	133	4.7	325	17	US-10-424-599-59828	Sequence 59828, A
c 891	134	4.7	1678	18	US-10-425-115-71345	Sequence 71345, A	133	4.7	325	18	US-10-021-323-8658	Sequence 8658, Ap
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c 893	134	4.7	1803	17	US-10-374-780A-1279	Sequence 1279, Ap	133	4.7	338	18	US-10-425-115-65485	Sequence 65485, A

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c 974	133	4.7	378	18	US-10-425-115-60509	Sequence 80509, A	1047	133	4.7	539	17	US-10-424-599-76890	Sequence 76890, A
c 975	133	4.7	391	18	US-10-425-115-13025	Sequence 13025, A	1048	133	4.7	539	18	US-10-425-115-152949	Sequence 152949, A
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c 980	133	4.7	396	17	US-10-361-811-53	Sequence 53, App1	1053	133	4.7	543	18	US-10-437-963-40831	Sequence 40831, A
c 981	133	4.7	396	17	US-10-369-186-53	Sequence 53, App1	1054	133	4.7	544	18	US-10-425-115-26104	Sequence 26104, A
c 982	133	4.7	398	18	US-10-021-323-7863	Sequence 7863, App	1055	133	4.7	545	17	US-10-424-599-48829	Sequence 4829, App
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c 986	133	4.7	406	10	US-09-814-353-11195	Sequence 11195, A	1059	133	4.7	547	18	US-10-021-323-8671	Sequence 8671, App
c 987	133	4.7	408	18	US-10-357-930-34697	Sequence 34697, A	c1060	133	4.7	547	18	US-10-021-323-16890	Sequence 16890, A
c 988	133	4.7	408	18	US-10-357-930-43554	Sequence 43554, A	c1061	133	4.7	549	18	US-10-021-323-7101	Sequence 7101, App
c 989	133	4.7	411	18	US-10-021-323-7694	Sequence 7694, App	1062	133	4.7	549	18	US-10-437-963-43799	Sequence 43799, A
c 990	133	4.7	419	17	US-10-424-599-58948	Sequence 58948, A	c1063	133	4.7	552	18	US-10-021-323-17351	Sequence 17351, A
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c1290	132	4.6	970	17	US-10-264-049-91	Sequence 91, Appl	1363	129	4.5	421	9	US-09-960-352-9222	Sequence 9222, App
c1291	132	4.6	1389	18	US-10-723-860-5322	Sequence 5322, App	1364	129	4.5	422	18	US-10-425-115-54417	Sequence 54417, A
c1292	132	4.6	1468	18	US-10-425-115-155043	Sequence 155043, A	1365	129	4.5	432	17	US-10-424-599-83231	Sequence 83231, A
c1293	132	4.6	2110	18	US-10-425-115-181585	Sequence 181585, A	1366	129	4.5	460	9	US-09-960-352-4953	Sequence 4953, App
c1294	132	4.6	2394	9	US-09-800-729-33	Sequence 33, Appl	1367	129	4.5	497	17	US-10-424-599-47120	Sequence 47120, A
c1295	132	4.6	2585	18	US-10-425-115-54177	Sequence 54177, A	1368	129	4.5	502	18	US-10-357-930-57784	Sequence 57784, A
c1296	132	4.6	2721	18	US-10-425-115-26594	Sequence 26594, A	1369	129	4.5	513	18	US-10-425-115-90741	Sequence 90741, A
c1297	132	4.6	6775	18	US-10-433-793-189	Sequence 189, App	1370	129	4.5	513	17	US-10-424-599-141420	Sequence 141420, A
c1298	131	4.6	131	9	US-09-770-696-616	Sequence 616, App	1371	129	4.5	538	17	US-10-424-599-8435	Sequence 8435, App
c1299	131	4.6	358	17	US-10-242-535A-16192	Sequence 16192, A	c1372	129	4.5	548	18	US-10-021-323-16019	Sequence 16019, A
c1300	131	4.6	358	17	US-10-085-783A-16192	Sequence 16192, A	1373	129	4.5	560	18	US-10-021-323-12602	Sequence 12602, A
c1301	131	4.6	362	18	US-10-425-115-36607	Sequence 36607, A	1374	129	4.5	569	17	US-10-424-599-50759	Sequence 50759, A
c1302	131	4.6	459	18	US-10-437-963-6545	Sequence 6545, App	c1375	129	4.5	578	18	US-10-021-323-7928	Sequence 7928, App
c1303	131	4.6	505	18	US-10-425-115-43909	Sequence 43909, A	1376	129	4.5	588	18	US-10-437-963-55397	Sequence 55397, A
c1304	131	4.6	526	17	US-10-424-599-89355	Sequence 89355, A	1377	129	4.5	595	17	US-10-424-599-128362	Sequence 128362, A
c1305	131	4.6	527	18	US-10-425-115-133198	Sequence 133198, A	1378	129	4.5	639	18	US-10-767-795-230	Sequence 230, App
c1306	131	4.6	539	17	US-10-424-599-61810	Sequence 61810, A	1379	129	4.5	650	17	US-10-424-599-8610	Sequence 8610, App
c1307	131	4.6	559	18	US-10-425-115-130331	Sequence 130331, A	1380	129	4.5	662	18	US-10-425-115-104281	Sequence 104281, App
c1308	131	4.6	576	18	US-10-425-115-86318	Sequence 86318, A	1381	129	4.5	679	18	US-10-425-115-54897	Sequence 54897, A
c1309	131	4.6	589	18	US-10-437-963-16840	Sequence 16840, A	1382	129	4.5	703	18	US-10-425-115-165037	Sequence 165037, A
c1310	131	4.6	597	18	US-10-425-115-176033	Sequence 176033, A	1383	129	4.5	710	17	US-10-424-599-30592	Sequence 30592, A
c1311	131	4.6	603	18	US-10-425-115-152926	Sequence 152926, A	1384	129	4.5	972	18	US-10-425-115-51692	Sequence 51692, A
c1312	131	4.6	612	18	US-10-425-115-56968	Sequence 56968, A	1385	129	4.5	1045	17	US-10-424-599-60872	Sequence 60872, A
c1313	131	4.6	840	17	US-10-424-599-496138	Sequence 49578, A	1386	129	4.5	1051	9	US-09-893-238-10	Sequence 10, Appl
c1314	131	4.6	1015	17	US-10-424-599-96137	Sequence 96137, A	1387	129	4.5	1163	18	US-10-425-115-173100	Sequence 173100, A
c1315	131	4.6	1088	18	US-10-425-115-95565	Sequence 95565, A	1388	129	4.5	1380	18	US-10-411-120-36	Sequence 36, Appl
c1316	131	4.6	1302	18	US-10-425-115-56162	Sequence 56162, A	1389	129	4.5	1811	17	US-10-425-115-44753	Sequence 44753, A
c1317	131	4.6	1372	19	US-10-887-553A-1050	Sequence 1050, App	1390	129	4.5	2045	18	US-10-739-930-3948	Sequence 3948, App
c1318	131	4.6	1635	18	US-10-425-115-85095	Sequence 85095, A	1391	129	4.5	2634	18	US-10-425-115-148096	Sequence 148096, A
c1319	131	4.6	1806	18	US-10-775-920-225	Sequence 225, App	c1392	129	4.5	6577	15	US-10-311-455-1329	Sequence 1329, App
c1320	131	4.6	1812	18	US-10-425-115-53485	Sequence 53485, A	c1393	129	4.5	6577	17	US-10-221-613-181	Sequence 181, App
c1321	131	4.6	2827	18	US-10-357-930-22992	Sequence 22992, A	c1394	128	4.5	152	9	US-09-960-352-6995	Sequence 6995, App
c1322	131	4.6	2827	18	US-10-357-930-28857	Sequence 28857, A	1395	128	4.5	365	9	US-09-960-352-5456	Sequence 5456, App
c1323	131	4.6	3101	17	US-10-424-599-95087	Sequence 95087, A	1396	128	4.5	375	17	US-10-424-599-20347	Sequence 20347, A
c1324	131	4.6	4670	18	US-10-723-860-2449	Sequence 2449, App	1397	128	4.5	391	18	US-10-425-115-12313	Sequence 12313, A
c1325	131	4.6	4672	18	US-10-723-860-6624	Sequence 6624, App	1398	128	4.5	429	9	US-09-960-352-11097	Sequence 11097, A
c1326	130	4.6	320	18	US-10-425-115-138457	Sequence 138457, A	c1399	128	4.5	444	18	US-10-425-115-666130	Sequence 666130, A
c1327	130	4.6	399	18	US-10-425-115-150156	Sequence 150156, A	1400	128	4.5	489	18	US-10-425-115-14467	Sequence 14467, A
c1328	130	4.6	449	18	US-10-425-115-47881	Sequence 47881, A	1401	128	4.5	510	17	US-10-424-599-34481	Sequence 34481, A
c1329	130	4.6	467	18	US-10-425-115-148915	Sequence 148915, A	1402	128	4.5	511	18	US-10-425-115-63146	Sequence 63146, A
c1330	130	4.6	468	18	US-10-021-323-8271	Sequence 8271, App	1403	128	4.5	549	18	US-10-425-115-114423	Sequence 114423, A
c1331	130	4.6	474	18	US-10-021-323-10842	Sequence 10842, A	1404	128	4.5	555	18	US-10-425-115-90821	Sequence 90821, A

1405	128	4.5	556	18	US-10-021-323-14847	Sequence 14847, A
c1406	128	4.5	563	18	US-10-425-115-10912	Sequence 10912, A
1407	128	4.5	567	18	US-10-425-115-143483	Sequence 143483, A
c1408	128	4.5	571	18	US-10-425-115-861	Sequence 861, App
c1409	128	4.5	577	18	US-10-021-323-162	Sequence 162, App
1410	128	4.5	579	18	US-10-357-930-58709	Sequence 58709, A
1411	128	4.5	581	18	US-10-425-115-36960	Sequence 36960, A
1412	128	4.5	582	18	US-10-425-115-83069	Sequence 83069, A
c1413	128	4.5	584	18	US-10-021-323-6395	Sequence 6395, App
1414	128	4.5	600	18	US-10-425-115-81134	Sequence 81134, A
1415	128	4.5	603	18	US-10-425-115-40308	Sequence 40308, A
c1416	128	4.5	606	18	US-10-425-115-147131	Sequence 147131, A
1417	128	4.5	637	18	US-10-425-115-48251	Sequence 48251, A
1418	128	4.5	663	18	US-10-425-115-114479	Sequence 114479, A
1419	128	4.5	1093	17	US-10-424-599-95648	Sequence 95648, A
1420	128	4.5	1099	18	US-10-425-115-36774	Sequence 36774, A
1421	128	4.5	1269	18	US-10-425-115-119668	Sequence 119668, A
c1422	128	4.5	1629	18	US-10-425-115-72646	Sequence 72646, A
1423	128	4.5	1881	17	US-10-424-599-12512	Sequence 12512, A
1426	128	4.5	1985	9	US-09-905-291A-212	Sequence 212, App

Search completed: May 8, 2005, 16:05:52

Job time : 1113 secs



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OM protein - protein search, using sw model

Run on: May 8, 2005, 15:25:38 ; Search time 23 Seconds  
(without alignments)  
3012.003 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 79:\*\*

1: Piri:\*\*

2: Piri2:\*\*

3: Piri3:\*\*

4: Piri4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	949	24.1	181	2 T08805	hypothetical prote
2	672	17.0	2	A38738	coagulation factor
3	482	12.2	699	1 I54763	Ra-reactive factor
4	403.5	10.2	705	1 C1HURB	complement subcomp
5	400.5	10.2	686	1 A59271	Ra-reactive factor
6	378.5	9.6	695	1 S05008	complement subcomp
7	354	9.0	1524	2 T30337	polyprotein - Afri
8	340.5	8.6	694	2 JC6554	complement subcomp
9	334	8.5	688	1 C1HUS	complement subcomp
10	331.5	8.4	1019	1 A56318	enteropeptidase (E
11	330.5	8.4	1034	1 A53663	enteropeptidase (E
12	320	8.1	461	1 JX0210	protein C (activat
13	317.5	8.0	1035	1 A43090	enteropeptidase (E
14	314.5	8.0	475	1 EXCH	coagulation factor
15	313	7.9	855	2 JC7731	membrane-bound arg
16	310.5	7.9	461	1 KXHU	protein C (activat
17	299.5	7.6	443	2 I46932	coagulation factor
18	293.5	7.4	407	1 KFB07	coagulation factor
19	292	7.4	461	1 S18994	protein C (activat
20	285.5	7.2	452	1 A30351	coagulation factor
21	283.5	7.2	482	1 EXRT	coagulation factor
22	282	7.1	456	1 KXBO	protein C (activat
23	281.5	7.1	558	2 JC5878	plasma hyaluronan-
24	281	7.1	492	1 EXBO	coagulation factor
25	280.5	7.1	264	2 I38136	chymotrypsin-like
26	280	7.1	562	1 UKHU	t-plasminogen acti
27	278.5	7.1	466	1 KFHU7	coagulation factor
28	278	7.0	488	1 JX0315	coagulation factor
29	278	7.0	1113	2 JE0315	low-density lipopr

30	277	7.0	559	1 A29941	t-plasminogen acti
31	277	7.0	559	1 A35029	hepatocyte growth
32	276.5	7.0	655	1 A46688	thrombin (EC 3.4.2
33	273	6.9	625	1 TBBO	plasma hyaluronan-
34	273	6.8	560	1 JC4795	t-plasminogen acti
35	270	6.8	477	2 JS0597	t-plasminogen acti
36	264.5	6.7	431	2 JS0599	thrombin (EC 3.4.2
37	264.5	6.7	618	2 A35827	coagulation factor
38	262.5	6.7	461	1 KFHU	t-plasminogen acti
39	262	6.6	477	2 JS0598	u-plasminogen acti
40	261.5	6.6	442	1 UKPG	u-plasminogen acti
41	261	6.6	431	1 UKHU	u-plasminogen acti
42	261	6.6	433	1 JN0560	u-plasminogen acti
43	260	6.6	477	1 A34369	chymotrypsin B - A
44	259	6.6	244	2 S72219	coagulation factor
45	259	6.6	416	1 KFB0	serine proteinase
46	258.5	6.6	786	1 A47547	29K serine protein
47	258	6.5	251	2 PC1235	u-plasminogen acti
48	258	6.5	433	1 UKBAY	complement factor
49	257.5	6.5	1004	2 T30338	thrombin (EC 3.4.2
50	255.5	6.5	763	2 I50807	thrombin (EC 3.4.2
51	254	6.4	617	2 S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2 T31069	thrombin (EC 3.4.2
53	249.5	6.3	400	1 A48050	coagulation factor
54	249.5	6.3	986	1 B58788	procollagen C-endo
55	248.5	6.3	459	2 JQ0419	coagulation factor
56	248	6.3	263	2 A31299	chymotrypsin (EC 3
57	248	6.3	638	1 KQHUP	plasma kallikrein
58	247.5	6.3	991	2 I49540	procollagen C-endo
59	247	6.3	275	2 A32410	trypsin (EC 3.4.2
60	247	6.3	764	1 BBHU	complement factor
61	246.5	6.2	347	2 G00006	haptoglobin - blac
62	246.5	6.2	622	1 TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2 C42696	thrombin (EC 3.4.2
64	246	6.2	812	1 PLBO	plasmin (EC 3.4.21
65	245	6.2	234	2 F42696	thrombin (EC 3.4.2
66	244	6.1	638	1 KQMSPL	plasma kallikrein
67	242.5	6.1	730	1 BMHU1	procollagen C-endo
68	241.5	6.1	823	1 A58788	procollagen C-endo
69	240	6.1	242	2 S49489	trypsin (EC 3.4.21
70	239.5	6.1	406	1 HPHU2	haptoglobin precur
71	239	6.1	245	1 KYBOA	chymotrypsin (EC 3
72	238	6.0	237	1 TRCY1	trypsin (EC 3.4.21
73	238	6.0	263	2 A21195	chymotrypsin (EC 3
74	238	6.0	347	1 HPHU1	haptoglobin precur
75	238	6.0	375	1 A23689	limulus clotting e
76	237.5	6.0	810	2 I46260	plasmin (EC 3.4.21
77	237	6.0	263	1 KRTTB	chymotrypsin (EC 3
78	236.5	6.0	274	2 JC4171	trypsin (EC 3.4.2
79	236.5	6.0	707	2 JC2218	procollagen C-endo
80	235	6.0	270	2 S56160	mast cell tryptase
81	235	6.0	345	2 I36941	haptoglobin - chlm
82	235	6.0	1420	2 A32869	apolipoprotein(a)
83	233.5	5.9	263	2 S47537	chymotrypsin (EC 3
84	232	5.9	416	1 S33777	hepsin (EC 3.4.21.
85	232	5.9	638	1 KORTPL	plasma kallikrein
86	229.5	5.8	329	1 HPDG	haptoglobin precur
87	228.5	5.8	235	2 E42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1 HPMS	haptoglobin precur
89	228.5	5.8	861	2 A48825	Notch homolog Motc
90	228.5	5.8	2531	2 A46019	notch-1 protein -
91	228	5.8	812	1 PLMS	plasmin (EC 3.4.21
92	227.5	5.8	242	2 S31775	trypsin (EC 3.4.21
93	227.5	5.8	349	2 I36944	haptoglobin - chlm
94	227	5.8	242	2 S31776	trypsin (EC 3.4.21
95	227	5.8	1464	2 S58984	development protei
96	226.5	5.7	238	2 S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2 JCS759	brain-specific ser
98	226	5.7	394	2 JS0600	t-plasminogen acti
99	226	5.7	625	1 KFHU1	coagulation factor
100	225	5.7	615	1 KFHU12	coagulation factor
101	224.5	5.7	271	1 ELKT2	pancreatic elastas
102	224	5.7	245	1 KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-relate	177	198.5	5.0	229	1	TRB0TR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21.	178	198.5	5.0	232	1	KQPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21	180	198	5.0	250	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastas	181	198	5.0	279	2	B29934	pancreatic elastas
109	222	5.6	275	2	B35863	trypsin (EC 3.4.2	182	198	5.0	760	1	C2MS	classical-comple
110	221.5	5.6	231	2	S18188	notch protein homo	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	I36947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2	185	196.5	5.0	269	2	C26823	pancreatic elastas
113	220.5	5.6	1057	1	A32888	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	235	2	A35863	trypsin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2	188	196.5	5.0	2524	2	A35844	xotch protein - Af
116	219.5	5.6	271	2	A25528	pancreatic elastas	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BBSW	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig(f
118	219	5.6	343	1	A57014	protease (EC 3.4.	191	195	5.0	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	serine proteinase (	192	194.5	4.9	246	1	TRRT1	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	venom proteinase (	193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	pancreatic elastas	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2	196	193.5	4.9	347	1	HPRT	haptoglobin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24420	notch protein - fr	198	193	4.9	240	1	CPBOA3	procarboxypeptidas
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2	199	193	4.9	246	1	DBHU	complement factor
127	216.5	5.5	346	2	I36942	haptoglobin - chim	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	216	2	A57096	nudel protein prec	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	PLHU	plasmin (EC 3.4.21	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	247	1	TRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	JC7629	membrane-type friz
131	215.5	5.5	248	2	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	P-selectin precurs
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	fibropellin Ia - s
133	215	5.4	268	2	S68826	pancreatic elastas	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S13813	trypsin (EC 3.4.21	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JE0105	testicular serine	208	189	4.8	246	2	JQ1472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	trypsin (EC 3.4.2	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	235	2	D42696	thrombin (EC 3.4.2	211	189	4.8	258	4	S70439	pancreatic elastas
139	213.5	5.4	232	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	260	2	I58559	neuropsin - mouse	213	189	4.8	646	2	UN0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A36154	mast cell protein	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	1	UKMS	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	JQ1471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	haptoglobin Hp - C	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	thrombin (EC 3.4.2	221	187	4.7	271	2	S25239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	pancreatic elastas	222	186	4.7	1594	2	T230549	hensin - rabbit
150	207	5.2	238	1	TRWV5Y	trypsin-like prote	223	185.5	4.7	927	1	JQ0948	macrophage-stimula
151	206.5	5.2	246	1	TRRT2	trypsin (EC 3.4.21	224	185.5	4.7	711	1	A47136	A5 antigen precurs
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	apoprotein(a) (EC	227	183	4.6	265	1	KQRTP	tissue kallikrein
155	205.5	5.2	269	2	B32410	mastocytoma protel	228	183	4.6	392	1	A30100	serine proteinase
156	205.5	5.2	460	2	B61545	plasmin (EC 3.4.21	229	182.5	4.6	482	2	JCS092	E-selectin - pig
157	204.5	5.2	367	2	JE0104	testicular serine	230	182.5	4.6	722	2	I48324	DELTA-like 1 - mou
158	204.5	5.2	752	1	C2HU	complement C2 prec	231	182.5	4.6	2531	2	T31070	notch homolog - se
159	204.5	5.2	1203	2	A49175	Notch B protein -	232	182	4.6	261	1	TRMSM5	tissue kallikrein
160	203.5	5.2	247	1	S25852	trypsin (EC 3.4.21	233	181.5	4.6	247	1	PRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	serine proteinase
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	2	S18407	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	probable trypsin V	238	181	4.6	418	2	A37344	acrosin (EC 3.4.21
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	1291	2	T21694	hypothetical prote
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	trypsin (EC 3.4.21
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	275	2	I46712	factor IX - rabbit
169	200.5	5.1	226	1	KCUF	bradykinin (EC 3.4	242	180.5	4.6	436	2	JX0172	acrosin (EC 3.4.21
170	200.5	5.1	231	1	TRP0TR	trypsin (EC 3.4.21	243	180	4.6	254	2	S49329	trypsin-like prote
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21
174	199.5	5.1	258	2	G02959	haptoglobin - rhes	247	179.5	4.6	259	1	WNMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	I50719	C-Delta-1 - chicke	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	masquerade precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	ELPG	pancreatic elastas	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	JH40403	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	JH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic repetit
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	1827	2	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KFHU13	coagulation factor
257	177	4.5	268	2	JQ1473	pancreatic elastas	330	160	4.1	662	1	A31372	granzyme A (EC 3.4
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	fibrillin-1 precur
259	177	4.5	747	2	I51579	complement factor	332	159.5	4.0	1722	2	E89753	protein FlkC7.4 [i
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A44284	tissue kallikrein
261	176	4.5	261	2	A29745	tissue kallikrein	334	159	4.0	261	2	A28062	gamma-renin (EC 3.
262	176	4.5	261	2	A31136	tissue kallikrein	335	159	4.0	2907	2	A57278	fibrillin-2 precur
263	176	4.5	264	2	S32794	trypsin-like prote	336	158.5	4.0	247	2	S59135	mast cell proteina
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	835	2	S53718	homotetic protein d
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	gene Delta protein
266	175	4.4	270	2	A29834	pancreatic elastas	339	158	4.0	610	2	T16761	hypothetical prote
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	fibrillin-2 precur
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A56740	sperm-egg recognit
269	174.5	4.4	246	1	TRDC	trypsin (EC 3.4.21	342	157.5	4.0	907	2	T27317	hypothetical prote
270	174	4.4	259	2	A29746	tissue kallikrein	343	157	4.0	261	2	JE0236	tissue kallikrein
271	174	4.4	261	1	KQWS1	tissue kallikrein	344	157	4.0	610	2	A35046	E-selectin precurs
272	174	4.4	1295	2	A32901	glpl protein precu	345	156.5	4.0	252	2	A36172	procytotoxic T-lym
273	173.5	4.4	548	2	D82175	probable trypsin v	346	156.5	4.0	275	2	JC8506	tumor necrosis fac
274	173	4.4	229	1	TRDFS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homotetic protein 1
275	173	4.4	768	2	I53821	p-selectin - rat	348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
276	172.5	4.4	248	1	PRMSC2	granzyme C (EC 3.4	349	156	4.0	259	1	KQRTTN	tonin (EC 3.4.21.-
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	261	2	A29586	tissue kallikrein
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T16832	hypothetical prote
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	fibriolytic prote
280	172	4.4	254	2	S65465	trypsin-like prote	353	155.5	3.9	485	2	S36772	E-selectin - bovin
281	172	4.4	261	2	A24378	tissue kallikrein	354	155.5	3.9	533	2	JC7985	brain-specific CUB
282	172	4.4	415	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	kallikrein, glandu
283	171.5	4.3	230	2	A27802	hypodermin C (EC 3	356	155	3.9	2489	2	I73012	complement C3b/C4b
284	171.5	4.3	262	1	KQHU	tissue kallikrein	357	154.5	3.9	252	2	A34877	C4b-binding protei
285	171.5	4.3	2403	2	A59386	sanko - human	358	154	3.9	669	2	S65551	factor H - bovine
286	171	4.3	257	2	B45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
287	171	4.3	260	2	A45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49175	Motch A protein -
288	171	4.3	266	1	ELRT1	pancreatic elastas	361	153.5	3.9	551	1	I46709	endothelial leukoc
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMMSB1	laminin beta-1 cha
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	complement factor
291	170	4.3	248	2	S33756	granzyme-like prot	364	153	3.9	254	1	TRWV3Y	trypsin-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	fibrillin I - bovi
293	169.5	4.3	251	2	T10262	mast cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65663	granzyme F (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	560	2	T16833	hypothetical prote	369	152.5	3.9	422	1	KXHUZ	plasma protein 2 p
297	169	4.3	214	2	S17680	fibriolytic prote	370	152	3.9	281	1	A61021	granzyme B (EC 3.4
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	152	3.9	686	2	JC7569	Delta-4 protein -
299	169	4.3	259	2	B31136	tissue kallikrein	372	151.5	3.8	261	2	A40322	tissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone pGM31	373	151.5	3.8	716	1	A40332	macrophage-stimula
301	168.5	4.3	248	2	S31755	metalloproteinase	374	151.5	3.8	977	2	I52657	seizure-related pr
302	168	4.3	597	2	S71352	complement recepto	375	151	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	2014	2	I36936	semenogelase (EC 3	376	151	3.8	261	2	A41020	tissue kallikrein
304	167.5	4.2	261	1	A32297	delta-like homeoti	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	383	2	S53716	granzyme-like prot	378	150.5	3.8	247	2	S43259	granzyme-like prot
306	167	4.2	247	2	A45113	trypsin-like prote	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	260	2	A37938	tissue kallikrein	380	150.5	3.8	285	2	T35195	probable serine pr
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	JC7570	Delta-4 protein -
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	probable complemen
310	164.5	4.2	449	1	NBHUHS	complement factor	383	150	3.8	263	1	MMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHUH	complement factor	384	150	3.8	267	1	ELHVL	leukocyte elastase
312	164	4.2	230	2	I48685	mast cell proteina	385	150	3.8	601	2	B36346	fibulin 1 precurs
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precur	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T20239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A47290	TSG-6 homolog PS4	389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
317	162.5	4.1	1290	2	A57190	ebnerin precursor	390	149.5	3.8	13288	2	T03099	mucin, submaxillar
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	391	149	3.8	216	1	KVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	tissue kallikrein	392	149	3.8	683	2	C36346	fibulin 1 precurs
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T00204	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYVH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	proteinase 7 - buf
397	148	3.8	1469	2	B36665	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36665	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell proteina	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	C4BP alpha chain p	474	132	3.3	246	2	A38678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	JC5377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	C4BP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	I50421	aggreacan precursor
405	147	3.7	259	2	D23863	tissue kallikrein	478	132	3.3	3871	2	T28112	hypothetical prote
406	147	3.7	262	1	JC4803	venombin A (EC 3.4	479	131.5	3.3	302	1	WMBE1E	secretory compleme
407	147	3.7	716	1	JC5061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMHUBA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	snake venom factor	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	JG0169	venombin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	L-selectin precurs
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B26359	decay-accelerating
414	145	3.7	263	1	C36838	complement control	487	129.5	3.3	440	2	A26359	decay-accelerating
415	145	3.7	372	1	A32375	L-selectin precurs	488	129	3.3	235	1	S65621	venombin AB (EC 3
416	145	3.7	782	2	A61625	tenascin-like prote	489	128.5	3.3	255	2	A27122	cathepsin G (EC 3
417	144.5	3.7	246	2	B38678	mast cell proteina	490	128.5	3.3	321	2	T33161	hypothetical prote
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRFGAZ	azurocidin - pig
419	144.5	3.7	360	2	T42921	complement control	492	128	3.2	5147	1	IJPFMT	cadherin-related t
420	144	3.7	263	2	B72152	B18L protein - var	493	127.5	3.2	1531	2	T42218	slit-1 protein hom
421	144	3.7	685	2	S78040	fibulin, splice fo	494	127	3.2	258	2	I56220	trypsinase 2 - rat
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1609	1	MMHUB2	laminin gamma-1 ch
423	143	3.6	3075	2	S14458	laminin alpha-1 ch	496	127	3.2	1751	1	MMHUMH	laminin alpha-2 ch
424	142.5	3.6	260	2	S26043	chymase (EC 3.4.21	497	127	3.2	3106	1	S53868	laminin alpha-2 ch
425	142	3.6	272	2	JC4170	trypsin-like prote	498	126.5	3.2	1025	2	T42626	secreted leucine-r
426	141.5	3.6	310	2	S41055	metalloproteinase	499	126	3.2	265	2	A38894	serine proteinase
427	141.5	3.6	385	1	A34015	L-selectin precurs	500	126	3.2	265	2	J50260	serine proteinase
428	141	3.6	225	2	S43556	probable serine pr	501	126	3.2	330	2	I56100	complement factor
429	141	3.6	246	2	A32692	cytotoxic T-lympho	502	126	3.2	642	2	S53433	plasma protein S p
430	140.5	3.6	234	1	A46504	chymase (EC 3.4.21	503	125.5	3.2	254	2	S35585	chymotrypsin-like
431	140.5	3.6	1234	1	NBMHS	complement factor	504	125.5	3.2	265	2	I48679	neutrophil elastas
432	140.5	3.6	2406	2	A54148	odz protein - frui	505	125.5	3.2	597	1	NBHUC4	C4b-binding protei
433	140.5	3.6	2515	2	S47008	tenascin-like prot	506	125	3.2	152	2	S35209	serine proteinase
434	140	3.5	396	1	KXBOZ	plasma protein Z -	507	125	3.2	323	1	S09702	L-selectin precurs
435	139.5	3.5	258	1	S44184	chymotrypsin (EC 3	508	125	3.2	1790	1	MMFFB1	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	hypothetical prote	509	124.5	3.2	248	2	A33412	cytotoxic T-lympho
437	139.5	3.5	319	2	I51569	UVS 2 protein - Af	510	124.5	3.2	548	2	T16642	hypothetical prote
438	139	3.5	1820	2	A55494	latent transformin	511	124	3.1	330	2	T46256	brevican - human (
439	138.5	3.5	244	2	S26042	chymase (EC 3.4.21	512	124	3.1	710	1	I51283	hepatocyte growth
440	138.5	3.5	247	1	KYHUCM	chymase (EC 3.4.21	513	124	3.1	883	2	S43126	brevican precursor
441	138.5	3.5	705	2	S34968	fibulin, splice fo	514	124	3.1	1221	2	A49457	fibulin-2 precursor
442	138.5	3.5	1111	2	T26972	hypothetical prote	515	124	3.1	1523	2	T13953	MEGF5 protein - ra
443	137.5	3.5	191	2	S54115	complement factor	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	808	2	D35069	complement factor	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	258	2	S57960	C4BP protein beta	518	123.5	3.1	151	2	S35205	proteinase 5 - buf
446	137	3.5	372	2	S23936	L-selectin precurs	519	123.5	3.1	259	1	S43129	chymotrypsin (EC 3
447	137	3.5	2823	2	F87908	protein T2A3.8 (i	520	123.5	3.1	370	2	S22124	L-selectin precurs
448	137	3.5	2823	2	T23064	hypothetical prote	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	laminin alpha chai	522	123.5	3.1	1184	2	A55184	fibulin-2 precurs
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	248	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	2	T42017	cysteine rich prot	524	123	3.1	308	2	JC7125	epidermal growth f
452	136	3.4	360	1	WMBE2E	membrane-bound com	525	123	3.1	340	2	I56234	decay-accelerating
453	136	3.4	676	2	A45900	complement C3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MEGF6 protein - ra	527	123	3.1	2844	2	S28291	hypothetical prote
455	136	3.4	1607	1	MMHUB2	laminin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	JE0151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	I46002	C4BP beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NBMSC4	C4b-binding protei	532	122	3.1	1810	1	A32230	tenascin precursor
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	AGCH	agrin precursor -
461	135	3.4	343	2	G35070	apolipoprotein H-r	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBUH	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	1	I46001	C4b-binding protei
464	134.5	3.4	601	2	T22025	hypothetical prote	537	121.5	3.1	5376	2	T42215	zonadhesin - mouse
465	134.5	3.4	601	2	D89711	protein F40E10.4 [	538	121	3.1	647	2	A43902	tenascin - eastern
466	134	3.4	232	1	A54361	venombin A (EC 3.4	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	versican precursor

541	120.5	3.1	247	2	S64708	chymase (EC 3.4.21	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	hypothetical prote	615	112	2.8	228	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	apolipoprotein H p	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	complement regulat	617	112	2.8	1353	1	JM0675	restrictin precurs
545	120.5	3.1	646	2	S38819	plasma protein S -	618	112	2.8	1639	1	MM0622	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	fibulin, splice fo	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	fibulin 1, splice	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	hepatocyte growth	621	111.5	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A56226	transforming growt	622	111.5	2.8	370	2	JC7592	spinal cord-derive
550	120.5	3.1	1801	1	MMRTS	laminin beta-2 cha	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	venombin B (EC 3.4	624	111.5	2.8	1328	2	T43060	agrin - electric r
552	120	3.0	363	2	B45900	complement C3d/Bps	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	JC5621	epidermal growth f	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	fibulin-ID precurs	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	serine proteinase	628	111.5	2.8	4351	2	T00252	MEGF1 protein - ra
556	120	3.0	1548	2	S34583	versican precursor	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	versican precursor	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	2397	1	A55535	versican precursor	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	versican precursor	632	110.5	2.8	297	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	I48158	coagulation factor	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A34924	complement C3b/C4b	634	110.5	2.8	583	2	A29154	complement factor
562	119.5	3.0	675	1	KXBOS	plasma protein S p	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	2	JP0076	nel protein - chic	636	110.5	2.8	692	2	T32980	hypothetical prote
564	119.5	3.0	1247	1	MMHUND	nidogen precursor	637	110.5	2.8	961	1	TSHP4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	integumentary muc	638	110.5	2.8	1217	1	EGMSMG	epidermal growth f
566	119	3.0	258	2	A57290	venom plasminogen	639	110.5	2.8	1894	2	JC4980	plexin 1 precursor
567	119	3.0	513	2	D88991	protein apx-1 [imp	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	I55476	growth potentiatio	641	110	2.8	1124	1	I58388	protein-tyrosine k
569	118.5	3.0	728	1	A35644	hepatocyte growth	642	110	2.8	1905	2	I51553	Plexin - African c
570	118.5	3.0	738	1	JH0579	hepatocyte growth	643	109.5	2.8	198	2	S08176	cytotoxic T-lympho
571	118	3.0	133	2	S21114	spermadhesin AWN -	644	109.5	2.8	2215	2	T00348	ILK1 protein - mou
572	118	3.0	196	2	T08808	hypothetical prote	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	neurogenic repetit	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	hypothetical prote	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	brevican precursor	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	tissue kallikrein	649	108.5	2.8	2825	2	T14271	Doc4 protein, stre
577	117.5	3.0	259	2	T21011	hypothetical prote	650	108	2.7	251	1	TRH04Z	azurocidin precurs
578	117.5	3.0	642	2	S53434	plasma protein S p	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	JE0237	apolipoprotein E r	652	108	2.7	1700	2	S08167	Ballbani ring 3 pr
580	117.5	3.0	1160	2	F88369	protein unc-52 [im	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	protein unc-52 [im	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	hypothetical prote	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRU03	proteinase 3 (EC 3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	membrane cofactor	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	Wnt inhibitory fac	658	107	2.7	280	2	G02741	skeletal muscle LI
586	116.5	3.0	384	2	S01896	membrane cofactor	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	laminin Bk chain	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	osteonidogen - hum	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	complement recepto	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	protein ZC84.6 [im	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	furin (EC 3.4.21.7	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	EGU164	LIM protein, FHL4	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	epidermal growth f	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	complement factor	667	106	2.7	927	2	T21772	hypothetical prote
595	114.5	2.9	349	2	G02913	sperm CD46 - human	668	106	2.7	1133	1	EGRT	epidermal growth f
596	114.5	2.9	369	2	I57998	membrane cofactor	669	106	2.7	1142	2	T30272	hypothetical prote
597	114.5	2.9	1798	2	S53869	laminin beta-2 cha	670	106	2.7	1522	2	H88380	protein T22F7.3 [i
598	114	2.9	255	1	A28169	venombin A (EC 3.4	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	hypothetical prote	672	106	2.7	2195	2	T34264	hypothetical prote
600	114	2.9	846	2	A30888	integrin beta chai	673	105.5	2.7	346	2	T46914	hypothetical prote
601	114	2.9	1069	2	T42681	hypothetical prote	674	105.5	2.7	596	2	A45664	variant-specific s
602	113.5	2.9	293	2	T22919	hypothetical prote	675	105.5	2.7	673	2	A48089	growth arrest-spec
603	113.5	2.9	502	2	T20130	hypothetical prote	676	105	2.7	860	1	QRHULD	LDL receptor precu
604	113.5	2.9	558	2	T17324	hypothetical prote	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	protein B0244.8 [i	678	105	2.7	1746	1	SI5694	tenascin precursor
606	113.5	2.9	879	1	QRRTLD	LDL receptor precu	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	masking protein pr	680	104.5	2.7	345	1	NBMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	coagulation factor	681	104.5	2.6	1360	2	T33922	hypothetical prote
609	112.5	2.9	264	2	A28942	pancreatic elastase	682	104	2.6	345	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	JC7591	spinal cord-derive	683	104	2.6	360	1	A55198	transcription fact
611	112.5	2.9	677	2	A42125	trophozoite cystei	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	multimerin, endoth	685	104	2.6	473	2	T23226	hypothetical prote
613	112.5	2.9	1797	2	T21889	hypothetical prote	686	104	2.6	2101	2	S57245	insulin receptor (

687	104	2.6	4135	2	T42629	tenascin-X - bovin	760	98	2.5	102	2	B55885	chondroitin sulfat
688	103.5	2.6	383	2	T21946	hypothetical prote	761	98	2.5	357	2	S23403	sperm surface prot
689	103	2.6	431	2	A45222	complement factor	762	98	2.5	909	1	QRXLL1	LDL receptor 1 pre
690	103	2.6	321	2	S72579	hypothetical prote	763	98	2.5	937	2	I53282	gene PAC4 protein
691	103	2.6	1296	2	T16859	hypothetical prote	764	98	2.5	1087	2	T31100	probable potassium
692	103	2.6	2148	1	A56081	insulin receptor -	765	98	2.5	1748	1	JN0786	integrin beta-4 ch
693	102.5	2.6	153	2	S35204	proteinase 4 - buf	766	98	2.5	2588	2	T14342	NSD1 protein - mou
694	102.5	2.6	473	2	T43283	ADAM 4 protein pre	767	98	2.5	4660	2	T42737	gp330 protein prec
695	102.5	2.6	565	2	T16408	hypothetical prote	768	97.5	2.5	577	2	A60501	thrombomodulin pre
696	102.5	2.6	873	1	QR8BVD	VLDR receptor prec	769	97.5	2.5	837	1	A29512	LDL receptor precu
697	102	2.6	149	2	S35208	serine proteinase	770	97.5	2.5	878	2	B71460	probable outer mem
698	102	2.6	280	2	G01884	LIM protein FHU-1,	771	97.5	2.5	884	2	T18649	hypothetical prote
699	102	2.6	380	2	G01639	transmembrane prot	772	97.5	2.5	1162	2	T21557	hypothetical prote
700	102	2.6	411	2	D88087	protein B0454.7 fi	773	97.5	2.5	2946	2	T15840	hypothetical prote
701	102	2.6	718	2	T29448	hypothetical prote	774	97	2.5	126	2	A23473	chymotrypsin-like
702	102	2.6	863	1	S51789	VLDR receptor prec	775	97	2.5	379	2	T27350	hypothetical prote
703	102	2.6	1168	2	I56985	kalinin B1 - mouse	776	97	2.5	429	2	T21113	hypothetical prote
704	102	2.6	1713	2	A55347	adhesive ligand ep	777	97	2.5	626	2	T27319	hypothetical prote
705	102	2.6	4006	2	T09070	probable tenascin	778	97	2.5	799	1	IUMSPB	fibronectin recept
706	101.5	2.6	379	2	T16213	APX-1 protein homo	779	97	2.5	808	2	T23129	hypothetical prote
707	101.5	2.6	1106	2	T18739	hypothetical prote	780	97	2.5	862	2	S43922	versican - pig-tai
708	101.5	2.6	1959	1	AGRT	agrin - rat	781	97	2.5	915	1	A48225	subilisin-like pr
709	101.5	2.6	2415	1	A39086	aggreccan precursor	782	97	2.5	1138	1	S24066	protein-tyrosine k
710	101	2.6	377	2	C88710	protein C43G2.5 fi	783	97	2.5	1193	2	A44018	laminin B2t chain
711	101	2.6	463	2	T26655	hypothetical prote	784	97	2.5	1292	2	T09229	galactose binding
712	101	2.6	557	2	A48434	variant-specific s	785	96.5	2.4	149	1	KQMSM	tissue kallikrein
713	101	2.6	1371	2	A33837	insulin-like growt	786	96.5	2.4	317	2	D42526	B5R protein - vacc
714	101	2.6	1378	1	I48751	protein-tyrosine k	787	96.5	2.4	613	2	A69535	aldehyde ferredoxi
715	101	2.6	1875	2	A36429	integrin beta-4 ch	788	96.5	2.4	956	2	A57121	thrombospondin 3 p
716	100.5	2.5	417	2	T20199	hypothetical prote	789	96.5	2.4	1149	2	I38006	M130 antigen precu
717	100.5	2.5	670	2	S77463	transketolase (EC	790	96.5	2.4	1193	2	T21133	hypothetical prote
718	100.5	2.5	802	2	T24293	hypothetical prote	791	96.5	2.4	1297	2	T30274	proteolialisin - se
719	100.5	2.5	949	2	T24294	hypothetical prote	792	96.5	2.4	3133	2	S52093	hemocytin - silkw
720	100.5	2.5	956	1	A46016	thrombospondin 3 -	793	96	2.4	116	2	S17567	AQN-3 protein - pl
721	100.5	2.5	1252	2	S36016	coocyst wall protei	794	96	2.4	116	2	S39434	spermadhesin AQN-3
722	100.5	2.5	1356	2	A45445	janusin precursor,	795	96	2.4	256	2	A56593	trypsin-related pr
723	100	2.5	152	2	S35203	janine proteinase,	796	96	2.4	392	2	T25213	hypothetical prote
724	100	2.5	421	2	T23383	hypothetical prote	797	96	2.4	798	2	A28193	integrin beta-1 ch
725	100	2.5	667	2	A48579	trophozoite surfac	798	96	2.4	886	2	A57172	probable hormone r
726	100	2.5	873	1	A49729	VLDR receptor prec	799	96	2.4	4753	1	A47437	LDL-receptor-relat
727	100	2.5	1122	2	I54237	protein-tyrosine k	800	96	2.4	177	2	S23505	chymase (EC 3.4.21
728	100	2.5	1123	1	JN0712	protein-tyrosine k	801	95.5	2.4	218	2	H70770	probable regulator
729	100	2.5	1125	1	JH0771	protein-tyrosine k	802	95.5	2.4	330	2	B82415	probable serine pr
730	100	2.5	1151	2	I38004	M130 antigen precu	803	95.5	2.4	427	2	JC4915	ags protein precu
731	100	2.5	1156	2	I38005	M130 antigen precu	804	95.5	2.4	561	2	T27318	hypothetical prote
732	100	2.5	1251	2	A57293	latent transformin	805	95.5	2.4	1042	2	A57534	mucin SAC (clone L
733	100	2.5	1299	2	T43251	furin (EC 3.4.21.7	806	95.5	2.4	1135	1	JQ1928	G2-G1 polypeptide
734	99.5	2.5	330	2	I55975	X/Y protein - mous	807	95.5	2.4	1270	2	T22615	hypothetical prote
735	99.5	2.5	640	1	A30452	uromodulin precurs	808	95.5	2.4	3191	2	T22945	peptidyl prollyl ci
736	99.5	2.5	686	2	S43562	K08E5.3 protein -	809	95.5	2.4	463	2	T39621	gastric mucin MUC5
737	99.5	2.5	914	1	S07047	iodide peroxidase	810	95	2.4	850	2	S56015	VLDR receptor prec
738	99.5	2.5	1280	2	A39117	170K lectin precu	811	95	2.4	869	1	JC4858	hypothetical prote
739	99.5	2.5	1350	2	S00647	finger protein - A	812	95	2.4	989	2	T01519	nitrogen precursor
740	99.5	2.5	1766	2	A42125	trophozoite cystel	813	95	2.4	1245	1	MMMSND	mucin MUC5B, trach
741	99.5	2.5	1847	2	T18308	probable vitellog	814	95	2.4	1321	2	JE0352	spermadhesin AQN-1
742	99.5	2.5	1984	2	T13171	probable vitellog	815	95	2.4	111	2	S21211	hypothetical prote
743	99	2.5	589	2	B38128	epithelin/granulin	816	94.5	2.4	643	2	T25473	TMDC 1 protein - c
744	99	2.5	591	1	I48141	acroganin - guine	817	94.5	2.4	736	2	S47645	LDL receptor precu
745	99	2.5	675	1	KXMS	plasma protein S p	818	94.5	2.4	862	1	QRMSLD	hypothetical prote
746	99	2.5	805	2	S68441	leptin receptor, s	819	94.5	2.4	1216	2	T26104	protein ZC94.1 [im
747	99	2.5	892	2	S68439	leptin receptor, s	820	94.5	2.4	1416	2	E88550	epidermal growth f
748	99	2.5	894	2	S68437	leptin receptor, s	821	94.5	2.4	1717	1	A45558	insulin-like growt
749	99	2.5	900	2	S68440	leptin receptor, s	822	94.5	2.4	258	1	K37252	platelet-derived g
750	99	2.5	900	2	S68440	leptin receptor, s	823	94	2.4	370	2	JC7998	hypothetical prote
751	99	2.5	1162	2	S68438	two-component hybr	824	94	2.4	634	2	T02594	neuregulin-3 limpo
752	99	2.5	1558	2	AB2457	G-cadherin - sea u	825	94	2.4	713	2	T44447	hypothetical prote
753	99	2.5	2809	2	T30213	hypothetical prote	826	94	2.4	736	2	T06757	subilisin-like pr
754	98.5	2.5	317	2	T28605	H7R protein - vari	827	94	2.4	899	2	G02428	subilisin-like pr
755	98.5	2.5	317	2	F72172	B7R protein - vari	828	94	2.4	915	2	JC6148	subilisin-like pr
756	98.5	2.5	317	2	G36855	PAS-6/7 protein pr	829	94	2.4	932	2	I52527	thrombospondin pre
757	98.5	2.5	427	2	S74211	hypothetical prote	830	94	2.4	1381	2	T31083	neurexin IV - mous
758	98.5	2.5	1178	1	A39804		831	94	2.4	1385	2	T14158	
759	98	2.5	82	2	T46510		832	94	2.4				

833	94	2.4	3097	2	T00021	DN-cadherin - frui	906	89.5	2.3	854	1	QRHYLD	LDL receptor precu
834	93.5	2.4	258	2	A45403	insulin-like growt	907	89.5	2.3	1164	2	T01871	RNA-directed DNA p
835	93.5	2.4	317	2	JQ1799	B5R protein precu	908	89.5	2.3	1258	2	A12155	WD-repeat protein
836	93.5	2.4	449	2	T35048	probable ATP/GTP	909	89.5	2.3	1364	2	T00250	MEGF2 protein - hu
837	93.5	2.4	456	2	T31483	hypothetical prote	910	89	2.3	319	2	A53502	folliastatin - Afri
838	93.5	2.4	486	2	A49820	PRK1 protein - Ara	911	89	2.3	354	2	T22274	hypothetical prote
839	93.5	2.4	612	2	JH0799	laminin-related pr	912	89	2.3	369	2	F81178	histone deacetylase
840	93.5	2.4	739	2	B88553	protein K04H4.2b [	913	89	2.3	390	2	C90208	hypothetical prote
841	93.5	2.4	1115	2	S04241	G protein-coupled	914	89	2.3	469	1	NM1V27	exo-alpha-sialidas
842	93.5	2.4	1136	1	S57845	protein-tyrosine k	915	89	2.3	525	2	T31357	hypothetical prote
843	93	2.4	104	2	T19868	hypothetical prote	916	89	2.3	907	2	I50404	p50B/p97 (Lyt-10)
844	93	2.4	329	2	A48805	insulin-like growt	917	89	2.3	1110	1	B42544	G2-C1 polyprotein
845	93	2.4	873	1	I48952	VNDR receptor prec	918	89	2.3	1170	2	A40558	thrombospondin 1 p
846	93	2.4	846	2	A56599	embryo kinase 5 -	919	88.5	2.2	317	2	T37442	SEV gp42,ps/hr pro
847	93	2.4	2767	1	UIHU	alpha-2-macroglobu	920	88.5	2.2	356	2	T20656	hypothetical prote
848	93	2.4	4545	1	S25111	human CR1 homolog	921	88.5	2.2	438	2	T40509	lim domain protein
849	92.5	2.3	211	2	A46458	hypothetical prote	922	88.5	2.2	693	2	I37570	zinc finger protei
850	92.5	2.3	736	2	T19366	hypothetical prote	923	88.5	2.2	754	2	T47886	transketolase-like
851	92.5	2.3	756	2	T47656	TMDC II protein -	924	88.5	2.2	905	2	S55059	probable cysteine-
852	92.5	2.3	803	1	IJCH3	integrin, band 3 p	925	88.5	2.2	1077	2	T41146	feritin alpha-1 -
853	92.5	2.3	955	2	A45441	thrombospondin 4 -	926	88.5	2.2	1096	2	T16875	hypothetical prote
854	92.5	2.3	1367	1	IGHUR1	insulin-like growt	927	88.5	2.2	1170	1	TSHUP1	thrombospondin 1 p
855	92	2.3	334	2	T23027	hypothetical prote	928	88.5	2.2	1978	2	T07081	acetyl-CoA carboxy
856	92	2.3	650	2	A34498	glycoprotein antig	929	88	2.2	621	2	I38467	low density lipopr
857	92	2.3	719	2	T00268	hypothetical prote	930	88	2.2	656	2	JC2005	integrin beta-5 ch
858	92	2.3	915	2	B48225	probable protease	931	88	2.2	798	2	B27079	fibronectin recept
859	92	2.3	964	2	JC5545	integrin beta-4 pr	932	88	2.2	799	2	A38308	integrin beta-5 ch
860	92	2.3	1097	2	S68685	adenylate cyclase	933	88	2.2	962	2	JC5571	subtilisin-like pr
861	92	2.3	1444	2	T18856	angiogenesis inhib	934	88	2.2	1085	2	C96797	unknown protein [i
862	92	2.3	1895	2	T15881	hypothetical prote	935	88	2.2	1175	2	S52417	E-selectin ligand-
863	92	2.3	2533	2	T28675	alpha-51D immobili	936	88	2.2	1192	2	S69000	laminin gamma 2 ch
864	92	2.3	3869	2	A48205	All-1 protein +GFE	937	87.5	2.2	554	2	A45818	cytolysin precuro
865	91.5	2.3	237	2	I47031	insulin-like growt	938	87.5	2.2	580	2	A37107	complement C8 alph
866	91.5	2.3	250	2	T30124	hypothetical prote	939	87.5	2.2	584	1	C8HUA	hypothetical prote
867	91.5	2.3	303	2	H35068	apolipoprotein H-r	940	87.5	2.2	667	2	T01999	hypothetical prote
868	91.5	2.3	511	2	T17298	hypothetical prote	941	87.5	2.2	914	1	UN0550	iodide peroxidase
869	91.5	2.3	588	2	T33815	hypothetical prote	942	87.5	2.2	1807	2	JC6319	integrin beta-4 ch
870	91.5	2.3	640	2	S49932	MET30 protein - ye	943	87.5	2.2	1816	1	S68960	extracellular prot
871	91.5	2.3	1101	2	T16840	hypothetical prote	944	87	2.2	387	2	I38449	laminin alpha-4 ch
872	91.5	2.3	1161	2	D83076	type 4 fibrial bi	945	87	2.2	706	2	S74610	hypothetical prote
873	91.5	2.3	2144	2	S71490	ashl protein - fru	946	87	2.2	743	2	T40521	hypothetical prote
874	91.5	2.3	2672	2	A48126	translation activa	947	87	2.2	860	2	T16892	hypothetical prote
875	91.5	2.3	2910	2	T42214	otogelin - mouse	948	87	2.2	970	2	I78842	receptor protein-t
876	91	2.3	94	2	PC2013	tissue kallikrein	949	87	2.2	975	2	JC5570	subtilisin-like pr
877	91	2.3	293	2	T03065	hypothetical prote	950	87	2.2	1042	2	T26644	mucin MUC5B, trach
878	91	2.3	319	1	I50370	transcription fact	951	87	2.2	1056	2	A53767	protein-tyrosine k
879	91	2.3	398	2	E71539	hypothetical prote	952	87	2.2	1134	1	JN0711	plexin A - fruit f
880	91	2.3	435	2	I54182	tumor necrosis fac	953	87	2.2	1945	2	T13937	fibronectin - Afri
881	91	2.3	478	2	S47040	gene T52 protein	954	87	2.2	2481	2	A43908	trithorax homolog
882	91	2.3	909	1	QRXLL2	LDL receptor 2 pre	955	87	2.2	3968	2	A44265	hypothetical prote
883	91	2.3	2543	2	T31687	surface antigen - P	956	86.5	2.2	222	2	S72795	hypothetical prote
884	91	2.3	4543	1	A53102	alpha-2-macroglobu	957	86.5	2.2	264	2	T16271	hypothetical prote
885	90.5	2.3	53	2	S17294	epidermal growth f	958	86.5	2.2	336	2	D69074	polyferredoxin 4x2
886	90.5	2.3	330	1	JN0561	urokinase-type pla	959	86.5	2.2	391	2	T34284	hypothetical prote
887	90.5	2.3	642	1	JP0079	LIM protein kinase	960	86.5	2.2	471	2	I79528	alkaline phosphata
888	90.5	2.3	746	1	HYHUMA	mepirin A (EC 3.4.2	961	86.5	2.2	585	2	I46686	complement compone
889	90.5	2.3	776	2	S28258	androgen-regulated	962	86.5	2.2	632	2	T22288	hypothetical prote
890	90.5	2.3	960	2	JEO356	gamma-aminobutyric	963	86.5	2.2	632	2	T21602	hypothetical prote
891	90.5	2.3	1104	2	I38869	transcription fact	964	86.5	2.2	638	2	AE3463	flagellar protein
892	90.5	2.3	1148	1	GNVUNE	M polyprotein prec	965	86.5	2.2	641	2	F71810	type III DNA modif
893	90.5	2.3	1357	2	T16860	hypothetical prote	966	86.5	2.2	651	2	T05869	hypothetical prote
894	90.5	2.3	1436	2	A46496	antigen WC1.1 prec	967	86.5	2.2	700	2	A32392	protein kinase C (
895	90.5	2.3	2813	1	VWHU	von Willebrand fac	968	86.5	2.2	734	2	C81399	isocitrate dehydro
896	90	2.3	156	2	B23863	tissue kallikrein	969	86.5	2.2	1172	2	A42587	thrombospondin 2 p
897	90	2.3	340	2	T34423	hypothetical prote	970	86.5	2.2	1376	1	UJ1534	E2 glycoprotein pr
898	90	2.3	409	2	T11743	pp47 protein - pig	971	86.5	2.2	1418	2	D75281	ribonucleoside-dip
899	90	2.3	417	2	T29864	hypothetical prote	972	86.5	2.2	1473	2	A20872	ovostatin precuro
900	90	2.3	522	2	T29767	hypothetical prote	973	86.5	2.2	3712	1	YGCEVC	alpha-aminoadipyl-
901	90	2.3	577	2	B37057	integrin beta-6 ch	974	86	2.2	455	2	B82525	conserved hypothet
902	90	2.3	814	1	I39627	nicotine dehydroge	975	86	2.2	713	2	A35502	major surface-labe
903	90	2.3	2533	2	T28674	alpha-51D-immobili	976	86	2.2	738	2	S40992	hypothetical prote
904	89.5	2.3	417	2	T39939	DNA binding protei	977	86	2.2	905	2	T23229	hypothetical prote
905	89.5	2.3	748	2	S24134	endopeptidase 2 (E	978	86	2.2	906	2	A71438	probable resistanc



979	2.2	933	1	OPRHUT	iodide peroxidase	1052	83.5	2.1	311	2	JC7873	L-thamnose-binding
980	86	969	1	A39490	subtilisin-like pr	1053	83.5	2.1	344	2	A32141	folliculin 1 prec
981	86	1487	2	S48719	phospholipase-A(2)	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	1572	2	T00027	brain-specific ang	1055	83.5	2.1	354	2	G64475	GTP-binding protei
983	86	1650	2	S53457	dominant autoantig	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2233	2	T28669	surface protein 51	1057	83.5	2.1	366	2	I53035	trithorax homolog
985	85.5	2.2	317	A39493	ps/hr protein - va	1058	83.5	2.1	491	2	H83770	hypothetical prote
986	85.5	2.2	340	B55973	transcription fact	1059	83.5	2.1	579	2	H84192	pyruvate kinase [i
987	85.5	2.2	344	A27701	folliculin precu	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	B64427	carbamoyl-phosphat	1061	83.5	2.1	697	2	H86457	78.1K hypothetical
989	85.5	2.2	463	A36479	milk fat globule m	1062	83.5	2.1	873	2	D88482	protein C5D11.8 [
990	85.5	2.2	515	T05863	hypothetical prote	1063	83.5	2.1	1106	2	T13938	gene shuttle craft
991	85.5	2.2	638	S22491	acetolactate synth	1064	83.5	2.1	2120	2	T30243	alpha tectorin - c
992	85.5	2.2	663	T21010	hypothetical prote	1065	83.5	2.1	2704	2	S09118	G surface protein
993	85.5	2.2	798	S01659	integrin beta-1 ch	1066	83.5	2.1	4302	2	A38971	polycystic kidney
994	85.5	2.2	1162	PC4184	leptin receptor, O	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	H84465	hypothetical prote	1068	83	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1 RNQ2L	DNA-directed RNA p	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	T18492	hypothetical prote	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	T42678	hypothetical prote	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	I38098	t-plasminogen acti	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	H86342	hypothetical prote	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	S55369	folliculin - chic	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	I51734	transcription fact	1075	83	2.1	770	2	D89447	protein F5C12.1 [
1003	85	2.2	413	T23098	hypothetical prote	1076	83	2.1	771	2	A45839	leukocyte adhesion
1004	85	2.2	542	A84554	hypothetical prote	1077	83	2.1	800	2	S54623	probable mitochon
1005	85	2.2	552	T83417	sulfite reductase	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	S43118	finger protein - m	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	S22490	acetolactate synth	1080	83	2.1	1066	2	B95037	hyaluronidase limp
1008	85	2.2	653	T23098	hypothetical prote	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	UYVP19	noncapsid protein	1082	83	2.1	1373	2	JE0095	gastric mucin MUC5
1010	85	2.2	752	T26508	hypothetical prote	1083	83	2.1	2116	1	ZLVNSY	genome polyprotein
1011	85	2.2	794	F88508	protein H1A12.6 [	1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	S74225	leptin receptor, i	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	S26985	probable DNA-dirc	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	T79707	hyaluronate lyase	1087	82.5	2.1	486	2	S29302	alliin lyase (EC 4
1015	85	2.2	1148	1 JQ1604	M polyprotein prec	1088	82.5	2.1	591	1	C8HUB	complement C8 beta
1016	85	2.2	1533	T00344	hypothetical prote	1089	82.5	2.1	753	2	T19338	hypothetical prote
1017	85	2.2	1538	S73296	glutamate synthase	1090	82.5	2.1	761	2	E82223	ribonucleoside-dip
1018	85	2.2	2150	T32497	hypothetical prote	1091	82.5	2.1	781	2	S43534	integrin beta3 - c
1019	84.5	2.1	271	T21783	OX40 antigen precu	1092	82.5	2.1	984	2	T00326	hypothetical prote
1020	84.5	2.1	337	I47079	folliculin - shee	1093	82.5	2.1	1175	2	I57549	adenosine deaminas
1021	84.5	2.1	344	I45894	folliculin - bovi	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1022	84.5	2.1	429	T16656	hypothetical prote	1095	82	2.1	188	2	A39787	teratocarcinoma-de
1023	84.5	2.1	494	A99683	alkaline phosphata	1096	82	2.1	235	2	AE0114	deoxyribonuclease
1024	84.5	2.1	505	E85533	alkaline phosphata	1097	82	2.1	318	2	S65019	chitinase (EC 3.2.
1025	84.5	2.1	505	A46570	H+-transporting tw	1098	82	2.1	343	2	S45321	folliculin - mous
1026	84.5	2.1	615	S06546	finger protein (cl	1099	82	2.1	349	2	D72175	G2R protein - vari
1027	84.5	2.1	654	T30136	hypothetical prote	1100	82	2.1	432	2	D83904	carbon storage regu
1028	84.5	2.1	696	A12849	GGDP family prote	1101	82	2.1	528	2	B42560	4-chlorobenzoate-C
1029	84.5	2.1	696	G97626	hypothetical prote	1102	82	2.1	583	2	T34121	steroid/thyroid/re
1030	84.5	2.1	744	A43353	ascites sialoglyco	1103	82	2.1	599	2	B82439	formate-tetrahydro
1031	84.5	2.1	746	F87243	isocitrate dehydro	1104	82	2.1	711	2	T27358	hypothetical prote
1032	84.5	2.1	760	A40195	meprin A (EC 3.4.2	1105	82	2.1	868	2	T02635	D2 protein homolog
1033	84.5	2.1	788	A28547	platelet glycoprot	1106	82	2.1	1530	2	I45944	neurexin 1-alpha -
1034	84.5	2.1	789	S28259	androgen-regulated	1107	82	2.1	1609	2	S44821	F44E2.4 protein -
1035	84.5	2.1	864	T49574	probable carnitine	1108	82	2.1	1661	2	T31330	head-activator bin
1036	84.5	2.1	917	T48950	telencephalin prec	1109	82	2.1	2214	2	T16305	hypothetical prote
1037	84.5	2.1	950	T28793	diacylglycerol kin	1110	82	2.1	4861	2	S71752	giant protein p619
1038	84	2.1	278	T21718	hypothetical prote	1111	81.5	2.1	209	2	T02394	hypothetical prote
1039	84	2.1	335	T32657	hypothetical prote	1112	81.5	2.1	251	2	A55035	cysteine-rich prot
1040	84	2.1	349	T36858	gene G4R protein -	1113	81.5	2.1	349	2	S57453	polyferredoxin 4x2
1041	84	2.1	413	D34123	hypothetical prote	1114	81.5	2.1	383	2	D89633	protein F5G83.2 [i
1042	84	2.1	471	A84741	probable myosinas	1115	81.5	2.1	429	2	S01919	knirps protein - f
1043	84	2.1	520	G88846	protein T12A7.2 [i	1116	81.5	2.1	432	2	A25483	env polyprotein, r
1044	84	2.1	567	T49942	hypothetical prote	1117	81.5	2.1	443	2	T29147	hypothetical prote
1045	84	2.1	972	A30363	glycoprotein GP330	1118	81.5	2.1	460	2	S67174	lysine decarboxyla
1046	84	2.1	1034	JC5598	mucin - rat	1119	81.5	2.1	482	2	A83655	probable finger pr
1047	84	2.1	1047	T34946	probable isoleucyl	1120	81.5	2.1	496	2	T08674	transketolase (EC
1048	84	2.1	1599	T16210	hypothetical prote	1121	81.5	2.1	519	2	S54300	probable finger pr
1049	84	2.1	2153	T14893	scavenger receptor	1122	81.5	2.1	604	1	HMNZCD	hemagglutinin - ca
1050	83.5	2.1	202	A44247	C4b-binding protei	1123	81.5	2.1	625	2	S35317	hematopoietic grow
1051	83.5	2.1	278	AH0282	probable pepetides	1124	81.5	2.1	626	2	S37622	proto-oncogene - m

1125	81.5	2.1	724	2	A48569	antigen Em100 - Ei	1198	80	2.0	644	2	I84634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	2	PN0510	integrin beta-3 ch
1128	81.5	2.1	1210	2	D88013	protein K1084.1 [i	1201	80	2.0	713	2	JC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40228	neurexin I-alpha p	1202	80	2.0	741	2	G84888	probable transket
1130	81	2.1	180	2	AE1010	conserved hypothet	1203	80	2.0	746	2	G84605	hypothetical prote
1131	81	2.1	236	2	C81906	hypothetical prote	1204	80	2.0	753	2	JC7386	retinovin - chicke
1132	81	2.1	348	2	A56247	natural killer cel	1205	80	2.0	817	2	T24063	hypothetical prote
1133	81	2.1	428	2	T04472	penicillin binding	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	491	2	I40455	hypothetical prote	1207	80	2.0	1138	2	T36406	hypothetical prote
1135	81	2.1	501	2	JC7181	maternal transcrip	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jasmonate-induced	1210	80	2.0	1385	2	H85669	protein K03H1.5 [1
1138	81	2.1	732	2	T52588	wall-associated se	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	fertilin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	735	2	J48101	ADAM 6 protein pre	1213	80	2.0	2229	2	T16199	hypothetical prote
1141	81	2.1	769	1	JC1121	leukocyte adhesio	1214	80	2.0	2643	2	T29149	hypothetical prote
1142	81	2.1	787	2	T49614	related to tol pro	1215	80	2.0	3140	2	S47508	genome polyprotein
1143	81	2.1	799	2	JC4126	integrin beta olig	1216	79.5	2.0	3171	2	A59412	KoB-bearing platel
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	conserved hypothet
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	insulin-like growt
1146	81	2.1	1344	2	H84557	hypothetical prote	1219	79.5	2.0	254	2	JC1464	insulin-like growt
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	transaldolase (EC
1148	81	2.1	1438	2	A48216	neurexin III-alpha	1221	79.5	2.0	318	2	S43317	chitinase (EC 3.2.
1149	81	2.1	1471	2	B48218	neurexin III-alpha	1222	79.5	2.0	324	2	S20981	chitinase (EC 3.2.
1150	81	2.1	1578	2	I48216	neurexin III-alpha	1223	79.5	2.0	356	2	A25918	thrombomodulin - b
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	391	2	S49300	AWJ1236 protein -
1152	81	2.1	3898	2	S57437	genome polyprotein	1225	79.5	2.0	457	2	C86464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	tubulointerstitial
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	conserved hypothet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hemorrhagic protei	1229	79.5	2.0	661	2	B90861	hypothetical prote
1157	80.5	2.0	431	2	S49821	PRL2 protein - Ara	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	454	2	T26654	hypothetical prote	1231	79.5	2.0	700	1	HYHUMB	mepirin A (EC 3.4.2
1159	80.5	2.0	471	1	PAECA	alkaline phosphata	1232	79.5	2.0	713	2	I65253	disintegrin-like c
1160	80.5	2.0	479	2	D86182	protein Fl3M7.11 [	1233	79.5	2.0	741	2	T05015	transketolase (EC
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	868	2	G84674	probable selenium-
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	952	2	T28792	diacylglycerol kin
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1161	1	S31213	nidogen precursor
1164	80.5	2.0	555	2	T12028	hypothetical prote	1237	79.5	2.0	1178	2	S08405	hypothetical prote
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1260	2	A86323	protein Fl4D16.3 [
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1390	2	S51364	sperm tail-specifi
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	hypothetical prote
1168	80.5	2.0	656	2	B49423	hypothetical prote	1241	79.5	2.0	2261	2	T07084	acetyl-CoA carboxy
1169	80.5	2.0	658	2	A68628	semaphorin I - fru	1242	79.5	2.0	2499	1	A30788	mannose 6-phosphat
1170	80.5	2.0	673	2	A49878	transketolase (EC	1243	79.5	2.0	171	2	S57894	laminin - Hydra vu
1171	80.5	2.0	704	2	A48040	coagulation factor	1244	79	2.0	188	2	A30362	teratocarcinoma-de
1172	80.5	2.0	741	2	B81143	mepirin A (EC 3.4.2	1245	79	2.0	192	1	B57143	thiosulfate-dithio
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79	2.0	192	2	AC0763	thiosulfate reduct
1174	80.5	2.0	773	2	I46059	beta-1 integrin su	1247	79	2.0	206	2	D97285	ribosomal protein
1175	80.5	2.0	1055	2	T05663	hypothetical prote	1248	79	2.0	360	2	S32695	Wnt-2 protein - Ca
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 [i	1249	79	2.0	364	2	T24153	hypothetical prote
1177	80.5	2.0	1245	1	VHW82	structural polypro	1250	79	2.0	392	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VGIHJ2	Ez glycoprotein pr	1251	79	2.0	393	2	A64036	hypothetical prote
1179	80.5	2.0	1382	1	INHUR	insulin receptor p	1252	79	2.0	415	2	T08724	probable membrane
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79	2.0	417	2	T08724	hypothetical prote
1181	80.5	2.0	1558	2	C89114	protein C37C3.6a [	1254	79	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	602	2	B81420	GTP-binding protei
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	606	2	T22105	hypothetical prote
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	630	2	T48369	hypothetical prote
1185	80	2.0	211	1	CYRFB3	beta-crystallin B3	1258	79	2.0	660	2	S71949	metalloproteinase
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	687	2	T16352	hypothetical prote
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	729	2	A45716	leukemia virus cel
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	738	2	T41730	hypothetical prote
1189	80	2.0	335	2	A39743	u-plasminogen acti	1262	79	2.0	753	2	B36268	platelet glycoprot
1190	80	2.0	395	2	S64299	probable membrane	1263	79	2.0	773	2	JB0387	exo-alpha-sialidas
1191	80	2.0	398	1	S24802	polyferredoxin 6x2	1264	79	2.0	788	2	A60798	platelet glycoprot
1192	80	2.0	437	2	S05478	properdin - mouse	1265	79	2.0	788	2	I77349	platelet glycoprot
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79	2.0	790	2	D81668	phenylalanine-tRNA
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0	826	2	A60385	monocyte surface a
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0	871	2	T04867	hypothetical prote
1196	80	2.0	642	2	C89124	protein K07c11.9 [	1269	79	2.0	952	2	T18900	disintegrin and me
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79	2.0	1023	2	T30257	19G Fc binding pro

1271	79	2.0	1389	1	RMXRR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	JT0747	epiregulin - rat
1273	79	2.0	1313	2	A54895	muclin 2, intestina	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-1
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H96776	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prote	1349	77.5	2.0	295	2	JC5559	lectin-B - Virgini
1277	79	2.0	1777	2	AC2088	serine/threonine k	1350	77.5	2.0	296	2	G81111	conserved hypothet
1278	78.5	2.0	116	2	S65875	spermadhesin PSP-1	1351	77.5	2.0	400	2	A55647	phyllolopod - fruit
1279	78.5	2.0	307	1	S18523	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phosphoribulokinas
1280	78.5	2.0	327	2	A55356	urokinase-type pla	1353	77.5	2.0	407	2	C82428	glucose-1-phosphat
1281	78.5	2.0	341	2	I61725	natural killer cell	1354	77.5	2.0	413	4	FOHUE2	retrovirus-related
1282	78.5	2.0	345	2	I57698	follistatin - rat	1355	77.5	2.0	457	2	B85749	ATP-dependent RNA
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	469	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoprotein anti-g	1360	77.5	2.0	546	2	B75375	probable amidaase -
1288	78.5	2.0	436	2	S06884	virD2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	569	2	E85076	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FWFMLA	legumin A precursor	1365	77.5	2.0	721	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A63202	conserved hypothet
1294	78.5	2.0	600	2	I49281	fertilin alpha pre	1367	77.5	2.0	809	2	A57283	hypothetical prote
1295	78.5	2.0	638	2	D86477	protein F15O4.27 l	1368	77.5	2.0	809	2	E85079	integrin beta chai
1296	78.5	2.0	658	2	F85024	probable CHP-rich	1369	77.5	2.0	845	2	G82773	phage-related prot
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrite reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytotactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h+-transporting AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFVMI	gag-Rml1-env polyp
1301	78.5	2.0	763	2	T49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1323	2	E88257	protein let-23 [im
1303	78.5	2.0	1119	2	T16720	hypothetical prote	1376	77.5	2.0	1374	2	S70712	protein-tyrosine k
1304	78.5	2.0	1121	2	S57058	probable membrane	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1131	2	T30951	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T18625	atrial natriuretic	1379	77	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	JC4889	phosphatidylinosit	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	genome polyprotein	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	polyprotein - rice	1382	77	2.0	279	2	T16201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	protein C44E4.1a l	1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27778	hypothetical prote	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T03157	probable capsid as	1385	77	2.0	452	2	H84772	probable serine ca
1313	78	2.0	360	2	T26037	hypothetical prote	1386	77	2.0	476	2	T19786	hypothetical prote
1314	78	2.0	360	2	G82994	glycine-cleavage s	1387	77	2.0	500	2	AE2032	glycerol kinase [i
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	trp-asp repeat con
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	protein F25E5.10 l	1390	77	2.0	540	1	OYHUCR	natriuretic peptid
1318	78	2.0	415	2	T40553	Trp-Asp repeat pro	1391	77	2.0	591	2	S33542	catechol oxidase (
1319	78	2.0	441	2	E83377	oxidoreductase Atu	1392	77	2.0	713	2	T40729	WD repeat-containi
1320	78	2.0	446	2	AH2930	probable oxidoredu	1393	77	2.0	729	2	A49120	fibroblast growth
1321	78	2.0	454	1	QGMST1	tumor necrosis fac	1394	77	2.0	768	2	A87722	protein ZC123.1 [i
1322	78	2.0	468	2	B40228	neurexin I-beta pr	1395	77	2.0	821	1	S06943	brain-derived neur
1323	78	2.0	468	2	S26741	T-cell glycoprotei	1396	77	2.0	821	1	S06943	neuronal different
1324	78	2.0	468	2	S26741	T-cell glycoprotei	1397	77	2.0	1019	2	JC7538	hypothetical prote
1325	78	2.0	482	2	T17250	hypothetical prote	1398	77	2.0	1302	2	T00038	DNA segregation Ar
1326	78	2.0	522	2	A46103	transmembrane glyc	1399	77	2.0	1498	2	B97355	T22111.2 protein -
1327	78	2.0	523	2	C95303	conserved hypothet	1400	77	2.0	1552	2	G86344	receptor DEC-205 -
1328	78	2.0	527	2	T04329	importin alpha - t	1401	77	2.0	1723	2	S58880	hypothetical prote
1329	78	2.0	539	2	JH0259	prostaglandin-endo	1402	77	2.0	1743	2	T28859	hypothetical prote
1330	78	2.0	723	2	PN0509	integrin beta-3 ch	1403	77	2.0	2165	2	T21371	hypothetical prote
1331	78	2.0	725	2	T27148	hypothetical prote	1404	77	2.0	2584	2	T24158	hypothetical prote
1332	78	2.0	843	2	A27131	epidermal growth f	1405	77	2.0	2606	2	T24157	thryoglobulin prec
1333	78	2.0	957	2	T15976	hypothetical prote	1406	77	2.0	2769	1	UIBO	genome polyprotein
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3033	1	GNWVJ8	dysatrophin, musc
1335	78	2.0	1016	2	G86295	hypothetical prote	1408	77	2.0	3660	1	S02041	ALR protein - huma
1336	78	2.0	1131	2	T38744	hypothetical prote	1409	77	2.0	4957	2	T03455	ALR protein - huma
1337	78	2.0	1245	1	VHWVB	structural polypro	1410	76.5	1.9	5262	2	T03454	platelet-aggregati
1338	78	2.0	1260	1	TVRTNU	protein-tyrosine k	1411	76.5	1.9	71	2	A59413	platelet aggregati
1339	78	2.0	1330	1	QGFPE	epidermal growth f	1412	76.5	1.9	146	2	G95995	phosphoribosylform
1340	78	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	216	2	JX0265	platelet aggregati
1341	78	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	224	2	AD2115	phosphoribosylform
1342	78	2.0	1658	2	D75489	hypothetical prote	1415	76.5	1.9	234	2	I48603	insulin-like growt
1343	78	2.0	3234	1	S58884	Ran-binding protei	1416	76.5	1.9	264	2	T22380	hypothetical prote
										272	2	E97451	hypothetical prote

1417 76.5 1.9 272 2 AG2669 enoyl-(acyl)-carrie  
1418 76.5 1.9 309 2 JC5665 four-and-a-half li  
1419 76.5 1.9 202 2 E82627 hypothetical prote  
1420 76.5 1.9 322 1 S37344 chitinase (EC 3.2.  
1421 76.5 1.9 323 2 T24836 hypothetical prote  
1422 76.5 1.9 327 2 AC0156 probable cobalamin  
1423 76.5 1.9 359 2 T30500 probable histidino  
1424 76.5 1.9 359 2 E82627 hypothetical prote  
1425 76.5 1.9 385 2 AH0793 probable lipopolys  
1426 76.5 1.9 386 2 T12527 hypothetical prote  
1427 76.5 1.9 388 1 E8WS ig epsilon chain C  
1428 76.5 1.9 420 2 S74388 gamma-glutamyl pho  
1429 76.5 1.9 435 2 T25350 hypothetical prote  
1430 76.5 1.9 481 2 A56346 transcription fact  
1431 76.5 1.9 483 2 T48328 importin alpha-lik  
1432 76.5 1.9 487 2 T21384 hypothetical prote  
1433 76.5 1.9 504 2 T33404 hypothetical prote  
1434 76.5 1.9 518 2 G88961 protein F59A7.8 li  
1435 76.5 1.9 520 2 C70311 hypothetical prote  
1436 76.5 1.9 536 1 A39036 H+-transporting tw  
1437 76.5 1.9 545 1 PW8YA H+-transporting tw  
1438 76.5 1.9 601 2 T34396 hypothetical prote  
1439 76.5 1.9 623 2 S56206 probable membrane  
1440 76.5 1.9 658 2 T47960 finger protein - m  
1441 76.5 1.9 707 2 S68858 hypothetical prote  
1442 76.5 1.9 712 2 T16338 hypothetical prote  
1443 76.5 1.9 772 2 S32659 integrin beta 2 ch  
1444 76.5 1.9 837 2 A42112 mucin-like peptide  
1445 76.5 1.9 849 2 I50617 protein-tyrosine k  
1446 76.5 1.9 1000 2 S47243 starch phosphoryla  
1447 76.5 1.9 1004 2 T31665 hypothetical prote  
1448 76.5 1.9 1056 2 T31167 hypothetical prote  
1449 76.5 1.9 1071 2 T18307 suppressor protein  
1450 76.5 1.9 1153 2 T00615 RNA polymerase III  
1451 76.5 1.9 1201 2 AD1107 RNA polymerase (be  
1452 76.5 1.9 1349 2 T01699 aldehyde oxidase (  
1453 76.5 1.9 1561 2 S46200 acetyl-CoA carboxy  
1454 76.5 1.9 1660 2 T18561 vitellinogen vit-6  
1455 76.5 1.9 1738 2 C84507 hypothetical prote  
1456 76.5 1.9 1985 2 I61776 Munc13-2 - rat  
1457 76.5 1.9 2098 2 T18397 protein CTBP - mal  
1458 76.5 1.9 2155 2 T30197 alpha tectorin - m  
1459 76.5 1.9 2395 1 S50820 surface protein ty  
1460 76.5 1.9 2562 2 T14266 xin protein - chic  
1461 76.5 1.9 3828 2 T13857 trithorax protein  
1462 76.5 1.9 4550 2 T19440 hypothetical prote  
1463 76.5 1.9 4836 2 T14346 herc2 protein - mo  
1464 76 1.9 96 2 A03208 tissue kallikrein  
1465 76 1.9 136 2 S72508 sperm motility inn  
1466 76 1.9 171 2 I49612 teratocarcinoma-de  
1467 76 1.9 233 2 T22396 hypothetical prote  
1468 76 1.9 261 2 G97190 rRNA methylase, YS  
1469 76 1.9 269 2 S36166 paired box transcr  
1470 76 1.9 287 2 A11072 conserved hypothet  
1471 76 1.9 333 2 T15257 hypothetical prote  
1472 76 1.9 349 1 I51739 transcription fact  
1473 76 1.9 374 2 A42264 membrane-associate  
1474 76 1.9 415 2 T32467 hypothetical prote  
1475 76 1.9 418 2 T24350 hypothetical prote  
1476 76 1.9 454 2 D75446 oxidoreductase - D  
1477 76 1.9 490 2 T35948 probable ADA-like  
1478 76 1.9 512 1 T22021 purH bifunctional  
1479 76 1.9 531 2 T22021 hypothetical prote  
1480 76 1.9 603 2 S22402 2-aminobenzoate-Co  
1481 76 1.9 605 2 T71630 metalloproteinase  
1482 76 1.9 612 2 T39666 WD-repeat protei  
1483 76 1.9 616 1 RRQWA probable RNA-dir  
1484 76 1.9 626 2 T09345 hypothetical prote  
1485 76 1.9 634 2 AG0252 probable DEAD box  
1486 76 1.9 670 2 A12223 transketolase [imp  
1487 76 1.9 837 2 S43656 furin [EC 3.4.21.7  
1488 76 1.9 860 2 JC5702 Erbb kinase activa  
1489 76 1.9 897 2 S67283 hypothetical prote

1490 76 1.9 908 2 T27117 hypothetical prote  
1491 76 1.9 925 2 T37475 lipoprotein recept  
1492 76 1.9 926 1 OPFGIT iodide peroxidase  
1493 76 1.9 934 1 A34372 complement C6 prec  
1494 76 1.9 967 2 T48210 hypothetical prote  
1495 76 1.9 1001 2 AG1979 hypothetical prote  
1496 76 1.9 1084 2 T18292 nicotinamide nucle  
1497 76 1.9 1097 2 S17308 leukemia inhibitor  
1498 76 1.9 1206 2 T18557 probable hydrogena  
1499 76 1.9 1245 1 VHWVB2 structural polypro  
1500 76 1.9 1385 2 S34230 156k protein - Pla

ALIGNMENTS

RESULT 1

T08805

hypothetical protein DKFp586H2123.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C:Accession: T08805

R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16472

A:Accession: T08805

A:Molecule type: mRNA

A:Residues: 1-181 <ANS>

A:Cross-references: UNIPROT:O9Y432; EMBL:AL050214

A:Experimental source: adult uterus; clone DKFp586H2123

C:Genetics:

A>Note: DKFp586H2123.1

Query Match 24.1%; Score 949; DB 2; Length 181;

Best Local Similarity 99.4%; Pred. No. 2.2e-56;

Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 540 SLQISAIILHPNYDPIILDADIAIKLDKARISTRVQPICLAASRDLSSTFQESHITVA 599

|||||

Db 1 SLRISAIILHPNYDPIILDADIAIKLDKARISTRVQPICLAASRDLSSTFQESHITVA 60

QY 600 GNNVLADVRSFGKNDTLRSVGVSVDLSLCEQEDHGIPVSVTDNMFCAWPTAPSD 659

|||||

Db 61 GNNVLADVRSFGKNDTLRSVGVSVDLSLCEQEDHGIPVSVTDNMFCAWPTAPSD 120

QY 660 ICTAETGGIAAVFFGRASPERPWHLMGLVSVSYDKTCSHRLSTAFKVLPFKDWIERNM 719

|||||

Db 121 ICTAETGGIAAVFFGRASPERPWHLMGLVSVSYDKTCSHRLSTAFKVLPFKDWIERNM 180

QY 720 K 720

Db 181 K 181

RESULT 2

A38738

coagulation factor C precursor - horseshoe crab (Tachyplesus tridentatus)

N:Alternate names: coagulation-complement factor C; Limulus factor C

N:Contains: coagulation factor C heavy chain; coagulation factor C light chain peptide

C:Species: Tachyplesus tridentatus

C>Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004

R:Mutu, T.; Miyata, T.; Misumi, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; I

J. Biol. Chem. 266, 6554-6561, 1991

A:Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic

A:Reference number: A38738; MUID:91177916; PMID:2007602

A:Accession: A38738

A:Molecule type: mRNA

A:Residues: 1-1019 <MUT>

A:Cross-references: UNIPROT:P28175; GB:D90271; NID:g217396; PID:d1015020; PID:g217397

A:Accession: B38738

A:Molecule type: mRNA

A:Residues: 1-466,616,'DN',619-620,'A',622 <MU2>

A;Cross-references: GB:D90272  
R;Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kuma, K.I.; Miyata, T.; Iwanaga, S.  
Eur. J. Biochem. 167, 405-416, 1987  
A;Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe crab is a novel type of serine protease.  
A;Reference number: S00105; MUID:88004461; PMID:3308457  
A;Accession: S00105  
A;Molecule type: protein  
A;Residues: 'S',27-39,'S',41,'T',43-54,'E',691-782,950-977 <TOK>  
C;Superfamily: coagulation factor C; C-type lectin homology; complement factor H repeat  
C;Keywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;126-690/Product: coagulation factor C heavy chain #status experimental <HCH>  
F;136-195/Domain: complement factor H repeat homology <FH01>  
F;199-254/Domain: complement factor H repeat homology <FH02>  
F;260-321/Domain: complement factor H repeat homology <FH03>  
F;436-564/Domain: C-type lectin homology <LCH>  
F;576-634/Domain: complement factor H repeat homology <FH04>  
F;685-747/Domain: complement factor H repeat homology #status atypical <PH05>  
F;691-762/Product: coagulation factor C light chain peptide A #status experimental <PPA>  
F;763-1015/Domain: trypsin homology <TRY>  
F;763-1015/Domain: trypsin homology <TRY>  
F;523,534,624,912/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;767/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;809,865,966/Active site: His, Asp, Ser #status predicted  
  
Query Match 17.0%; Score 672; DB 2; Length 1019;  
Best Local Similarity 25.6%; Pred. No. 4.5e-37;  
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;  
  
QY 34 PGAEWNIM---CRECEYDQIE--CVCPRKREVVGYTIPCCRNENECSLIHPGCT 86  
DB 184 PNCQWSFPKPCIRECAKVSSPHGKVNAPSGNMIEGATL-----RFSCHS-----PYYL 233  
  
QY 87 IFENCKSCR-NGSWGGLT-----CQVPGKREVVGYTIPCCRNENECSLIHPGCT 103  
DB 234 IQGETLTICQNGQWSQIIPQCKKLVPDLDPVNAEHQVIGVEQKYGFPGQTEVTVT 293  
  
QY 104 --DDFVVKGYCABCR--AGWYGG--DCMR-----CGQVLR--APKG 137  
DB 294 CSGNYFLMGFTLTKCPDGSWSGQSPCKVADREVDCHSKAVDFLDVYGEFVRHCPAG 353  
  
QY 138 QILLES-----YPLNAHCEWTIRA---KPGFVI-----Q 163  
DB 354 CSLTAGTVGTATYHELSSVCRAIIHAGKLPSGGVHVNVNPGYSDFLGSLDNGIKSBE 413  
  
QY 164 LRFVWLSLEBFDYM-----COYDYVEVRD-----GDNRDQGIKRVCGN--BRPAP 206  
DB 414 LKSLARSFRFDYVSSSTAGRSQCPDQGFVEEENCVVYTSQRAWERAQGVCTNMAARLAV 473  
  
QY 207 IQS--IGSSLHLVLFHSDG-SKNPDGFH-----AIYEITACSSSPCF 245  
DB 474 LDKDLPLSSLTETLRGKGLTTTWIGLRLDAEKPFWELMDRSNVVLDNLTFWASGEPG 533  
  
QY 246 HDGTCV-LDKAGS----YKCACLAGYTGQRCENLLBERN---CSDPGQVWNGYOKITGGP 297  
DB 534 NETNCVLDLRDQLQPVWTKSCFQSPSSFACMDLSDRNKAKCDDPOPLENGHATLHGQS 593  
  
QY 298 GLNGRHAIGTGVVSPFCNNYSVLSGNEKRTCOQNGEWSGKQPCIK--ACREPKISDLV 355  
DB 594 --IDGFYA--GSSIRYSCVHLVLSGTETVCTTNGTWSAPKPRCIKVITCQNPVPVSYG 649  
  
QY 356 RRRVLPMQVQSRTPPLHQLYSAAFSQKLO---SAPTKYPALPPGD-----LP 400  
DB 650 SVEIKE---PSRTNSISRVGSPFLRLPLRLPLARAAKPPPKPRSSQPSVTDLASKVKLP 706  
  
QY 401 MGYCHLHTLOQYECISIPFYRLGSSRRTCLRTGKWSGRAPSCIPICCKENITAP-----455  
DB 707 EGHYRVGSRAIYTCESRYEYLLSQGRCDNSGNWGRPASCIPVGRSDSPRSPIWNG 766  
  
QY 456 -KTQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAACHVTDLGKVTM 514  
DB 767 NSTEIGQWPMQAGISRWLA-----DHNMMWFQCGSLLNEXKIWTAAHCVTYSATAEI 819

QY 515 IKTADLKVVLGKPYFDDRRDEKTIQSIQISAILHPNYDPILLDADIALKLLDKARIST 574  
DB 820 IDPSQFKIYLGKYYDDSDDDYVQVREALEHVNPNYDPGNLNFIDIALIQLKTPVTLTT 879  
  
QY 575 RVQPICLAASRDLSSTFORESHI-----TVAGMNVLADVRSFGFKNDTLRSQVSVVDSL 628  
DB 880 RVQPICLPT--DITF---REHLKEGTALVAVTGWG-----LNENNTYSEMIQQAFLPVVAAS 930  
  
QY 629 LCEBQHEHDGIPVSTVDNMFCSWEPAPSDDICTAETGIAAVSPGRASPEPRWHLMLGL 688  
DB 931 TCEEGYKEADLPLTWTENNFCAGYK-KGRYDACSDDSGG--PLVFADDSRTERRWVLEGI 987  
  
QY 689 VWSYVDKTCSSH-RLSTAFPTKVLPEKDWTIER 717  
DB 988 VSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017  
  
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Ra-reactive factor (EC 3.4.21.-) 1 precursor - human  
N;Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)  
C;Species: Homo sapiens (man)  
C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004  
C;Accession: I54763; JN0883  
R;Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.  
Int. Immunol. 6, 665-669, 1994  
A;Title: Molecular characterization of a novel serine protease involved in activation o  
A;Reference number: I54763; MUID:94289349; PMID:8018603  
A;Accession: I54763  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-699 <SAT>  
A;Cross-references: UNIPROT:P48740; GB:D28593; NID:G790963; PIDN:BAA05928.1; PID:G47112  
R;Takada, F.; Takayama, Y.; Hattuse, H.; Kawakami, M.  
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993  
A;Title: A new member of the C1s family of complement proteins found in a bactericidal  
A;Reference number: JN0883; MUID:94059062; PMID:8240317  
A;Accession: JN0883  
A;Molecule type: mRNA  
A;Residues: 1-234, 'E',236-284, 'G',286-498, 'K',500-542, 'K',544-642, 'S',644-699 <TAK>  
A;Cross-references: DDBJ:D17525; NID:G439712; PIDN:BAA04477.1; PID:G439713  
A;Experimental source: liver  
C;Comment: This is a serum bactericidal factor that activates complement C4 and C2 comp.  
C;Genetics:  
A;Gene: GDB:MASP1; GDB:CRARF; CRARF1; PRSS5; MASP  
A;Cross-references: GDB:361104; GDB:330954; OMIM:600521  
A;Map position: 3q27-3q28  
C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol  
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydr  
F;1-17/Domain: signal sequence #status predicted <SIG>  
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F;19-135/Domain: C1r/C1s repeat homology <C1R1>  
F;143-181/Domain: EGF homology <EGF>  
F;185-294/Domain: C1r/C1s repeat homology <C1R2>  
F;301-362/Domain: complement factor H repeat homology <FH1>  
F;367-432/Domain: complement factor H repeat homology <FH2>  
F;449-699/Domain: trypsin homology <TRY>  
F;49,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572  
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F;448-449/Cleavage site: Arg-Ile (autolytic) #status predicted  
F;490,552,646/Active site: His, Asp, Ser #status predicted  
  
Query Match 12.2%; Score 482; DB 1; Length 699;  
Best Local Similarity 24.9%; Pred. No. 1.4e-24;  
Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;  
  
QY 69 CRNEECDCSLIHPCTIFENCKSCRNCSWGSGTLLDDFYVKGYCAECRAGWY---GGD 124  
DB 143 CKEREDEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 180  
  
QY 125 C-MRCQVLRAPKQGIILL-----ESYPLNAHCETTHAKPGFVIQURFVMSLEFDYM-- 176

Db 181 CRVCSNLTQRTGVITSPDFNPYPKSECLYITBLEEGFWNQLQFEDI----FDIQDH 237  
QY 177 ----COYDYVEVRDGNRQDQIIKRVCGNERPAPIQSIGSSLLVLFHSDGSKNFDFGHAI 232  
Db 238 PEVPCPYDIKIKVGP-----KVLGPFCEKAPPEISTQSHSVLLLFHSDNSAENRGWRL- 292  
QY 233 YEITACSSPCFHDGTCVLDKAGYKACLAGYTGQRCENLLBERNCSPGPGVNGYQK 292  
Db 293 -----SYRAA-----GNECPCL-----QP--PVH----- 309  
QY 293 ITGPGPLNGRHAKIGTVVSEFF-----CNNSV-VLSGNEKR-----TCQNGEWSGKQ 339  
Db 310 -----GKLEPSQAKY-----FFKDQVLVSCDTGKVLKONVEMDTFOIECLKDGTWSNKI 359  
QY 340 PIC- IKACREPKISDLVRRERVLPMQVQSRRETPHLQLYSAAFSKQKLSQAPTKKPPALFPFG 398  
Db 360 PTCKIVDCRAP----- 372  
QY 399 LPMGYOHLHT-----LOQYECISPFYRRLGSSR--RTCLRTGKWIS-----GRA-PSC 442  
Db 373 LEHLITFTSRNLLTYKSIKYSQBPYYKMLNNNTGIYCSAQGVMMNKVLGRSLPTC 432  
QY 443 IPICG-----KIENITAPKTQGLRWPQAAIYRRTSGVHDSGLHKGANFLVCSGA 492  
Db 433 LPVCGLPKFSRKLWAFIN-GRPAQKGT--PWIAML-----SHLNGQPF--CGGS 478  
QY 493 LVNERTVVAACHV--TDLGKVT-----MIKTADLVKLVGKPYRDDDRDEKTIQSLQIS 544  
Db 479 LLGSSMIVTAAACHLQSLDPGDTFLRSDLSLSPDFKILUGKHW--LRSDENEQHLGVK 536  
QY 545 AIIHLNYPDILLDADIAILKLDKARISTRVOPICLAASRDISTFQE-SHITVAGWNV 603  
Db 537 HTTLHQYDNTFENDVALVELLESFVLNAFVNPICLPEGPQ-----QEGAMVIVSGWK 591  
QY 604 LADVRSPGKNDTLRSQVSWVDSLCEBOHEDHGIPVSVTDNMFCASWEPTAPSDICTA 663  
Db 592 QFLQRFPP-----ETLMEIPIVDHSTCQKAYAP--LKVKVTRDMI CAG-EKEGGKDACAG 644  
QY 664 ETGGIAAVSPFGGRASPEPRHMLGLWSYDKTCSHRLSTAFKVLFPFKDWIER 717  
Db 645 DSGGPNVTLNRERG-----QWYLVGTVSWGDDCGKDRYG-VVSYIHHNKDWIOR 693  
RESULT 4  
CIRHUB  
Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Nov-1984 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: A24170; A29769; S02422; A00916; A37820; S68830  
R:Leytus, S.P.; Kurachi, K.; Sakuraiassen, K.S.; Davie, E.W.  
Biochemistry 25, 4855-4863, 1986  
A:Title: Nucleotide sequence of the cDNA coding for human complement C1r.  
A:Reference number: A24170; MUID:87026566; PMID:3021205  
A:Accession: A24170  
A:Molecule type: mRNA  
A:Residues: 1-705 <LEY>  
A:Cross-references: UNIPROT:P00736; GB:M14058; NID:G179643; PIDN:AAA51851.1; PID:G179644  
R:Journet, A.; Tosi, M.  
Biochem. J. 240, 783-787, 1986  
A:Title: Cloning and sequencing of full-length cDNA encoding the precursor of human complement subcomponent C1r.  
A:Reference number: A29768; MUID:87156625; PMID:3030286  
A:Accession: A29768  
A:Molecule type: mRNA  
A:Residues: 1-151, 'L', 153-705 <JOU>  
A:Cross-references: GB:X04701; NID:G29538; PIDN:CAA28407.1; PID:G29539  
R:Arlaud, G.J.; Willis, A.C.; Gagnon, J.  
Biochem. J. 241, 711-720, 1987  
A:Title: Complete amino acid sequence of the A chain of human complement-classical-pathway C1r.  
A:Reference number: A29769; MUID:87241248; PMID:3036070  
A:Accession: A29769  
A:Molecule type: protein  
A:Residues: 18-166, 'X', 168-463 <ARL>

A:Note: 152-Leu was also found  
R:Arlaud, G.J.; van Dorsselaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.  
FEBS Lett. 222, 129-134, 1987  
A:Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of human complement subcomponent C1r.  
A:Reference number: S02422; MUID:88005128; PMID:2820791  
A:Accession: S02422  
A:Molecule type: protein  
A:Residues: 152-186 <AR3>  
A:Note: 152-Leu was also found  
R:Arlaud, G.J.; Gagnon, J.  
Biochemistry 22, 1758-1764, 1983  
A:Title: Complete amino acid sequence of the catalytic chain of human complement subcomponent C1r.  
A:Reference number: A00916; MUID:83204782; PMID:6303394  
A:Accession: A00916  
A:Molecule type: protein  
A:Residues: 464-705 <AR2>  
R:Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.  
J. Biol. Chem. 265, 14469-14475, 1990  
A:Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH2-terminal domain of human complement subcomponent C1r.  
A:Reference number: A37820; MUID:90354439; PMID:2387866  
A:Accession: A37820  
A:Molecule type: protein  
A:Residues: 18-26, 'L', 153-160, 'XX', 252-255 <THI>  
R:Felloux, S.; Thielens, N.M.; Hudry-Clergeon, G.; Petillot, Y.; Filhol, O.; Arlaud, G.  
FEBS Lett. 386, 15-20, 1996  
A:Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human complement subcomponent C1r.  
A:Reference number: S68830; MUID:96221263; PMID:8635594  
A:Accession: S68830  
A:Molecule type: protein  
A:Residues: 133-137, 187-211, 610-613 <PEL>  
A:Experimental source: plasma  
C:Comment: C1r is a dimer of identical chains, each of which is activated by cleavage 1. A chain, while fragment gamma remains disulfide-bonded to the B chain to form C1r II. C:Comment: This protein is a serine protease that combines with C1q and C1s to form C1, n, activate C2 and C4.  
C:Genetics:  
A:Gene: GDB:C1R  
A:Cross-references: GDB:119729; OMIM:216950  
A:Map position: 12p13-12p13  
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homo  
C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; m  
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F:17-138/Domain: C1r/C1s repeat homology <C1R1>  
F:18-463/Product: complement C1r chain A #status experimental <ACH>  
F:146-189/Domain: EGF homology <EGF>  
F:193-302/Domain: C1r/C1s repeat homology <C1R2>  
F:297-463/Product: C1r gamma fragment #status experimental <GFR>  
F:309-371/Domain: complement factor H repeat homology <FH1>  
F:376-447/Domain: complement factor H repeat homology <FH2>  
F:464-705/Product: complement C1r chain B #status experimental <BCH>  
F:464-697/Domain: trypsin homology <TRY>  
F:71-89, 146-165, 161-174, 176-189, 193-220, 250-268, 309-358, 338-371, 376-429, 406-447, 451-577  
F:125, 221, 514, 581/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental  
F:206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental  
F:463-464/Cleavage site: Arg-Ile (autolytic) #status experimental  
F:502, 557, 654/Active site: His, Asp, Ser #status predicted  
Query Match 10.2%; Score 403.5; DB 1; Length 705;  
Best Local Similarity 22.9%; Pred. NO. 2.5e-19;  
Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;  
QY 44 ECCEYDQIEBC-----VC-----PKERWGVYTIPTCC-----RNEERNECD 77  
Db 69 ECGFDYVYKISADKSLGRFCQQLGSPGNPPKKEFMQGNKMLTFTDFSNEN--G 126  
QY 78 SCLIHPGCTIF--ENCKSCRNCSGGTLD-----DFYVYKGYCAECRAGW---- 120  
Db 127 TIMFYKGFLAYYQAVDLDECASRSKSGEDPQPCQHLCHNVYGVYFCS-CRPGYELQED 185  
QY 121 ----YGGDCMRCQGVLRAPKQGI-LLE---SYPLNAHCEWTHAKPGFVQLQAPVMSLEF 173  
Db 186 RHSCQAEC--SSELYTEASGYISSLEYPRSPYPPDLRCNYSIRVERGLTLHLKFE---PP 240



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QY 174 D-----YMCQDYVEVRDGDNRDGOIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFD 227
Db 241 DIDDHQVHCPCYDQIQI-----YANGKNIGCFCKQRPDLDTSSNAVDLLFFTFDGDGR 296
QY 228 GFHAIY-EEITACSSSPFHDGTCVLDKAGSYKACACLAGYTGQRCCNLLERNCSDPGGP 286
Db 297 GWKLRVTTLLIKCPQKPTLDEFTIIQNLQPOVQ-----FRDYFIATCK----- 339
QY 287 VNGYQKITGGPGGLNGRHAIGTFFVSCNNSYLVSGNEKRTQQQNGEWSGKQIPIC- IKA 345
Db 340 -QGYQLIEGNOVL-----HSPT-----AVCQDDGTWHRAMPCKIKD 375
QY 346 CREPKSLDVRRLVPMQVQSRTPHLQLYSAAFSKQKLSQAPTKKPALPFGDL-----PM 401
Db 376 CGQPR-----NLPNGDGRFYTTM 393
QY 402 GYCHLHTLOQYECISPFYR-----RLGSSRR-----TCLRTGKNWG-----RAPSCIPICGK 448
Db 394 GUNTYKARIQYCHEPYKMQTRAGSRESEQGVYTCTAQGIWKEQKGEKI PRCLPVCCK 453
QY 449 IEN-----IPAPKTQGLRMPWQAIIYRTSGVHDGSLHKGAWFLVCSGALVNERTVV 500
Db 454 PVNPVEORQRIIGQKAKGNFPQV-----FTNIHG-----RG-----GGALLGDRWIL 498
QY 501 VAAHCVTDLGKVTMIKTADLKVVILGKFYRDDDRDEKTIQSLQ-----ISAILLHPNY-- 552
Db 499 TAAHTLYPKHEHAQ-SNASLDVFLG-----HTNVEELMKLGNHPIRRVSVHPDYRQ 548
QY 553 -DFILADADAILKLDKARISFRVQPICLAASRDLSSTSFQESHITVAGMNVLAAD----- 606
Db 549 DESYFEGDIALLENSVTLGNLLPICLP-----DNDTFYDLGLMGVSGFGVWEKIAH 605
QY 607 ----VRSPGKNDLTRSGVVVVDLSLCEBQEDHGPVSVTDNMFCAWEPAPSICT 662
Db 606 DLRFVRLP-----VANPQACENWLGRKMRMDVFSQNMFCAG-HPSLKDQACQ 651
QY 663 AETGGTAANSVPGRASPEPRHMLGLVWSYDKTCSHRLSTARTKVLFPKDWIERNMK 720
Db 652 GDSGGVFAVRDPN-----TDRWATGIVSWGIG--CS-RGYGFTYKVLNLYVDWIKEME 702

RESULT 5
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59271
R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laureen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates C
A;Reference number: A59271; MUID:97242412; PMID:9087411
A;Accession: A59271
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-686 <JEN>
A;Cross-references: UNIPROT:O00187; GB:Y09926; NID:G4007626; PIDN:CAA71059.1; PID:G40076
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
C;Genetics:
A;Gene: GDB:MASP2
A;Cross-references: GDB:6071500
A;Map position: lp36.2-lp36.3
C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p
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F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: C1r/C1s repeat homology <C1R1>
F;142-180/Domain: EGF homology <EGF>
F;184-293/Domain: C1r/C1s repeat homology <C1R2>
F;300-361/Domain: complement factor H repeat homology <FH1>
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F;366-430/Domain: complement factor H repeat homology <FH2>

F;445-679/Domain: trypsin homology <TRY>  
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,  
F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F;444-445/Cleavage site: Arg-Ile (autolytic) #status predicted  
F;483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 400.5; DB 1; Length 686;  
Best Local Similarity 22.7%; Pred. No. 3.9e-19;  
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;

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QY 128 CQQLR--APK-----GOILLESYP-----LNAHCEWTTHAKPGFVIQIRFVMLSLEFDY 175
Db 11 CGSVATPLGPKPEPVFGRLASPGPGEVANDQERRRRLTAPGVRRLRYTFHFDLELGH 70
QY 176 MCQDYVEVRDGDNRDGOIKRVCGNE-----RPAP-----IQSIGSSHLVLFHSDGS--KN 225
Db 71 LCEYDFVKLSG-----AKVLATLCQOESTDTERAFKQDTFYSLGSLDTFFRSDYSNEKP 126
QY 226 FQGEHAIY--ERITACSSSP-----CFHDGTCVLDKAGSYKACACLAGYTGQR-----CENL 274
Db 127 FTGFEAFYAAEDIDECQVAPGEAPTCDHH-----CHNHLGGFYCSCRAGYVLRHNRKTCAL 183
QY 275 -----LEE----- 277
Db 184 CSGQVPTQSRSGELSPPEPRYPKLSSTCTSYISLESGFSVILDFVBSFDVETHPETLCPY 243
QY 278 -----RNCSDP 283
Db 244 DFLKIQTDRREHGPFCGKTLPHRIETKSNVTITFTVDESQDHTGKWHIYTTAHACPPY 303
QY 284 GGPVNGYQKITGGPGGLNGRHAH--IGTVVSFFCNSY-VLSG-----NEKRTCCQNGEW 335
Db 304 MAPPNGH-----VSPQAKYILKDSFIFCTGYELLOGLHPLKSFYAVCQKDGSW 354
QY 336 SGKQPIC- IKACREPKISDLVRRRVLPMQVQSRTPHLQLYSAAFSKQKLSQAPTKKPAL 394
Db 355 DRPMFACSI VDCGP--DDLPSGRV-----EVI TGP----- 383
QY 395 PFGDLPVMGQVHLHTLOQYECISPFY--RLGSSRRITCLRTGKNWG-----RAPSCIPICGK 448
Db 384 -----GVTTYKAVIQSYCETFTYTMKVDGKGYVCEADGFWTSSKGEKSLPVCPEVCG 436
QY 449 IENITAPKTQGLR-----WPWQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVA 502
Db 437 SARTTGRIYGGQAKPGDFPQWVLLGGTT-----AAGALLYDNWVLT 481
QY 503 AHCVTDLGKVTMIKTADLKVVILGKFYRDDDRDEKTIQSLQ-----ISAILLHPNY-DP 554
Db 482 AHAVYE-----QKHDSALDIRMG-----TLKRLSPHYTQAWSEAVFIHEGYTHD 526
QY 555 ILLDADAILKLDKARISFRVQPICLAASRDLSSTSFQESHITVAGMNVLAADVRSPEKXN 614
Db 527 AGFDNDIALIKLNKVNINSNITPICLRKBAESFMRTDDIGTASGQ-----LTQGFILA 582
QY 615 DTLRSGVSVVSDLSLCEBQEDHGP-VSVTDNMFCAWEPAPSICTAETAGIAAVSF 673
Db 583 RNLMYVDIPIVDHOKTAAYEKPPYPRGVSVTANMLCAGLE-SGCKDSKSGDSSG--ALVF 639
QY 674 PGRASPEPRHMLGLVWSYDKTCSHRLSTARTKVLFPKDWIE 716
Db 640 --LDSETERFWFGVIVSGMNGCEAGQGVYTKVINIYPWIE 680
```

RESULT 6

S05008  
complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster  
C;Species: Mesocricetus auratus [golden hamster]  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S05008  
R;Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajob-Ohmi, S.; Hamada, Y.; Isono, K.; Sa  
FEBS Lett. 250, 411-415, 1989  
A;Title: Complete primary structure of a calcium-dependent serine proteinase capable of





Db 745 --ELTDHMLCAGPPSKKXDAQCGDGGPLVCQ-----NEKEQFIYGLVSWG--EGCG- 794

Qy 700 RLST--AFYKVLFPKDWIERNMK 720

Db 795 RVSKPGVYTKVRLFFFTMIQNTQQ 817

RESULT 8

JC6554

complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004

C;Accession: JC6554

R;Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.

Gene 209, 87-94, 1998

A;Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement

A;Reference number: JC6554; MUID:98192519; PMID:9524231

A;Accession: JC6554

A;Molecule type: mRNA

A;Residues: 1-694 <SAK>

A;Cross-references: UNIPROT:O70542; DBJ:D88250; NID:g3080541; PIDN:BAA25797.1; PID:g308

C;Comment: This protein is involved in glial cell differentiation and cartilage remodeling

C;Genetics:

A;Gene: x-gsp

C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol

C;Keywords: differentiation; glycoprotein; hydrolase; serine proteinase

F;1-21/Domain: signal sequence #status predicted <SIG>

F;17-133/Domain: C1r/C1s repeat homology <C1R>

F;22-694/Product: serine protease homolog #status predicted <MAT>

F;141-177/Domain: EGF homology <EGF>

F;300-360/Domain: complement factor H repeat homology <FHR>

F;444-681/Domain: trypsin homology <TRY>

F;180.412/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;481.535.637/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 340.5; DB 2; Length 694;

Best Local Similarity 21.2%; Pred. No. 4e-15;

Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;

Qy 44 ECCEYDQIECVCGKRE-----VVGVTTPCCR-----NEE----- 73

Db 69 ENCAVDSVQIISGIEERLCQGRSSKSPNPTVEBFQFPYNNLQVFTSDFNSNEERFTG 128

Qy 74 -----NECDCLIHPCCTIFENCKSCRNNGTLLDPFYVKGFFCAECRACWYGG 123

Db 129 FAAYSADVNECTDFTDVP-CSHF-----CNN-----FIGGYFCS-CPPEYFLH 171

Qy 124 DCMR-----CGQVLRAPKQILLES-----YPLNHAHCWTIHAKPGFVIQLRFVMLSLEF 173

Db 172 DMRTCGVNCSDVFTALIGEIASPNYPNPENSRCEYQIRLOEGF--RLVLTIRREDF 229

Qy 174 DYCQDYVYEVVRDGNR-----DGQIIRKVCNERPAP--IQSIGSSLHVLPHSDG 222

Db 230 D-----VEPADSEGNCHDSLTFAAKNQOFGPYCGNGFPGPLTIKTSNTLIDIVQTDL 282

Qy 223 SKNFDGFHAIY-----BEITACS-----SSPCFHDCTCVLDKAGSKYKACLAGYTG 268

Db 283 TGQNGKWKLYHGDPIPCPKBEISANSIWEPEKAYVFKD-----VVKITC----- 327

Qy 269 QRCENLLEERNCDPGGPVNGYQKINGGPGGLINGRAKIGTVVVSFFCNNSYVLSGNEKRT 328

Db 328 -----VDGFVEVGNVG-----STSPY-----ST 346

Qy 329 CQNGEMSGK-----QFICIKACREPKISDLVRRVLPQVQSRKETPLHQLYSAFQKQL 384

Db 347 CQNGGWSNRLECPV---DCGVPE-----PIENGKVEDPEDTVFGSV----- 387

Qy 385 QSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFY--RRLGSSRRCTCLRTGKWSG----- 437

Db 388 -----IHYTCEEPYTYNEQEGGEYHCAANGSWNNQLGV 422

Qy 438 RAPSCIPICG-----KIEN--ITAPKTOGLRWPQAAIYRRTSGVHDGSLHKGAWFLVC 489

Db 423 ELPKCIPIVCGVTEPFKVOQRIFGGYSTKIQSPFMQVYFESPRGG----- 467

Qy 490 SCALVNERIVVVAACHVT--DLGKVTMIKTADLKVLGKFYRDDDRDEKTIQSIQISAIL 548

Db 468 -GALIDEXVWLTAHVVEGNSDPVMYVGSTLKI-----EKLRNAQLITERVII 516

Qy 549 HPNYDP-----ILLDADIAILKLDKARISTRVQPICLAAASRDILSTSFQESH-----TV 598

Db 517 HFSWKQEDDLNTRTFNDIALVOLKDPVKMGPTVAPICLP---ETFSYDNFSEVDLGLI 573

Qy 599 AGNVLADVRSPFGKNDTLRSGVSVVDSLLCE----EQEDHGIGIPVSTDMNMFCAWEP 654

Db 574 SCWG-RTEIRTVIQ---LRGAKLPITSLKCKQVKVENPKARSNDYVFTDNMICAGEKG 629

Qy 655 TAPSDICTAETGIIAAVSPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFYKVLFPKDW 714

Db 630 V---DSCEGDSGGAFALPVFN--VKDPKPYFVAGLVSWG--KKCG--TYGIYTKVRKNYVDW 680

Qy 715 IERNMK 720

Db 681 ILKTMQ 686

RESULT 9

C1HUS

complement subcomponent C1s (EC 3.4.21.42) precursor [validated] - human

N;Alternate names: C1 esterase precursor

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-May-2004

C;Accession: A40496; A27381; S00224; S26732; S05634; A05140; A25396; A38407; B37820

R;Kusumoto, H.; Hitosawa, S.; Salier, J.P.; Hagen, F.S.; Kurachi, K.

Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988

A;Title: Human genes for complement components C1r and C1s in a close tail-to-tail array

A;Reference number: A40496; MUID:89017187; PMID:2459702

A;Accession: A40496

A;Molecule type: mRNA

A;Residues: 1-688 <KUS>

A;Cross-references: GB:J04080; NID:g179645; PIDN:AAA51852.1; PID:g179646

R;Tosi, M.; Duponchel, C.; Meo, T.; Julier, C.

Biochemistry 26, 8516-8524, 1987

A;Title: Complete cDNA sequence of human complement C1s and close physical linkage of t

A;Reference number: A27381; MUID:88163522; PMID:2831944

A;Accession: A27381

A;Molecule type: mRNA

A;Residues: 1-688 <TOS>

A;Cross-references: GB:M18767; NID:g179647; PIDN:AAA51853.1; PID:g179648

R;Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E.

Eur. J. Biochem. 169, 547-553, 1987

A;Title: Molecular cloning of cDNA for human complement component C1s. The complete am

A;Reference number: S00224; MUID:88082788; PMID:3500856

A;Accession: S00224

A;Molecule type: mRNA

A;Residues: 1-688 <EMBL>

A;Cross-references: EMBL:X06596; NID:g29542; PIDN:CAA29817.1; PID:g763110

A;Accession: S26732

A;Molecule type: protein

A;Residues: 16-38/69-116;170-236;246-262;265-280;282-284;287-308,315-363;384-394;421-43

R;Tosi, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E.

J. Mol. Biol. 208, 709-714, 1989

A;Title: Complement genes C1r and C1s feature an intronless serine protease domain clos

A;Reference number: S05634; MUID:90040704; PMID:2553984

A;Accession: S05634

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 356-513,'G',514-688 <TO2>

R;Carter, P.E.; Dunbar, B.; Fothergill, J.E.

Biochem. J. 215, 565-571, 1983

A;Title: The serine proteinase chain of human complement component C1s. Cyanogen bromid

A;Reference number: A05140; MUID:84104122; PMID:6362661

A;Accession: A05140

A;Molecule type: protein

A;Residues: 438-483,'X',485-500;503-534;542-558;561-572,'A',574-601;617-623;626-644;647

R;Spycher, S.E.; Nick, H.; Rickli, E.E.

Eur. J. Biochem. 156, 49-57, 1986  
 A;Title: Human complement component C1s. Partial sequence determination of the heavy chain  
 A;Reference number: A25396; MUID:86164350; PMID:3007145  
 A;Accession: A25396  
 A;Molecule type: protein  
 A;Residues: 16-61;168-219;287-293,'X',295-334;384-445 <SPY>  
 R;Hess, D.; Schaller, J.; Richli, E.E.  
 Biochemistry 30, 2827-2833, 1991  
 A;Title: Identification of the disulfide bonds of human complement C1s.  
 A;Reference number: A38407; MUID:91175725; PMID:2007122  
 A;Accession: A38407  
 A;Molecule type: protein  
 A;Residues: 131-134,'X',136-146,'X',148-150;155,'X',157-162;166-170,'X',172-174,'X',176-  
 'X',387-402,'X',404-408;416-424,'X',426-431;547-556;592-597;617,'X',619-627,'X',629-635  
 R;Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.  
 J. Biol. Chem. 265, 14469-14475, 1990  
 A;Title: Chemical and functional characterization of a fragment of C1s containing the ep  
 A;Reference number: A38672; MUID:90283368; PMID:2141278  
 A;Contents: annotation; erythro-beta-hydroxyasparagine site, content  
 A;Note: about half of the A chains contain erythro-beta-hydroxyasparagine  
 C;Comment: This protein is a serine proteinase that combines with C1q and C1r to form C1  
 s C2 and C4.  
 C;Comment: C1s is a dimer of identical chains, each of which is activated by cleavage in  
 C;Genetics:  
 A;Gene: GDB:C1S  
 A;Cross-references: GDB:119730; OMIM:120580  
 A;Map position: 12p13-12p13  
 A;Introns: 291/1; 329/3; 356/1; 399/1; 424/1  
 A;Note: the list of introns may be incomplete  
 C;Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol  
 C;Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; du  
 F;1-15/Domain: signal sequence #status predicted <SIG>  
 F;11-127/Domain: C1r/C1s repeat homology <C1R1>  
 F;16-688/Product: complement subcomponent C1s #status experimental <MAT>  
 F;16-437/Product: complement subcomponent C1s chain A (heavy chain) #status experimental  
 F;135-171/Domain: EGF homology <EGF>  
 F;175-287/Domain: C1r/C1s repeat homology <C1R2>  
 F;294-354/Domain: complement factor H repeat homology <FH1>  
 F;359-421/Domain: complement factor H repeat homology <FH2>  
 F;438-688/Product: complement subcomponent C1s chain B (light chain) #status experimental  
 F;438-675/Domain: trypsin homology <TRY>  
 F;65-83;135-147;143-156;158-171;175-202;234-251;294-341;321-354;359-403;386-421;425-549,  
 F;149/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimental  
 F;174,406/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;437-438/Cleavage site: Arg-ile (complement subcomponent C1r) #status experimental  
 F;475,529,632/Active site: His, Asp, Ser #status predicted  
 Query Match  
 Best Local Similarity 21.7%; Pred. No. 1,1e-14;  
 Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;

295 GQGLIN-----GRHAK--I 307  
 254 GFGPLNIETKSNALDIIIFQDITGQKGWKLRYHGDPMPCPKEDTPNSWBEPAKAYVF 313  
 308 GTVVSPFCNNSY-VLSG-----NEKRTCOONGSEWSK-----QPICIKACREPISDLVRR 357  
 314 RDVQITCLDGGFEVVEGRVGATSYSTCOSNGKWSNKLKQBPV-----DCGIP----- 362  
 358 RVLPMQVSRETPLHQLYSAFASKQKQSAFTKCP-ALPFGDPLPMGYQHLLHTOLOQECIS 416  
 363 -----ESIENGKVEDPESTLFGSV-----IRTCBE 388  
 417 PPY--RRLGSSRRCTCLRTCKWSGRA-----PSCIPICGKIENITAPKTQGLRWPWQAAY 469  
 389 PYYVMENGSGGVEYHCAGNSWVNLGPELPCVPVCG-----VF-----REPFEEK-- 435  
 470 RTTSGVHDSLHKGAFLV-----CSGALVNETVTVVAACHVYDGLKVTMTKATADLKVL 524  
 436 QRITGGSDADIKNFPNQVFDPNPAWAGGALINEYWLTAHVVEGNREPTM-----YV 487  
 525 GKFYRDDDRDEKTIQSLQISAILLHPNYPDILL-----DADIALKLLDKARISTRVQ 577  
 488 GSTSVQTSRLAKS-KMLTPEHFVHPGWKLLEVPBGRTNFDNDIALVRLKDPVPMGPTVS 546  
 578 PICLAASRDLSFQESHITVAGWNLADVRSFPGKND---TLRSGVSVVSDSLLCSEQH 634  
 547 PICLPOTSDYNLMDGLISGWG-----RTE--KRDRAVRLKAARLPVAPLRKCKEVK 599  
 635 EDHGIPVS-----VTDNMFCASWEPTAPSDCTAETGIAAVSFPGRASPERPWHLMGL 688  
 600 VEK--PTADAEAYVFTPNNICAGGE--KGMDSCKGDSGGAFVQDP---NDKTKFYAAGL 652  
 689 VMSVDKTCSHRLSTAFTKVLFPKDWIERNMK 720  
 653 VSWG--PQCG--TYGLYTRKRYVDWIMKTMQ 680  
 RESULT 10  
 A56318  
 enteropeptidase (EC 3.4.21.9) precursor [validated] - human  
 N;Alternate names: enterokinase  
 C;Species: Homo sapiens (man)  
 C;Date: 19-May-1995 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
 C;Accession: A56318; B43090  
 R;Kitamoto, Y.; Veille, R.A.; Donis-Keller, H.; Sadler, J.E.  
 Biochemistry 34, 4562-4568, 1995  
 A;Title: cDNA sequence and chromosomal localization of human enterokinase, the proteoly.  
 A;Reference number: A56318; MUID:95234679; PMID:7718557  
 A;Accession: A56318  
 A;Molecule type: mRNA  
 A;Residues: 1-1019 <KIT>  
 R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994  
 A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease comp  
 A;Reference number: A43090; MUID:94329561; PMID:8052624  
 A;Accession: B43090  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 749-1019 <K12>  
 C;Cross-references: GDB:U09860  
 C;Comment: The mechanism of association with the membrane of the intestinal brush borde  
 (ated below) or with amino-terminal myristoylation of the heavy chain.  
 C;Genetics:  
 A;Gene: GDB:PRSS7  
 A;Cross-references: GDB:384083; OMIM:226200  
 A;Map position: 21q21-21q21  
 C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light  
 ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms invol  
 ducts.  
 C;Function:  
 A;Description: cleaves activation peptide from trypsinogen to produce active trypsin

A:Pathway: intestinal digestive hydrolase cascade  
C:Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat  
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen  
F:1-784/Product: enteropeptidase heavy chain #status predicted <HCH>  
F:22-38/Domain: transmembrane #status predicted <TM>  
F:184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:342-504/Domain: NAM homology <NAM>  
F:526-631/Domain: C1r/C1s repeat homology <C1r>  
F:643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC>  
F:785-1014/Product: enteropeptidase light chain #status predicted <LCH>  
F:785-1014/Product: trypsin homology <TRY>  
F:116-147, 179, 328, 335, 388, 440, 470, 503, 534, 630, 682, 706, 725, 848, 887, 909, 949/Binding site:  
F:772-896, 810-826, 910-977, 941-956, 967-995/bisulfide bonds: #status predicted  
F:825, 876, 971/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 331.5; DB 1; Length 1019;  
Best Local Similarity 22.9%; Pred. No. 2.4e-14;  
Matches 136; Conservative 90; Mismatches 225; Indels 143; Gaps 27;

QY 143 SYPLNAHCWTHAKPGFVIQLRFVMLSEFDYMCQYDVVEVDGNDRGQIIKRCVGN 202  
Db 545 YPNLAFVCWILNAQKGNQLHF-----QEFLENINADVVEIRDGEADSLLLAVTG-- 598  
QY 203 RPAIQSIGSLH-----VLPHSDGSKNF-DGFHAIYEEITACSSSPCFHDGTCV 251  
Db 599 -PGPVKDFSTNRMVLTINDVLARGGFKANFTTGYHLGIPE-----PC----- 643  
QY 252 LDKAGSYKC---ACLA-----GYTQRCENLLEERNCSDPGPGVNGYQKITGGPGLNG 302  
Db 644 --KADHFQCKNGCEVPLNLCGHL--HCDGSDGDEADC-----VRFNGTNNNGLVRF 693  
QY 303 RHAKIGTVVFFCNNSYVLSGNEKRTCQONGEWSGKQPIKACREPDKISDLVRRVLP 362  
Db 694 RIQSIW-----HTACAENWTQTISNDVC-----QLLGL 721  
QY 363 QVQSRRTPLHOLYSAAFSKQKLOSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFYRL 422  
Db 722 GSGNSKPIFSTDGGPF--VKLNTAPD-----GHLIITPQQCLQDSLRL 765  
QY 423 GSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHK 482  
Db 766 QCNHKSC-----GKLAQAQDITPKI--VGSNAKEGAWPVVGLY-----YGR--- 807  
QY 483 GAWFLVCSGALNVNRTVVAACHCVTDLGKVTMLKTADLKVKLVKFRDDEKTIQSLQ 542  
Db 808 ----LLCGASLVSSDWLVAACHCV--YGR--NLEPSKWTAILGLHMKSNLTSPTVPRL- 858  
QY 543 ISAILHPNVPILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITVAGWN 602  
Db 859 IDEIVNPHNRRRKNDIAMHLEFKVNYVDYIQICLPEENQVPPGR--NCSITAGWG 916  
QY 603 VLADVRSPGFKNDLRSVVVDSLLCEQEDHGIPIVSVTDNMFCAWEPAPSIDICT 662  
Db 917 T---VYQGTANILQEADVPLLSNRCQQQMPY---NITENMICAGYE-BGGIDSCQ 968  
QY 663 AETGGIAVSPGRASPERPWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIE 716  
Db 969 GDSGG-----PLMCQENNRWFLAGVTSFGYKCALPNR-PGVYARVSRFETMIQ 1015

RESULT 11  
A53663  
enteropeptidase (EC 3.4.21.9) precursor [validated] - pig  
N:Alternate names: enterokinase  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 07-Oct-1994 #sequence\_revision 09-Aug-1996 #text\_change 28-Apr-2003  
C:Accession: A53663  
R:Matsumura, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Teukada, S.; Miki, K.; Kurokawa,  
J. Biol. Chem. 269, 19976-19982, 1994  
A:Title: Structural characterization of porcine enteropeptidase.  
A:Reference number: A53663; MUID:94327548; PMID:8051081  
A:Accession: A53663

A:Molecule type: mRNA  
A:Residues: 1-1034 <MAT>  
A:Cross-references: GB:D30799; MID:g505122; PIDN:BAR06459.1; PID:g505123  
A:Note: parts of this sequence, including the amino ends of three chains isolated from t  
C:Comment: The mechanism of association with the membrane of the intestinal brush border  
ated below) or with amino-terminal myristoylation of the heavy chain.  
C:Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)  
ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv  
C:Function:  
A:Description: cleaves activation peptide from trypsinogen to produce active trypsin  
A:Pathway: intestinal digestive hydrolase cascade  
C:Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding rep  
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen  
F:22-38/Domain: transmembrane #status predicted <TM>  
F:52-117/Product: enteropeptidase mini chain #status predicted <MCH>  
F:118-799/Product: enteropeptidase heavy chain #status predicted <HCH>  
F:199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F:357-519/Domain: NAM homology <NAM>  
F:541-646/Domain: C1r/C1s repeat homology <C1r>  
F:658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F:693-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC>  
F:800-1034/Product: enteropeptidase light chain #status predicted <LCH>  
F:800-1034/Product: trypsin homology <TRY>  
F:116,147,170,194,283,343,350,403,455,485,518,549,645,697,701,721,740,761,804,863,902,936  
F:787-911,825-841,925-992,956-971,982-1010/Disulfide bonds: #status predicted  
F:840,891,986/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 330.5; DB 1; Length 1034;  
Best Local Similarity 22.9%; Pred. No. 2.9e-14;  
Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;

QY 143 SYPLNAHCWTHAKPGFVIQLRFVMLSEFDYMCQYDVVEVDGNDRGQIIKRCVGN 202  
Db 560 NYPNOAFVCWILNAQKGNQLHF-----QEFLENINADVVEIRDGEADSLLLAVTG-- 613  
QY 203 RPAIQSIGSS---LHVLPHSDGSS-----KNF-DGFHAIYEEITACSSSPCFHD--- 247  
Db 614 -PGPVKDFSTNRMVLTINDVLARGGFKANFTTGYHLGIPE-----PKEDNFQC 665  
QY 248 --GTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGPGVNGYQKITGGPGLNGRIA 305  
Db 666 ENGECVL-----LVNLCDFGSHCKDGSDEAHCVRFNLGNTANNSSLGVFRITQ 711  
QY 306 KIGTVVFFCNNSYVLSGNEKRTCQONGEWSGKQPIKACREPDKISDLVRRVLP 365  
Db 712 SIW-----HTACAENWTQTISDDVC-----QLLGLGTG 739  
QY 366 SRETPLHOLYSAAFSKQKLOSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFYRLGSS 425  
Db 740 NSSMPFFSSGGGPF--VKLNTAPNGSLILTASE-----QCFEDSLILLQCN 783  
QY 426 RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPQAAIYRRTSGVHDQS 479  
Db 784 HKSC---GK-----KQVAQEVSPKIVGGNDSREGAWPVVVALY-----YNGQ 822  
QY 480 LHKGAFLVCSGALNVNRTVVAACHCVTDLGKVTMLKTADLKVKLVKFRDDEKTIQ 539  
Db 823 -----LLCGASLVSRDMLVAACHCV--YGR--NLEPSKWTAILG-LHMTSNLTSFQIV 870  
QY 540 SIQISAILHPNVPILLDADIAILLKLDKARISTRVQPICLAASRDLSFQESHITV 598  
Db 871 TRLIDEIVNPHNRRRKNDIAMHLEFKVNYVDYIQICLPEENQV---PPGGRICSI 927  
QY 599 AGNVLADVRSPGFKNDLRSVVVDSLLCEQEDHGIPIVSVTDNMFCAWEPAPS 658  
Db 928 AGWKGVIYQGSFA---DILQEADVPLLSNRCQQQMPY---NITENMWCAQYE-EGGI 979  
QY 659 DICTAETGGIAVSPGRASPERPWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIE 716  
Db 980 DSCQDGGSG-----PLMCLENRRWLLAGVTSFGYKCALPNR-PGVYARVPKTEWIIQ 1030

RESULT 12

JX0210  
Protein C (activated) (EC 3.4.21.69) precursor - mouse  
N;Alternate names: vitamin K-dependent serine proteinase  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: JX0210  
R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
J. Biochem. 111, 491-495, 1992  
A;Title: Isolation and characterization of a mouse protein C cDNA.  
A;Reference number: JX0210; MUID:92316897; PMID:1618739  
A;Accession: JX0210  
A;Molecule type: mRNA  
A;Residues: 1-461 <TAD>  
A;Cross-references: UNIPROT:P33587; GB:D10445; NID:g2203085; PIDN:BAA01235.1; PID:g2203086  
A;Experimental source: liver  
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
s.  
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
F;1-33/Domain: signal sequence #status predicted <SIG>  
F;27-85/Domain: Gla domain homology <GLA>  
F;34-41/Domain: propeptide #status predicted <PRO>  
F;42-196/Domain: protein C #status predicted <PC>  
F;42-196/Domain: light chain #status predicted <PCL>  
F;91-130/Domain: EGF homology <EG1>  
F;139-174/Domain: EGF homology <EG2>  
F;199-461/Domain: heavy chain #status predicted <PCH>  
F;199-211/Domain: activation peptide #status predicted <ACT>  
F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <ACT>  
F;212-445/Domain: trypsin homology <TRY>  
F;47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxylglutamic acid (Glu) #status  
F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F;121-130,139-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
F;214,290,355/Binding site: carbohydrate (Aen) (covalent) #status predicted  
F;253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 8.1%; Score 320; DB 1; Length 461;  
Best Local Similarity 23.9%; Pred. No. 6e-14;  
Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;

QY 152 WTI-----HAKPGF-----VIOLRFVMLSEFDYMCQYDVEYRDNDRDQGIKKRV 198  
DB 14 WGISSIPALHPDPVFSSEHAHQVLRVRRANSFLF-----EMRPG-SLERECWEEI 62

QY 199 CGNERPAPI-QSIGSSHLVLFHSDGSKNFDGFAHYEETITACSSSPCFHDGTCVLDKAGS 257  
DB 63 CDFEERAQEIFQNVEDTLAFWI-----KYFDGQCSAPPLDHCQDSFCCGHGTCT-DGIGS 116

QY 258 YKACLAGYTGQRCENLLBERNSCDPGPVNGVQKITGGPL-----INGRHAKIGTVV 311  
DB 117 FSCGCDKGWEGKFCQQLRFPQC-----RVNNGGCLHYCLEESNGRCA----- 160

QY 312 SPFCNNSYVLGNKEK-----TCQNGEWSGKQPIKACREPISDLVRRVLPQV 364  
DB 161 ----CAGYELADHMKCKSTVNPFCGKGRWIEK-----KKKIL----- 196

QY 365 QSRETPHLQLYSAFSAFQKLSQAPTKKPPALPGDLPNGYQHLHTQLQYECISPFYRRLGS 424  
DB 197 -KEDTUL-----EDELPPD----- 210

QY 425 SRRTLRTGWSGRAPSCIPICCKIENITAPKTQGLRWPMQAAYVRTSGVHDGSLHKA 484  
DB 211 -----RIVNGTLTK-QG-DSPQAAIL-----DSKKK-- 235

QY 485 WELVCSGALVNERTVVVAACHVTDLCKVMTKADIKVVLGKPYRDRDRDEKTIQSLQIS 544  
DB 236 --LACGVLHTSWLTAACHVEGTGKLT-----VRLGEY--DLRRDRHWELDLDTK 283

QY 545 AILTHPNYDPIILDADIALIKLADKARISTRVOPICL-----AASRDLSTSFQESHITVAG 600  
DB 284 EILVHNYTRSSDNDIALRLAQAATLKTIVPICLPNGLAQQLTGAQGETVVT--G 341

QY 601 WNVLADVRSPGFKNDTL-----RSGVVSVVDSLLCEEQBEDHGIPVSVTDNMF 649

Db 342 WGYQSDRIKDGRRNRTFILTFRIPVARNECEVVMKNV-----VSENMLC 387  
QY 650 ASMEPTAPSDICTAETGGIAAASFPGRASPEPRWHLMLGLVSWGYDKTCSHRLSTA-PTKV 708  
Db 388 AGIIGNT-RDACDGDGGPMVFRG-----TWFLVGLVSWG--EGCGHTNNGYITKV 438  
QY 709 LPFKDWI 715  
Db 439 GSYLKI 445

## RESULT 13

A43090  
enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine  
N;Alternate names: enterokinase  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A43090; A48874; A61436  
R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994  
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease comp  
A;Reference number: A43090; MUID:94329561; PMID:8052624  
A;Accession: A43090  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1035 <KIT>  
A;Cross-references: UNIPROT:P98072; GB:U09859; NID:g746410; PIDN:AAB40026.1; PID:g74641  
A;Experimental source: small intestine  
R;LaVallie, E.R.; Rehentulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;  
J. Biol. Chem. 268, 23311-23317, 1993  
A;Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of  
A;Reference number: A48874; MUID:94043122; PMID:8226855  
A;Accession: A48874  
A;Molecule type: mRNA  
A;Residues: 801-1035 <LAV>  
A;Cross-references: GB:D19663; NID:9416131; PIDN:AAA16035.1; PID:g416132  
A;Note: Parts of this sequence, including the amino end of the mature protein, were con  
R;Light, A.; Janska, H.  
J. Protein Chem. 10, 475-480, 1991  
A;Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.  
A;Reference number: A61436; MUID:92189715; PMID:1799406  
A;Accession: A61436  
A;Molecule type: protein  
A;Residues: 801-807, 'Y', 809-827 <LIG>  
C;Comment: The mechanism of association with the membrane of the intestinal brush borde  
embrane attachment using a signal-anchor sequence  
C;Comment: Conversion from membrane-bound to soluble forms may involve further processi  
C;Complex: mature enteropeptidase is variously reported to contain two (heavy and light  
l)ide linked  
C;Function:  
A;Description: cleaves propeptide from trypsinogen to produce active trypsin  
A;Pathway: intestinal digestive hydrolase cascade  
C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding re  
C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protei  
F;22-38/Domain: transmembrane #status predicted <TRM>  
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>  
F;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>  
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F;358-520/Domain: MAM homology <MAM>  
F;542-647/Domain: C1r/C1s repeat homology <C1r>  
F;659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F;694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SR  
F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>  
F;801-1030/Domain: trypsin homology <TRY>  
F;116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Bindi  
F;788-912,826-926,926-993,957-972,983-1011/Disulfide bonds: #status predicted  
F;841,892,987/Active site: His, Asp, Ser #status predicted

Query Match 8.0%; Score 317.5; DB 1; Length 1035;  
Best Local Similarity 24.6%; Pred. No. 2.1e-13;  
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;





Search completed: May 8, 2005, 16:06:45  
Job time : 40 secs

A;Cross-references: UNIPROT:Q9JJI7; DBJ:AB049189  
A;Experimental source: strain Male, 7-week-old  
R;Satomi, S.; Yanasaki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.  
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001  
A;Title: A role for membrane-type serine protease (MT-Sp1) in intestinal epithelial turn  
A;Reference number: JC7775; PMID:11573963  
A;Contents: Small intestine  
A;Accession: JC7775  
A;Molecule type: mRNA  
A;Residues: 1-855 <SAT>  
A;Cross-references: DBJ:AB037898  
C;Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease  
of specific proteins or peptides on the brushborder membranes. It also participates in  
lial migration and/or cell loss.  
C;Genetics:  
A;Gene: mt-spl  
A;Map position: basolateral cell surface  
C;Superfamily: membrane-bound arginine-specific serine proteinase  
C;Keywords: protein digestion

Query Match 7.9%; Score 313; DB 2; Length 855;  
Best Local Similarity 21.4%; Pred. No. 3.4e-13;  
Matches 151; Conservative 78; Mismatches 227; Indels 250; Gaps 33;

QY 82 HPG--CTIFENCKSRNGSGTLLDDFYVKGFCACRAGWYGGDCMRCQGVLRAPKGQI 139  
DB 324 HPGFEATFFQLPKM---SSCGLLSE--AQGTSSP-----YYPG----- 358  
QY 140 LLESSYPLNAHCEWTHAKPGFVLQRFVMLSLEFDYM---CQYDYVEVRDGNRDGQII 195  
DB 359 ---HYPPNINCTWNKVPNNRNKVRFKLFYLDPNIPVGSCTKYDVEING----- 406  
QY 196 KRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACSSSPC-----FHDGTC 250  
DB 407 EKCGERSQFVSSNSSKITVHFSDHSYTDGTGLAEY--LSYDSNDPCPGMFMCKTGRC 464  
QY 251 VL-----DKAGSYKACLAGY-----TGRCENLL-----ERNCS 281  
DB 465 IRKDLRCDGWADCPDYSDERHRCNATHQPMCKNQCFKPLFWVCDSVNDCGDSDEGCS 524  
QY 282 DPGGPNVGYQKITGGPOLINGRAKIGTVVSFFCNNSYVL-----SGNEKETCOQNGEWSG 337  
DB 525 CPAG-----SFKCSNGKCLPQSQQCNGKDDCGDGGDEAS 558  
QY 338 KQPICIKACREPKISDLVRRRLVPMQVQSRETPHLQLYSAAFSKQLQSAPTCKPALPFG 397  
DB 559 CDNVNAVSC----- 567  
QY 398 DPMGYOHLHTLOYEICISPFYRLGSSRRTCRLRTGWSGRAPSCIPICOKIENITAPKT 457  
DB 568 -----TKTYRC-----QNGLCNLKGN-----PEC---DGKDCSDGSD 599  
QY 458 Q-----GLR-----WPMQAAIYRTSGVHDSGLHKGAWFLVCSGALVN 495  
DB 600 KNCDCGLRSTKQARVVGGTNADEGEMPMQVSLHALGQG-----H-----LCGASLIS 647  
QY 496 ERTVVAACHCVTLGKVTMIKTAD---LKVVLGKFYRDDDRDEKTIQSLQISAIILHPNY 552  
DB 648 PDLVLSAACHCFQD---ETIFKYSHTMTWTAFLG--LLDQSKRSASGVQEHKRLIITHPSF 703  
QY 553 DPILLADADIALKLLDKARISTRVQPICLAAASRDLSSTFOESHITVAGMNVLADVRSPPG 612  
DB 704 NDFTFDYDIALLELEKPAEYSTVVRPICLPDNTHTVPAGKA--IWTGW---GHTKEGGT 758  
QY 613 KNDTLRSVVVVDLSLLCEEHEDHGPVSVTDNMFCASWEPTAPSDICTAETGG-IAAV 671  
DB 759 GAILQKEIRVINQTTCEEL-----LPQOITPRMMCVGF--LSGGVSDSCQDGGPLSSV 812  
QY 672 SPFGRASPERHMLGLVMSYDKTCSHRLST-AFTKVLFPKDWIE 716  
DB 813 EKDGRI-----FQAGVWSWG--EGCAQRNKPQVYTRIPEVRDWIK 850



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 8, 2005, 16:05:58 ; Search time 62 Seconds  
(without alignments)  
3874.051 Million cell updates/sec

Perfect score: 3945  
Sequence: 1 MELGCWTQGLTFLQLLLIS.....LSTAFKVLPPKDWIERNNK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA.\*

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3: /cgn2\_6/protdata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/protdata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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18: /cgn2\_6/protdata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/protdata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
27	3945	100.0	720	10	US-09-997-428-231
562	3945	100.0	720	14	US-10-174-587-170
626	3945	100.0	720	14	US-10-063-742-38
741	3945	100.0	720	17	US-10-972-317-38
742	3939	99.8	720	14	US-10-004-551-4
743	3939	99.8	720	14	US-10-098-871-26
744	3921.5	99.4	737	16	US-10-408-765A-1796
745	3500.5	88.7	649	15	US-10-274-639-17
746	3500.5	88.7	649	15	US-10-333-574-17
747	3089.5	78.3	567	14	US-10-004-551-2
748	2946.5	74.7	570	13	US-10-067-422-9
749	2413	61.2	455	11	US-09-833-245-1401
750	1708.5	43.3	323	11	US-09-833-245-1402
751	672	17.0	1019	14	US-10-183-992-4

752	665	16.9	1019	14	US-10-183-992-8	Sequence 8, Appli
753	665	16.9	1019	16	US-10-638-125-4	Sequence 4, Appli
754	665	16.9	1083	14	US-10-183-992-6	Sequence 6, Appli
755	665	16.9	1083	16	US-10-638-125-2	Sequence 2, Appli
756	476	12.1	699	15	US-10-388-322-2	Sequence 2, Appli
757	471	11.9	728	14	US-10-148-671-5	Sequence 5, Appli
758	469.5	11.9	679	9	US-09-874-198-6	Sequence 6, Appli
759	469.5	11.9	679	9	US-09-874-238-6	Sequence 6, Appli
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761	403.5	10.2	688	9	US-09-874-198-7	Sequence 7, Appli
762	403.5	10.2	688	9	US-09-874-238-7	Sequence 7, Appli
763	403.5	10.2	705	9	US-09-808-602-94	Sequence 94, Appli
764	403.5	10.2	705	10	US-09-800-188-81	Sequence 81, Appli
765	403.5	10.2	705	15	US-10-257-021-66	Sequence 66, Appli
766	401.5	10.2	686	9	US-09-874-198-2	Sequence 2, Appli
767	401.5	10.2	686	9	US-09-874-238-2	Sequence 2, Appli
768	400.5	10.2	686	15	US-10-388-322-3	Sequence 3, Appli
769	400.5	10.2	686	15	US-10-332-713-2	Sequence 2, Appli
770	398.5	10.1	671	15	US-10-332-713-3	Sequence 3, Appli
771	336	8.5	760	9	US-09-925-301-1024	Sequence 1024, Ap
772	334	8.5	673	9	US-09-874-198-8	Sequence 8, Appli
773	334	8.5	673	9	US-09-874-238-8	Sequence 8, Appli
774	332	8.4	855	15	US-10-072-012-354	Sequence 354, App
775	332	8.4	855	15	US-10-072-012-420	Sequence 420, App
776	332	8.4	855	15	US-10-037-417-132	Sequence 132, App
777	331.5	8.4	1019	10	US-09-776-191-64	Sequence 64, Appli
778	331.5	8.4	1019	14	US-10-157-031-267	Sequence 267, App
779	331.5	8.4	1019	15	US-10-156-214A-31	Sequence 31, Appli
780	331.5	8.4	1019	16	US-10-729-807-37	Sequence 37, Appli
781	330.5	8.4	1019	16	US-10-408-765A-2243	Sequence 2243, Ap
782	329.5	8.4	3389	15	US-10-016-248-47	Sequence 47, Appli
783	329.5	8.4	3389	16	US-10-408-765A-2286	Sequence 2286, Ap
784	329.5	8.4	3508	15	US-10-016-248-46	Sequence 46, Appli
785	329	8.3	3564	15	US-10-016-248-45	Sequence 45, Appli
786	328.5	8.3	1274	15	US-10-467-042-11	Sequence 11, Appli
787	328.5	8.3	1783	14	US-10-276-934-12	Sequence 12, Appli
788	328.5	8.3	1800	14	US-10-276-934-10	Sequence 10, Appli
789	328.5	8.3	1826	14	US-10-276-934-9	Sequence 9, Appli
790	328.5	8.3	2008	14	US-10-276-934-11	Sequence 11, Appli
791	328.5	8.3	2306	14	US-10-276-934-14	Sequence 14, Appli
792	328.5	8.3	2352	14	US-10-276-934-13	Sequence 13, Appli
793	328	8.3	762	16	US-10-723-807-1	Sequence 1, Appli
794	328	8.3	851	15	US-10-276-774-1798	Sequence 1798, Ap
795	328	8.3	851	15	US-10-296-115-1143	Sequence 1143, Ap
796	328	8.3	855	15	US-10-295-027-1185	Sequence 1185, Ap
797	328	8.3	855	15	US-10-072-012-353	Sequence 353, App
798	328	8.3	855	15	US-10-072-012-412	Sequence 412, App
799	328	8.3	855	15	US-10-072-012-419	Sequence 419, App
800	327.5	8.3	449	9	US-09-925-302-612	Sequence 612, App
801	327.5	8.3	449	10	US-09-925-302-612	Sequence 612, App
802	327	8.3	688	15	US-10-453-827-884	Sequence 884, App
803	327	8.3	757	15	US-10-072-012-44	Sequence 44, Appli
804	327	8.3	855	10	US-09-776-191-2	Sequence 2, Appli
805	327	8.3	855	14	US-10-099-700A-2	Sequence 2, Appli
806	327	8.3	855	14	US-10-190-030B-2	Sequence 2, Appli
807	327	8.3	855	14	US-10-302-840B-2	Sequence 2, Appli
808	327	8.3	855	14	US-10-267-219-2	Sequence 2, Appli
809	327	8.3	855	14	US-10-112-221A-2	Sequence 2, Appli
810	327	8.3	855	14	US-10-104-271-2	Sequence 2, Appli
811	327	8.3	855	15	US-10-147-211A-2	Sequence 2, Appli
812	327	8.3	855	15	US-10-156-214A-2	Sequence 2, Appli
813	327	8.3	855	15	US-10-072-012-352	Sequence 352, App
814	327	8.3	855	15	US-10-072-012-411	Sequence 411, App
815	327	8.3	855	15	US-10-072-012-418	Sequence 418, App
816	327	8.3	855	15	US-10-600-187-2	Sequence 2, Appli
817	319.5	8.1	455	15	US-10-406-031-17	Sequence 17, Appli
818	318	8.1	2669	15	US-10-016-248-4	Sequence 4, Appli
819	318	8.1	3104	15	US-10-016-248-2	Sequence 2, Appli
820	314.5	8.0	454	15	US-10-406-031-11	Sequence 11, Appli
821	314	8.0	855	9	US-09-900-751-2	Sequence 2, Appli
822	314	8.0	855	15	US-10-072-012-355	Sequence 355, App
823	314	8.0	855	15	US-10-072-012-413	Sequence 413, App
824	313	7.9	855	15	US-10-072-012-356	Sequence 356, App

825	313	7.9	855	15	US-10-072-012-414	Sequence 414, App	981	280	7.1	562	15	US-10-411-049-26	Sequence 26, Appl
826	313	7.9	855	15	US-10-072-012-417	Sequence 417, App	982	280	7.1	562	16	US-10-410-930-26	Sequence 26, Appl
827	312	7.9	419	15	US-10-168-407-5	Sequence 8, Appl	983	280	7.1	562	16	US-10-410-937-26	Sequence 26, Appl
828	312	7.9	467	15	US-10-168-407-8	Sequence 8, Appl	984	280	7.1	562	16	US-10-411-012-26	Sequence 26, Appl
829	312	7.9	1031	15	US-10-451-168-80	Sequence 80, Appl	985	280	7.1	562	16	US-10-287-994-26	Sequence 26, Appl
830	311	7.9	419	15	US-10-168-407-3	Sequence 3, Appl	986	280	7.1	562	16	US-10-410-913-26	Sequence 26, Appl
831	311	7.9	419	15	US-10-168-407-6	Sequence 6, Appl	987	280	7.1	562	17	US-10-741-600-911	Sequence 911, App
832	310.5	7.9	415	15	US-10-670-628-2	Sequence 2, Appl	988	280	7.1	562	17	US-10-410-980-26	Sequence 26, Appl
833	310.5	7.9	419	10	US-09-997-623-4	Sequence 4, Appl	989	279.5	7.1	932	14	US-10-097-340-312	Sequence 312, App
834	310.5	7.9	419	10	US-09-978-917A-4	Sequence 4, Appl	990	279	7.1	932	15	US-10-363-937-6	Sequence 6, Appl
835	310.5	7.9	419	14	US-10-182-263-1	Sequence 1, Appl	991	279	7.1	970	9	US-09-888-615-101	Sequence 101, App
836	310.5	7.9	419	15	US-10-168-407-1	Sequence 1, Appl	992	278.5	7.1	264	10	US-09-978-418-34	Sequence 34, Appl
837	310.5	7.9	453	15	US-10-406-031-14	Sequence 14, Appl	993	278.5	7.1	466	14	US-10-017-122-2	Sequence 2, Appl
838	310.5	7.9	461	10	US-09-997-623-2	Sequence 2, Appl	994	278.5	7.1	466	15	US-10-375-741-14	Sequence 14, Appl
839	310.5	7.9	461	10	US-09-978-917A-2	Sequence 2, Appl	995	278.5	7.1	481	16	US-10-741-601-501	Sequence 501, App
840	310.5	7.9	461	14	US-10-182-263-2	Sequence 2, Appl	996	278.5	7.1	481	16	US-10-741-601-502	Sequence 502, App
841	310.5	7.9	461	15	US-10-168-407-2	Sequence 2, Appl	997	278.5	7.1	701	16	US-10-617-619-6	Sequence 6, Appl
842	310	7.9	419	14	US-10-182-263-6	Sequence 6, Appl	998	278	7.0	488	15	US-10-406-031-27	Sequence 27, Appl
843	310	7.9	419	15	US-10-168-407-4	Sequence 4, Appl	999	278	7.0	1113	15	US-10-464-368-78	Sequence 78, Appl
844	309.5	7.8	799	15	US-10-072-012-410	Sequence 410, App	1000	277.5	7.0	476	17	US-10-494-004-1	Sequence 1, Appl
845	309.5	7.8	799	15	US-10-072-012-416	Sequence 416, App	1001	276.5	7.0	426	10	US-09-951-121A-1	Sequence 1, Appl
846	309	7.8	419	14	US-10-182-263-3	Sequence 3, Appl	1002	276.5	7.0	426	10	US-09-848-107-1	Sequence 1, Appl
847	309	7.8	419	14	US-10-182-263-5	Sequence 5, Appl	1003	276.5	7.0	426	14	US-10-295-682-1	Sequence 1, Appl
848	308	7.8	419	14	US-10-182-263-4	Sequence 4, Appl	1004	276.5	7.0	655	14	US-10-172-712-28	Sequence 28, Appl
849	301.5	7.6	229	10	US-09-825-751A-72	Sequence 72, Appl	1005	276	7.0	249	9	US-09-961-721-5	Sequence 5, Appl
850	299.5	7.6	467	15	US-10-406-031-2	Sequence 2, Appl	1006	276	7.0	249	14	US-10-170-789-46	Sequence 46, Appl
851	298	7.6	397	15	US-10-104-047-3904	Sequence 3904, App	1007	276	7.0	251	9	US-09-961-721-4	Sequence 4, Appl
852	296	7.5	229	15	US-10-051-874-101	Sequence 101, App	1008	276	7.0	251	14	US-10-170-789-45	Sequence 45, Appl
853	296	7.5	230	10	US-09-981-151A-87	Sequence 87, App	1009	276	7.0	259	15	US-10-107-782-214	Sequence 214, App
854	296	7.5	230	10	US-09-981-151A-96	Sequence 96, App	1010	276	7.0	259	15	US-10-038-854-100	Sequence 100, App
855	296	7.5	230	14	US-10-032-189-66	Sequence 66, App	1011	276	7.0	396	16	US-10-700-778-1	Sequence 1, Appl
856	296	7.5	230	15	US-10-074-978A-221	Sequence 221, App	1012	275.5	7.0	405	15	US-10-360-101-225	Sequence 225, App
857	296	7.5	230	15	US-10-074-978A-222	Sequence 222, App	1013	275.5	7.0	406	10	US-09-782-587B-1	Sequence 1, Appl
858	296	7.5	230	15	US-10-055-569A-96	Sequence 96, App	1014	275.5	7.0	406	10	US-09-782-587B-3	Sequence 3, Appl
859	296	7.5	230	15	US-10-042-865-155	Sequence 155, App	1015	275.5	7.0	406	14	US-10-109-498-1	Sequence 1, Appl
860	296	7.5	230	15	US-10-072-012-804	Sequence 804, App	1016	275.5	7.0	406	14	US-10-285-032-1	Sequence 1, Appl
861	296	7.5	230	15	US-10-072-012-804	Sequence 812, App	1017	275.5	7.0	406	14	US-10-727-1	Sequence 1, Appl
862	296	7.5	230	15	US-10-037-417-135	Sequence 135, App	1018	275.5	7.0	406	15	US-10-386-898-7	Sequence 7, Appl
863	293	7.4	986	14	US-10-114-153-50	Sequence 50, App	1019	275.5	7.0	406	15	US-10-383-898-1	Sequence 1, Appl
864	291.5	7.4	516	17	US-10-741-600-909	Sequence 909, App	1020	275.5	7.0	406	15	US-10-617-500-1	Sequence 1, Appl
865	291	7.4	376	15	US-10-406-031-31	Sequence 31, App	1021	275.5	7.0	406	15	US-10-263-205B-2	Sequence 2, Appl
866	289.5	7.3	658	10	US-09-776-191-10	Sequence 10, App	1022	275.5	7.0	406	16	US-10-617-619-1	Sequence 1, Appl
867	289.5	7.3	658	15	US-10-156-214A-10	Sequence 10, App	1023	275.5	7.0	406	16	US-10-701-294-1	Sequence 1, Appl
868	289.5	7.3	802	10	US-09-776-191-8	Sequence 8, Appl	1024	275.5	7.0	406	16	US-10-669-537-1	Sequence 1, Appl
869	289.5	7.3	802	15	US-10-156-214A-8	Sequence 8, Appl	1025	275.5	7.0	406	16	US-10-738-777-2	Sequence 2, Appl
870	288.5	7.3	802	9	US-09-888-615-113	Sequence 113, App	1026	275.5	7.0	406	17	US-10-900-490-1	Sequence 1, Appl
871	288.5	7.3	802	14	US-10-167-749-169	Sequence 169, App	1027	275.5	7.0	406	17	US-10-725-843-3	Sequence 3, Appl
872	288.5	7.3	802	15	US-10-170-481A-169	Sequence 169, App	1028	275.5	7.0	444	15	US-10-411-037-8	Sequence 8, Appl
873	288.5	7.3	802	15	US-10-210-028-169	Sequence 169, App	1029	275.5	7.0	444	15	US-10-382-248-34	Sequence 34, Appl
874	288.5	7.3	802	15	US-10-162-521A-169	Sequence 169, App	1030	275.5	7.0	444	15	US-10-411-026-8	Sequence 8, Appl
875	288.5	7.3	802	17	US-10-918-851-169	Sequence 169, App	1031	275.5	7.0	444	15	US-10-411-049-8	Sequence 8, Appl
876	288.5	7.3	802	17	US-10-805-667-169	Sequence 169, App	1032	275.5	7.0	444	15	US-10-263-205B-3	Sequence 3, Appl
877	288.5	7.3	802	17	US-10-897-359-169	Sequence 169, App	1033	275.5	7.0	444	16	US-10-410-930-8	Sequence 8, Appl
878	288.5	7.3	802	17	US-10-893-802-169	Sequence 169, App	1034	275.5	7.0	444	16	US-10-410-937-8	Sequence 8, Appl
879	288.5	7.3	802	17	US-10-897-360-169	Sequence 169, App	1035	275.5	7.0	444	16	US-10-411-012-8	Sequence 8, Appl
880	288.5	7.3	902	15	US-10-333-743-3	Sequence 3, Appl	1036	275.5	7.0	444	16	US-10-287-994-8	Sequence 8, Appl
881	288.5	7.3	902	15	US-10-600-187-10	Sequence 10, App	1037	275.5	7.0	444	16	US-10-410-913-8	Sequence 8, Appl
882	288.5	7.3	902	16	US-10-297-987B-11	Sequence 11, App	1038	275.5	7.0	444	16	US-10-410-980-8	Sequence 8, Appl
883	287	7.3	467	15	US-10-406-031-5	Sequence 5, Appl	1039	275.5	7.0	444	16	US-10-738-777-3	Sequence 3, Appl
884	287	7.2	925	16	US-10-865-978-25	Sequence 25, App	1040	275.5	7.0	444	17	US-10-410-980-8	Sequence 8, Appl
885	281	7.1	488	14	US-10-348-504-44	Sequence 44, App	1041	275.5	7.0	459	16	US-10-741-601-503	Sequence 503, App
886	281	7.1	488	14	US-10-407-123-27	Sequence 27, App	1042	275.5	7.0	459	16	US-10-741-601-504	Sequence 504, App
887	280	7.1	527	10	US-09-987-457-18	Sequence 18, App	1043	275.5	7.0	641	16	US-10-617-619-8	Sequence 6, Appl
888	280	7.1	527	10	US-09-987-457-18	Sequence 18, App	1044	275.5	7.0	671	17	US-10-841-250-6	Sequence 6, Appl
889	280	7.1	527	15	US-10-360-101-203	Sequence 203, App	1045	275.5	7.0	679	16	US-10-617-619-11	Sequence 11, Appl
890	280	7.1	527	15	US-10-432-842-1	Sequence 1, Appl	1046	275	7.0	1113	17	US-10-926-083-4	Sequence 4, Appl
891	280	7.1	562	9	US-09-969-271-7	Sequence 7, Appl	1047	273	6.9	560	9	US-09-912-559-3	Sequence 3, Appl
892	280	7.1	562	9	US-09-974-298-145	Sequence 145, App	1048	273	6.9	560	9	US-09-912-559-4	Sequence 4, Appl
893	280	7.1	562	14	US-10-193-656-8	Sequence 8, App	1049	273	6.9	560	14	US-10-172-712-32	Sequence 32, Appl
894	280	7.1	562	14	US-10-443-701-4	Sequence 4, App	1050	273	6.9	560	15	US-10-391-215-5	Sequence 5, Appl
895	280	7.1	562	15	US-10-411-037-26	Sequence 26, App	1051	273	6.9	560	15	US-10-391-215-6	Sequence 6, Appl
896	280	7.1	562	15	US-10-411-026-26	Sequence 26, App	1052	273	6.9	560	15	US-10-391-215-7	Sequence 7, Appl
897	280	7.1	562	15	US-10-410-962-26	Sequence 26, App	1053	273	6.9	560	15	US-10-391-215-8	Sequence 8, Appl

1054	273	6.9	560	17	US-10-930-754-3	Sequence 3, Appli	1127	261.5	6.6	415	9	US-09-118-748-2	Sequence 2, Appli
1055	273	6.9	560	17	US-10-930-754-4	Sequence 4, Appli	1128	261.5	6.6	443	17	US-10-741-600-830	Sequence 830, App
1056	272.5	6.9	296	14	US-10-148-671-17	Sequence 17, Appl	1129	261	6.6	431	14	US-10-193-656-4	Sequence 4, Appli
1057	272	6.9	488	15	US-10-712-332-1	GENERAL INFORMA	1130	260.5	6.6	437	15	US-10-712-332-2	GENERAL INFORMA
1058	271.5	6.9	244	14	US-10-097-340-169	Sequence 169, App	1131	260	6.6	431	15	US-10-282-174-562	Sequence 562, App
1059	271.5	6.9	244	14	US-10-282-907-2	Sequence 2, Appli	1132	260	6.6	431	17	US-10-600-009-562	Sequence 562, App
1060	271.5	6.9	244	14	US-10-301-822-97	Sequence 97, Appl	1133	259.5	6.6	227	13	US-10-865-978-34	Sequence 34, Appl
1061	271.5	6.9	244	15	US-10-295-027-530	Sequence 530, App	1134	259	6.6	227	13	US-10-045-367A-4	Sequence 4, Appli
1062	271.5	6.9	244	15	US-10-173-999-131	Sequence 131, App	1135	259	6.6	227	14	US-10-170-789-54	Sequence 54, Appl
1063	271.5	6.9	244	15	US-10-344-394-25	Sequence 25, Appl	1136	258.5	6.6	411	9	US-09-880-503-3	Sequence 3, Appli
1064	271.5	6.9	244	16	US-10-757-262-28	Sequence 28, Appl	1137	258.5	6.6	411	15	US-10-407-821-2	Sequence 2, Appli
1065	271.5	6.9	1006	15	US-10-210-130-62	Sequence 62, Appl	1138	257.5	6.6	591	16	US-10-865-978-17	Sequence 17, Appl
1066	271	6.9	650	15	US-10-401-077-1	Sequence 1, Appli	1139	257	6.5	215	15	US-10-051-874-102	Sequence 102, App
1067	269	6.8	643	9	US-10-416-952-2	Sequence 2, Appli	1140	257	6.5	217	10	US-09-981-151A-88	Sequence 88, Appl
1068	269	6.8	643	9	US-09-808-602-103	Sequence 103, App	1141	257	6.5	217	10	US-09-981-151A-97	Sequence 97, Appl
1069	269	6.8	643	10	US-09-800-198-86	Sequence 86, Appl	1142	257	6.5	217	14	US-10-032-189-67	Sequence 67, Appl
1070	269	6.8	643	15	US-10-099-322-113	Sequence 113, App	1143	257	6.5	217	15	US-10-074-978A-223	Sequence 223, App
1071	269	6.8	643	15	US-10-044-564-113	Sequence 113, App	1144	257	6.5	217	15	US-10-055-569A-97	Sequence 97, Appl
1072	267	6.8	462	15	US-10-411-037-10	Sequence 10, Appl	1145	257	6.5	217	15	US-10-042-865-156	Sequence 156, App
1073	267	6.8	462	15	US-10-411-026-10	Sequence 10, Appl	1146	257	6.5	217	15	US-10-072-012-805	Sequence 805, App
1074	267	6.8	462	15	US-10-410-962-10	Sequence 10, Appl	1147	257	6.5	217	15	US-10-072-012-813	Sequence 813, App
1075	267	6.8	462	15	US-10-411-049-10	Sequence 10, Appl	1148	257	6.5	217	15	US-10-037-417-136	Sequence 136, App
1076	267	6.8	462	16	US-10-410-930-10	Sequence 10, Appl	1149	257	6.5	529	16	US-10-398-037-2	Sequence 2, Appli
1077	267	6.8	462	16	US-10-410-997-10	Sequence 10, Appl	1150	257	6.5	1039	16	US-10-865-978-30	Sequence 30, Appl
1078	267	6.8	462	16	US-10-411-012-10	Sequence 10, Appl	1151	256	6.5	207	15	US-10-004-378A-147	Sequence 147, App
1079	267	6.8	462	16	US-10-287-994-10	Sequence 10, Appl	1152	255.5	6.5	244	9	US-09-796-294-11	Sequence 11, Appl
1080	267	6.8	462	16	US-10-410-913-10	Sequence 10, Appl	1153	255.5	6.5	244	14	US-10-461-787-11	Sequence 11, Appl
1081	267	6.8	462	17	US-10-410-980-10	Sequence 10, Appl	1154	255.5	6.5	441	17	US-10-741-600-829	Sequence 829, App
1082	265	6.7	419	15	US-10-382-248-36	Sequence 36, Appl	1155	254.5	6.5	437	15	US-10-712-332-3	GENERAL INFORMA
1083	264.5	6.7	900	16	US-10-865-978-15	Sequence 15, Appl	1156	254	6.4	431	9	US-09-264-4688-1	Sequence 1, Appli
1084	264	6.7	431	14	US-10-247-671-149	Sequence 149, App	1157	253.5	6.4	464	9	US-09-808-602-95	Sequence 95, Appl
1085	263	6.7	431	13	US-10-076-421-2	Sequence 2, Appli	1158	253.5	6.4	487	9	US-09-808-602-93	Sequence 93, Appl
1086	263	6.7	431	14	US-10-171-311-184	Sequence 184, App	1159	253.5	6.4	487	10	US-09-800-198-80	Sequence 80, Appl
1087	263	6.7	431	14	US-10-301-822-161	Sequence 161, App	1160	253.5	6.4	1043	15	US-10-016-248-48	Sequence 48, Appl
1088	263	6.7	431	14	US-10-131-985-21	Sequence 21, Appl	1161	253.5	6.4	1048	15	US-10-016-248-49	Sequence 49, Appl
1089	263	6.7	431	15	US-10-295-027-114	Sequence 414, App	1162	253	6.4	273	14	US-10-148-671-25	Sequence 25, Appl
1090	263	6.7	431	15	US-10-295-027-1275	Sequence 1275, Ap	1163	252.5	6.4	452	9	US-09-808-602-21	Sequence 21, Appl
1091	263	6.7	431	15	US-10-411-037-34	Sequence 34, Appl	1164	252	6.4	789	16	US-10-865-978-16	Sequence 16, Appl
1092	263	6.7	431	15	US-10-411-026-34	Sequence 34, Appl	1165	252	6.4	819	16	US-10-865-978-22	Sequence 22, Appl
1093	263	6.7	431	15	US-10-410-962-34	Sequence 34, Appl	1166	251.5	6.4	487	9	US-09-808-602-17	Sequence 17, Appl
1094	263	6.7	431	15	US-10-411-049-34	Sequence 34, Appl	1167	251.5	6.4	487	9	US-09-808-602-19	Sequence 19, Appl
1095	263	6.7	431	16	US-10-410-930-34	Sequence 34, Appl	1168	251.5	6.4	487	10	US-09-800-198-17	Sequence 17, Appl
1096	263	6.7	431	16	US-10-410-997-34	Sequence 34, Appl	1169	251.5	6.4	487	10	US-09-800-198-19	Sequence 19, Appl
1097	263	6.7	431	16	US-10-411-012-34	Sequence 34, Appl	1170	251	6.4	433	16	US-10-372-966-5	Sequence 5, Appli
1098	263	6.7	431	16	US-10-287-994-34	Sequence 34, Appl	1171	249.5	6.3	403	9	US-09-880-503-6	Sequence 6, Appli
1099	263	6.7	431	16	US-10-410-913-34	Sequence 34, Appl	1172	249.5	6.3	822	9	US-09-147-947-6	Sequence 6, Appli
1100	263	6.7	431	17	US-10-741-600-1265	Sequence 1265, Ap	1173	249.5	6.3	875	16	US-10-757-262-34	Sequence 34, Appl
1101	263	6.7	431	17	US-10-741-600-1266	Sequence 1266, Ap	1174	249.5	6.3	875	17	US-10-843-239-2	Sequence 2, Appli
1102	263	6.7	431	17	US-10-901-417-21	Sequence 21, Appl	1175	249.5	6.3	986	9	US-09-285-385C-19	Sequence 19, Appl
1103	263	6.7	431	17	US-10-410-980-34	Sequence 34, Appl	1176	249	6.3	235	10	US-09-776-191-6	Sequence 6, Appli
1104	263	6.7	431	17	US-10-645-756-38	Sequence 38, Appl	1177	249	6.3	235	15	US-10-156-214A-6	Sequence 6, Appli
1105	263	6.7	437	13	US-10-087-192-594	Sequence 594, App	1178	249	6.3	251	11	US-09-789-210-47	Sequence 47, Appl
1106	262.5	6.7	415	16	US-10-466-988A-2	Sequence 2, Appli	1179	249	6.3	263	9	US-09-888-615-96	Sequence 96, Appl
1107	262.5	6.7	456	15	US-10-038-854-95	Sequence 95, Appl	1180	248.5	6.3	250	10	US-09-898-837A-45	Sequence 45, Appl
1108	262.5	6.7	456	15	US-10-038-854-96	Sequence 96, Appl	1181	248.5	6.3	250	11	US-09-789-210-51	Sequence 51, Appl
1109	262.5	6.7	461	9	US-09-884-901-3	Sequence 3, Appli	1182	248.5	6.3	251	10	US-09-898-837A-41	Sequence 41, Appl
1110	262.5	6.7	461	14	US-10-132-829-5	Sequence 5, Appli	1183	248	6.3	230	11	US-09-789-210-62	Sequence 62, Appl
1111	262.5	6.7	461	14	US-10-234-406-6	Sequence 6, Appli	1184	248	6.3	231	15	US-10-600-187-6	Sequence 6, Appli
1112	262.5	6.7	461	14	US-10-234-406-8	Sequence 8, Appli	1185	248	6.3	638	9	US-09-808-602-102	Sequence 102, App
1113	262.5	6.7	461	14	US-10-133-907-5	Sequence 5, Appli	1186	248	6.3	638	10	US-09-800-198-85	Sequence 85, Appl
1114	262.5	6.7	461	15	US-10-038-854-92	Sequence 92, Appl	1187	248	6.3	638	15	US-10-099-322-111	Sequence 111, App
1115	262.5	6.7	461	15	US-10-038-854-93	Sequence 93, Appl	1188	248	6.3	638	15	US-10-044-564-111	Sequence 111, App
1116	262.5	6.7	461	15	US-10-038-854-94	Sequence 94, Appl	1189	248	6.3	638	15	US-10-403-161-50	Sequence 50, Appl
1117	262.5	6.7	461	15	US-10-239-498A-5	Sequence 5, Appli	1190	248	6.3	638	15	US-10-287-226-400	Sequence 400, App
1118	262.5	6.7	461	17	US-10-741-600-832	Sequence 832, App	1191	248	6.3	638	15	US-10-287-226-558	Sequence 558, App
1119	262.5	6.7	696	17	US-10-841-250-8	Sequence 8, Appli	1192	248	6.3	638	16	US-10-741-601-303	Sequence 303, App
1120	262.5	6.7	1042	10	US-09-776-191-41	Sequence 62, Appl	1193	248	6.3	638	17	US-10-741-600-854	Sequence 854, App
1121	262.5	6.7	1042	15	US-10-156-214A-29	Sequence 29, Appl	1194	247.5	6.3	635	16	US-10-741-601-304	Sequence 304, App
1122	262.5	6.7	1042	16	US-10-865-978-2	Sequence 2, Appli	1195	247.5	6.3	635	17	US-10-741-600-855	Sequence 855, App
1123	262.5	6.7	1042	17	US-10-926-083-2	Sequence 2, Appli	1196	247	6.3	455	16	US-10-865-978-18	Sequence 18, Appl
1124	262.5	6.7	1044	16	US-10-865-978-9	Sequence 9, Appli	1197	247	6.3	619	15	US-10-403-161-52	Sequence 52, Appl
1125	262.5	6.7	1076	15	US-10-276-774-2345	Sequence 26, Appl	1198	247	6.3	619	15	US-10-287-226-404	Sequence 404, App
1126	262	6.6	280	14	US-10-148-671-26	Sequence 26, Appl	1199	247	6.3	623	15	US-10-403-161-48	Sequence 48, Appl

1200	247	6.3	638	15	US-10-099-322-30	Sequence 30, Appl	1273	239.5	6.1	3567	15	US-10-107-782-47	Sequence 47, Appl
1201	247	6.3	638	15	US-10-044-564-30	Sequence 30, Appl	1274	239.5	6.1	3594	9	US-09-911-842-4	Sequence 4, Appl
1202	247	6.3	638	15	US-10-403-161-46	Sequence 46, Appl	1275	239.5	6.1	3594	9	US-10-150-821-4	Sequence 4, Appl
1203	247	6.3	638	15	US-10-287-236-402	Sequence 402, Appl	1276	239	6.1	328	9	US-09-888-615-91	Sequence 91, Appl
1204	247	6.3	764	14	US-10-177-293-27	Sequence 27, Appl	1277	239	6.1	1093	15	US-10-156-214A-20	Sequence 20, Appl
1205	247	6.3	764	15	US-10-236-031B-44	Sequence 44, Appl	1278	238.5	6.0	482	17	US-10-741-600-910	Sequence 910, Appl
1206	247	6.3	986	10	US-09-918-715-242	Sequence 242, Appl	1279	238	6.0	335	15	US-10-094-886-128	Sequence 128, Appl
1207	247	6.3	986	10	US-10-366-345-33	Sequence 33, Appl	1280	238	6.0	335	10	US-09-987-457-13	Sequence 13, Appl
1208	246.5	6.2	259	11	US-09-789-210-52	Sequence 52, Appl	1281	238	6.0	335	10	US-09-987-455-14	Sequence 14, Appl
1209	246.5	6.2	259	16	US-10-872-198-5	Sequence 5, Appl	1282	238	6.0	343	10	US-09-987-457-15	Sequence 15, Appl
1210	246.5	6.2	259	17	US-10-872-198A-5	Sequence 5, Appl	1283	238	6.0	343	10	US-09-987-455-16	Sequence 16, Appl
1211	246.5	6.2	347	9	US-09-977-577-3	Sequence 3, Appl	1284	238	6.0	347	9	US-09-977-577-1	Sequence 1, Appl
1212	246.5	6.2	347	17	US-10-885-784-3	Sequence 3, Appl	1285	238	6.0	347	17	US-10-885-784-1	Sequence 1, Appl
1213	246.5	6.2	622	14	US-10-020-141-8	Sequence 8, Appl	1286	238	6.0	347	16	US-10-865-978-19	Sequence 19, Appl
1214	246.5	6.2	622	14	US-10-017-631-2	Sequence 2, Appl	1287	237.5	6.0	255	10	US-09-813-432-41	Sequence 41, Appl
1215	246.5	6.2	622	14	US-10-214-932-116	Sequence 116, Appl	1288	237.5	6.0	255	15	US-10-174-364-41	Sequence 41, Appl
1216	246.5	6.2	622	14	US-10-172-712-29	Sequence 29, Appl	1289	237.5	6.0	255	15	US-10-246-583-41	Sequence 41, Appl
1217	246.5	6.2	622	16	US-10-872-198-149	Sequence 149, Appl	1290	237.5	6.0	255	16	US-10-689-832-41	Sequence 41, Appl
1218	246.5	6.2	639	17	US-10-792-498-16	Sequence 16, Appl	1291	237.5	6.0	3568	15	US-10-028-248A-8	Sequence 8, Appl
1219	246.5	6.2	639	17	US-10-792-498-17	Sequence 17, Appl	1292	237.5	6.0	3568	15	US-10-107-782-8	Sequence 8, Appl
1220	246	6.2	812	10	US-09-825-751A-71	Sequence 71, Appl	1293	237.5	6.0	3570	15	US-10-028-248A-6	Sequence 6, Appl
1221	245.5	6.2	638	15	US-10-099-322-112	Sequence 112, Appl	1294	237.5	6.0	3570	15	US-10-107-782-6	Sequence 6, Appl
1222	245.5	6.2	638	15	US-10-044-564-112	Sequence 112, Appl	1295	236.5	6.0	308	10	US-09-987-457-16	Sequence 16, Appl
1223	245.5	6.2	823	15	US-10-112-944-309	Sequence 309, Appl	1296	236.5	6.0	308	10	US-09-987-455-17	Sequence 17, Appl
1224	245	6.2	445	15	US-10-360-101-266	Sequence 266, Appl	1297	236.5	6.0	331	10	US-09-987-457-11	Sequence 11, Appl
1225	244.5	6.2	269	9	US-09-981-123-2	Sequence 2, Appl	1298	236.5	6.0	331	10	US-09-987-455-12	Sequence 12, Appl
1226	244.5	6.2	280	14	US-10-148-671-23	Sequence 23, Appl	1299	236.5	6.0	339	10	US-09-987-457-12	Sequence 12, Appl
1227	244.5	6.2	292	14	US-10-029-386-31995	Sequence 23, Appl	1300	236.5	6.0	339	10	US-09-987-455-13	Sequence 13, Appl
1228	244	6.2	322	15	US-10-051-874-96	Sequence 96, Appl	1301	236.5	6.0	343	10	US-09-987-457-14	Sequence 14, Appl
1229	244	6.2	477	17	US-10-494-004-2	Sequence 2, Appl	1302	236.5	6.0	343	10	US-09-987-455-15	Sequence 15, Appl
1230	244	6.2	638	15	US-10-099-322-114	Sequence 114, Appl	1303	236.5	6.0	354	10	US-09-987-455-11	Sequence 11, Appl
1231	244	6.2	638	15	US-10-044-564-114	Sequence 114, Appl	1304	236.5	6.0	372	9	US-09-084-491A-3	Sequence 3, Appl
1232	244	6.2	638	15	US-10-287-236-672	Sequence 672, Appl	1305	236.5	6.0	372	13	US-10-102-704-3	Sequence 3, Appl
1233	243	6.2	273	15	US-10-028-248A-63	Sequence 63, Appl	1306	236.5	6.0	372	10	US-09-987-455-8	Sequence 8, Appl
1234	243	6.2	273	15	US-10-107-782-63	Sequence 63, Appl	1307	236.5	6.0	416	15	US-10-099-322-138	Sequence 138, Appl
1235	243	6.2	282	15	US-10-051-874-97	Sequence 97, Appl	1308	236.5	6.0	416	15	US-10-044-564-138	Sequence 138, Appl
1236	242.5	6.1	232	15	US-10-156-214A-276	Sequence 276, Appl	1309	236.5	6.0	871	9	US-09-893-238-19	Sequence 19, Appl
1237	242.5	6.1	326	16	US-10-865-978-37	Sequence 37, Appl	1310	236.5	6.0	1013	9	US-09-942-366-3	Sequence 3, Appl
1238	242.5	6.1	1019	15	US-10-016-248-99	Sequence 99, Appl	1311	236.5	6.0	1013	15	US-10-016-248-95	Sequence 95, Appl
1239	242.5	6.1	3571	16	US-10-603-283-2	Sequence 2, Appl	1312	236.5	6.0	1350	9	US-09-893-238-17	Sequence 17, Appl
1240	242	6.1	322	15	US-10-114-270-134	Sequence 134, Appl	1313	236.5	6.0	252	14	US-10-148-671-21	Sequence 21, Appl
1241	242	6.1	730	9	US-09-850-048A-2	Sequence 2, Appl	1314	236	6.0	275	14	US-10-117-323-27	Sequence 27, Appl
1242	241.5	6.1	416	9	US-09-815-876-2	Sequence 2, Appl	1315	236	6.0	411	16	US-10-372-966-6	Sequence 6, Appl
1243	241.5	6.1	823	15	US-10-016-248-98	Sequence 98, Appl	1316	236	6.0	992	15	US-10-016-248-40	Sequence 40, Appl
1244	241	6.1	346	9	US-09-977-577-8	Sequence 8, Appl	1317	236	6.0	325	14	US-10-311-955-2	Sequence 2, Appl
1245	241	6.1	346	17	US-10-885-784-8	Sequence 8, Appl	1318	235.5	6.0	293	14	US-10-148-671-18	Sequence 18, Appl
1246	241	6.1	986	9	US-09-850-048A-8	Sequence 4, Appl	1319	235	6.0	556	9	US-09-729-674-92	Sequence 92, Appl
1247	240.5	6.1	278	10	US-09-813-432-12	Sequence 12, Appl	1320	234.5	5.9	556	16	US-10-913-553-92	Sequence 92, Appl
1248	240.5	6.1	278	10	US-09-813-432-43	Sequence 43, Appl	1321	234.5	5.9	624	15	US-10-004-378A-143	Sequence 143, Appl
1249	240.5	6.1	278	15	US-10-174-364-12	Sequence 12, Appl	1322	234.5	5.9	296	15	US-10-072-012-90	Sequence 90, Appl
1250	240.5	6.1	278	15	US-10-174-364-43	Sequence 43, Appl	1323	234	5.9	296	15	US-10-051-874-99	Sequence 99, Appl
1251	240.5	6.1	278	15	US-10-246-583-12	Sequence 12, Appl	1324	234	5.9	296	15	US-09-789-210-72	Sequence 72, Appl
1252	240.5	6.1	278	15	US-10-246-583-43	Sequence 43, Appl	1325	233.5	5.9	253	11	US-10-600-187-8	Sequence 8, Appl
1253	240.5	6.1	278	16	US-10-689-832-12	Sequence 12, Appl	1326	233.5	5.9	253	15	US-10-600-187-8	Sequence 8, Appl
1254	240.5	6.1	278	16	US-10-689-832-43	Sequence 43, Appl	1327	233.5	5.9	268	10	US-09-987-457-17	Sequence 17, Appl
1255	240.5	6.1	430	16	US-10-372-966-4	Sequence 4, Appl	1328	233.5	5.9	268	10	US-09-987-455-18	Sequence 18, Appl
1256	240.5	6.1	970	15	US-10-016-248-42	Sequence 42, Appl	1329	233.5	5.9	275	14	US-10-131-409-20	Sequence 20, Appl
1257	240.5	6.1	3571	9	US-09-911-842-2	Sequence 2, Appl	1330	233.5	5.9	275	15	US-10-139-854-20	Sequence 20, Appl
1258	240.5	6.1	3571	13	US-10-150-821-2	Sequence 2, Appl	1331	233.5	5.9	275	15	US-10-150-813-20	Sequence 20, Appl
1259	240	6.1	242	17	US-10-926-083-34	Sequence 34, Appl	1332	233.5	5.9	273	15	US-10-150-811-20	Sequence 20, Appl
1260	240	6.1	1128	9	US-09-888-615-97	Sequence 97, Appl	1333	233	5.9	273	15	US-10-028-248A-64	Sequence 64, Appl
1261	240	6.1	1128	15	US-10-399-645-8	Sequence 8, Appl	1334	233	5.9	273	15	US-10-107-782-64	Sequence 64, Appl
1262	239.5	6.1	406	9	US-09-977-577-2	Sequence 2, Appl	1335	232.5	5.9	259	15	US-10-165-442-2	Sequence 2, Appl
1263	239.5	6.1	406	16	US-10-764-649-6	Sequence 6, Appl	1336	232.5	5.9	259	16	US-10-699-393-2	Sequence 2, Appl
1264	239.5	6.1	406	17	US-10-885-784-2	Sequence 2, Appl	1337	232.5	5.9	295	15	US-10-165-442-1	Sequence 1, Appl
1265	239.5	6.1	416	9	US-09-804-156-13	Sequence 13, Appl	1338	232.5	5.9	295	16	US-10-699-393-1	Sequence 1, Appl
1266	239.5	6.1	416	13	US-10-067-761-13	Sequence 13, Appl	1339	232.5	5.9	1013	9	US-09-942-366-5	Sequence 5, Appl
1267	239.5	6.1	416	14	US-10-319-519-13	Sequence 13, Appl	1340	232.5	5.9	1013	9	US-09-285-385C-20	Sequence 20, Appl
1268	239.5	6.1	1015	9	US-09-285-385C-2	Sequence 2, Appl	1341	232	5.9	416	15	US-10-099-322-137	Sequence 137, Appl
1269	239.5	6.1	1015	15	US-10-016-248-97	Sequence 97, Appl	1342	232	5.9	416	15	US-10-044-564-137	Sequence 137, Appl
1270	239.5	6.1	3557	15	US-10-295-027-430	Sequence 430, Appl	1343	232	5.9	638	14	US-10-316-253-82	Sequence 82, Appl
1271	239.5	6.1	3557	15	US-10-295-027-1297	Sequence 1297, Appl	1344	232	5.9	638	15	US-10-099-322-115	Sequence 115, Appl
1272	239.5	6.1	3567	15	US-10-028-248A-47	Sequence 47, Appl	1345	232	5.9	638	15	US-10-044-564-115	Sequence 115, Appl



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GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: May 8, 2005, 16:10:59 ; Search time 54 Seconds  
(without alignments)  
5156.805 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 720

Sequence: 1 MELGWTQLGTFLQLLLIS.....LSTAFKVLPPKDWIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980a.\*

2: Geneseqp1990a.\*

3: Geneseqp2000a.\*

4: Geneseqp2001a.\*

5: Geneseqp2002a.\*

6: Geneseqp2003a.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004a.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No. Score Match Length DB ID Description

RESULT 1

ID AAY66695 standard; protein; 720 AA.

DE Membrane-bound protein PRO1344.

PN WO9963088-A2.

PD 09-DEC-1999.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 3; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 2

ID AAU29108 standard; protein; 720 AA.

DE Human PRO polypeptide sequence #85.

PN WO20016848-A2.

PD 20-SEP-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 4; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 3

ID AAB87544 standard; protein; 720 AA.

DE Human PRO1344.

PN WO200116318-A2.

PD 08-MAR-2001.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 4; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 4

ID AAB65218 standard; protein; 720 AA.

DE Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.

PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 4; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 5

ID ABG95869 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.

PN US2002119130-A1.

PD 29-AUG-2002.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 5; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

RESULT 6

ID ABU5484 standard; protein; 720 AA.

DE Human PRO polypeptide #85.

PN US2003027272-A1.

PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

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Query Match 100.0%; Score 720; DB 6; Length 720;

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Query Match 100.0%; Score 720; DB 6; Length 720;

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Best Local Similarity 100.0%; Pred. No. 0;

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 17
ID AB68160 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID AB60542 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID AB96213 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 20
ID AB92644 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID AB008721 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22
ID AB002773 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ABR74927 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ABR94689 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 25
ID ABUI3924 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 26
ID ABUS662 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID AB98822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 28
ID AB98037 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID AB91743 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 30
ID AB89436 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 31
ID AB86277 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 32
ID AB67490 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 33
ID AB80518 standard; protein; 720 AA.
DE Human PRO protein #85.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 34
ID ABU72509 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 35
ID ABUS0894 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 36
ID ABO33953 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003009013-A1.
PD 09-JAN-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 37  
ID ABR99436 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 38  
ID ABR98826 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 39  
ID ABO16349 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 40  
ID ABR92249 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 41  
ID ABO18890 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 42  
ID ABR78311 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 43  
ID ABUT1970 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 44  
ID ABUS5047 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 45  
ID ABO00186 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 46  
ID ABO11518 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036124-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 47  
ID ABO02163 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 48  
ID ABUS8737 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 49  
ID ABUS3432 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 50  
ID ABO06233 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 51  
ID ABR59269 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 52  
ID ABO09331 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 53  
ID ABO19195 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 54  
ID ABO11213 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 55  
ID ABR66831 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 56  
ID ABO16044 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 57  
ID ABO11518 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036124-A1.  
PD 20-FEB-2003.

RESULT 57  
ID ABO13750 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 58  
ID ABU71524 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 59  
ID ABU65653 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, SEQ ID 170.  
PN US20030316156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 60  
ID ABO07501 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 61  
ID ABO03688 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 62  
ID ABR67136 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 63  
ID ABO15739 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 64  
ID ABUS6020 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 65  
ID ABU72305 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 66  
ID ABUS5348 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 67  
ID ABU95293 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 68  
ID ABU71196 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 69  
ID ABO07806 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 70  
ID ABR70047 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 71  
ID ABR69380 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 72  
ID ABO01521 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 73  
ID ABUS1323 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 74  
ID ABR60120 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 75  
ID ABU90978 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 76  
ID ABR67855 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 77  
ID ABR65243 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 78  
ID ABR68465 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 79  
ID ABR71877 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003021335-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 80  
ID ABUS9258 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 81  
ID ABUS5357 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 82  
ID ABUS9047 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 83  
ID ABUS3127 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US200302105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 84  
ID ABUS9493 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 85  
ID ABUS0531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 86  
ID ABUS4042 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 87  
ID ABUS3693 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 88  
ID ABO25955 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 89  
ID ABR64938 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 90  
ID ABO27299 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US200309012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 91  
ID ABR68770 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 92  
ID ABO06586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003031625-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 93  
ID ABR99131 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 94  
ID ABUS7015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 95  
ID ABUS9567 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 96  
ID ABUS2254 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003031636-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 97  
ID ABUS7265 standard; protein; 720 AA.

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DE Human PRO polypeptide #85.
PN US2003031638-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 98
ID ABU83737 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 99
ID ABO08111 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 100
ID ABU92494 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 101
ID ABU81822 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 102
ID ABU65986 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US20030316157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 103
ID ABU81164 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 104
ID ABR59815 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 105
ID ABU94003 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US20030316155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 106
ID ABU99856 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 107
ID ABR66526 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 108
ID ABR90944 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 109
ID ABO53279 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 110
ID ABU58964 standard; protein; 720 AA.
DE Human secreted/transmembrane protein, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 111
ID ABU94371 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 112
ID ABU79253 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 113
ID ABU66582 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 114
ID ABU66887 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 115
ID ABU94676 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 116
ID ABO04603 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
Result 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
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PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 118  
ID ABU92342 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 119  
ID ABUS98517 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 120  
ID ABR65916 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 121  
ID ABR64633 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 122  
ID ABUS9407 standard; protein; 720 AA.  
DE Novel human secreted or transmembrane protein PRO1109.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 123  
ID ABU79558 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 124  
ID ABUS2949 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 125  
ID ABUS95908 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 126  
ID ABUS91128 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 127  
ID ABUS90221 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036153-A1.  
PD 20-FEB-2003.

Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 128  
ID ABO09636 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 129  
ID ABO10908 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 130  
ID ABR70962 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 131  
ID ABUS98281 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 132  
ID ABUS7570 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 133  
ID ABUS91438 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 134  
ID ABUS9286 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 135  
ID ABUS4652 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 136  
ID ABR69742 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 137  
ID ABUS01119 standard; protein; 720 AA.  
DE Human PRO protein #85.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;



Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 138  
ID AB082493 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 139  
ID AB092173 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 140  
ID AB093388 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 141  
ID AB009941 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 142  
ID AB009026 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 143  
ID AB096457 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 144  
ID AB010879 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 145  
ID AB010594 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein #85.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 146  
ID AB081631 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US200217164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 147  
ID AB072127 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003023042-A1.

PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 148  
ID AB095603 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 149  
ID AB096812 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 150  
ID ABR70657 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 151  
ID AB005008 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 152  
ID AB008416 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 153  
ID AB088570 standard; protein; 720 AA.  
DE Human secreted and transmembrane polypeptide PRO1344.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 154  
ID AB034084 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 155  
ID AB005623 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 156  
ID ABR74012 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 157  
ID ABR95604 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 158  
ID ABR80901 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 159  
ID ABR81206 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 160  
ID ABR88504 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 161  
ID ABR88504 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 162  
ID ABR77325 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 163  
ID ABR28809 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 164  
ID ABR031554 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 165  
ID ABR07971 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 166  
ID ABR040451 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068682-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 167  
ID ABR035876 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 168  
ID ABR044015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 169  
ID ADA77922 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 170  
ID ABR24810 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 171  
ID ABR03078 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 172  
ID ABR90334 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ABR17248 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 174  
ID ABR94994 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 175  
ID ABR95299 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 176  
ID ABR040451 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068682-A1.

ID ADB17095 standard; protein; 720 AA.  
DE Human transmembrane PRO polypeptide (SeqID 38).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 177  
ID ABO21537 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003050471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 178  
ID ABR97801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 179  
ID ABR87589 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 180  
ID ABM77630 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 181  
ID ABM27860 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 182  
ID ABM06141 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 183  
ID ABM03647 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 184  
ID ABM35098 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 185  
ID ABM26335 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 186  
ID ABO48117 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 187  
ID ABR92859 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 188  
ID ABO24620 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 189  
ID ADA37742 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 190  
ID ABM11631 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 191  
ID ABM02732 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 192  
ID ABM16028 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 193  
ID ABO27589 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 194  
ID ABM29080 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068721-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 195  
ID ABM07056 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 196  
ID ABM21150 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 197  
ID ABM09496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 198  
ID AB041366 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 199  
ID ABO36181 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 200  
ID ABO43710 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 201  
ID ABM76410 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 202  
ID ABM76106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 203  
ID ABM25725 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 204  
ID ABM26030 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 205  
ID ADA21428 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 206  
ID ABO03383 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 207  
ID ABO02468 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 208  
ID ABO44257 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 209  
ID ABR90639 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 210  
ID ABR73707 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 211  
ID ABO16959 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 212  
ID ABR94384 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 213  
ID ABR75891 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 214  
ID ABR71267 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 215  
ID ABR93164 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 216  
ID ABR93469 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 217  
ID ADAL0215 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 218  
ID ABR87894 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 219  
ID ABO27894 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 220  
ID ABO30029 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 221  
ID ABO33238 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 222  
ID ABO4926 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 223  
ID ABO23705 standard; protein; 720 AA.

ID ABM0886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 224  
ID ABO36486 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 225  
ID ABO35571 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 226  
ID ABO39536 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 227  
ID ABM10411 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 228  
ID ABM11936 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 229  
ID ABO52082 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 230  
ID ABO52387 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 231  
ID ADAL1900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 232  
ID ABO23705 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 233  
ID ADB17283 standard; protein; 720 AA.  
DE Human transmembrane PRO polypeptide (seqID 38).  
FN US20030305465-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 234  
ID ADA17759 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
FN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 235  
ID ABR97191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 236  
ID ABR86979 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 237  
ID ABM11021 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 238  
ID ABM28165 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 239  
ID ABO32164 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 240  
ID ABM15291 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 241  
ID ABM06446 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068709-A1.  
PD 10-APR-2003.

PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 242  
ID ABM04257 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 243  
ID ABM22370 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 244  
ID ABM07666 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 245  
ID ABO40756 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 246  
ID ABM35403 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 247  
ID ABM33166 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 248  
ID ABO52692 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 249  
ID ABO50252 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 250  
ID ABU99246 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 251  
ID AB004298 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 252  
ID AB005928 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 253  
ID ABM18468 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 254  
ID ADA27867 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
FN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 255  
ID ABR97496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 256  
ID ABR80596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 257  
ID ABM01207 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 258  
ID ABR8809 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 259  
ID ABM13461 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 260  
ID ABM20845 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 261  
ID ABO41976 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 262  
ID ABO42586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 263  
ID ABM10106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 264  
ID ABO38621 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 265  
ID ABR32861 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 266  
ID ABM22675 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 267  
ID ABM74886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 268  
ID ADA79714 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 269  
ID ABR96276 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 270  
ID ABM02427 standard; protein; 720 AA.



DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 271  
ID ABR66369 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 272  
ID ABR86674 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 273  
ID ABR16638 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 274  
ID ABM29690 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 275  
ID ABO29114 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 276  
ID ABM23895 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 277  
ID ABM23285 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 278  
ID ABM22065 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 279  
ID ABO37706 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 280  
ID ABM28470 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 281  
ID ABM28775 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 282  
ID ABM66419 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 283  
ID ABM75801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 284  
ID ABM34081 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 285  
ID ABM34386 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 286  
ID ABO20317 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 287  
ID ABO21332 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 288  
ID ABO22147 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;

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RESULT 289
ID AD20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ABR99741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ABW00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ABW00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ABM29385 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ABO1654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 308  
ID ABR92554 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 309  
ID ABR81511 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 310  
ID ABR7935 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 311  
ID ABR89724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 312  
ID ABR26640 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 313  
ID ABR13766 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 314  
ID ABR28504 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 315  
ID ABR030334 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 316  
ID ABR07361 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003088702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 317  
ID ABR03952 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

FN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 318  
ID ABR037096 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 319  
ID ABR041671 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 320  
ID ABR035266 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 321  
ID ABR25115 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 322  
ID ABR047507 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 323  
ID ABR047812 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 324  
ID ABR048422 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 325  
ID ABR051472 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 326  
ID ABR051777 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003049767-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 327  
ID AB050557 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 328  
ID ABR79681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 329  
ID ABM16943 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 330  
ID ABO17975 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 331  
ID ABO20927 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 332  
ID ABR96886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 333  
ID ADA38672 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 334  
ID ABM12241 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 335  
ID ABM16333 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 336  
ID ABM24200 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 337  
ID ABM14681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 338  
ID ABM04562 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 339  
ID ABM06751 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 340  
ID ABM09191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 341  
ID ABO39231 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 342  
ID ABM75496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 343  
ID ABM25420 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 344  
ID ABM19930 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 345  
ID ABO46836 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 346  
ID ABO47141 standard; protein; 720 AA.  
DE Human secreted polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 347  
ID ADA83239 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 348  
ID ABR71572 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 349  
ID ABR72182 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 350  
ID ABR98521 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 351  
ID ABO06891 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 352  
ID ABR84844 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 353  
ID ABR73402 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 354  
ID ABR76496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 355  
ID ABR73097 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027270-A1.  
PD 06-FEB-2003.

Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 356  
ID ABM18163 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 357  
ID ABO20622 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 358  
ID ABO25365 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 359  
ID ABO25670 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 360  
ID ABR94079 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 361  
ID ADA92793 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 362  
ID ABR79986 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 363  
ID ABM11326 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 364  
ID ABO32933 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 365  
ID ABO30639 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 366  
ID ABO30944 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 367  
ID ABM27250 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 368  
ID ABM29995 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 369  
ID ABM05531 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 370  
ID ABM15596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 371  
ID ABM08581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 372  
ID ABO42281 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 373  
ID ABO38011 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 374  
ID ABO45921 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.

PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 375  
ID ABM66724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 376  
ID ADB20282 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 377  
ID ABM19625 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 378  
ID ABO49337 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 379  
ID ABO49642 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 380  
ID ADA78534 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 381  
ID ABR88199 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 382  
ID ADA00369 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 383  
ID ABM26945 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068739-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 384  
ID ABM03342 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 385  
ID ABO39841 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 386  
ID ABO49947 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 387  
ID ABO50862 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 388  
ID ABO05318 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 389  
ID ABR74622 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 390  
ID ABR77101 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 391  
ID ABM17858 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 392  
ID ABR95909 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 393  
ID ABO21842 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 394  
ID ABO20012 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 395  
ID ABO24315 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 396  
ID ABR86064 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 397  
ID ABM10716 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 398  
ID ABM76715 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 399  
ID ABR89419 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 400  
ID ABM12546 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 401  
ID ABM05836 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 402  
ID ABO34961 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.



Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 403  
ID ABM03037 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 404  
ID ABM19015 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 405  
ID ABM19320 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 406  
ID AB046531 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 407  
ID AB049032 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 408  
ID ABR69075 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 409  
ID ABR89114 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 410  
ID ABR72487 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 411  
ID ABR74317 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 412  
ID ABO18585 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 413  
ID ABR80291 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 414  
ID ABM01512 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 415  
ID ABM02122 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 416  
ID ABR87284 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 417  
ID ABM12851 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 418  
ID ABM30605 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 419  
ID ABM24505 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 420  
ID ABO29419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 421  
ID ABO31249 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068710-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 422  
ID ABM14376 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US200306886-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 423  
ID ABM09801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 424  
ID ABO38926 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 425  
ID ABM34691 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 426  
ID ABO51167 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 427  
ID ABO03993 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 428  
ID ABO10463 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 429  
ID ABO53170 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
FN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 430  
ID ABR77706 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 431  
ID ABR78916 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068731-A1.  
PD 10-APR-2003.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 432  
ID ABO24010 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 433  
ID ABR93774 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 434  
ID ABM01817 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 435  
ID ABM78240 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 436  
ID ABR90029 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 437  
ID ADA22354 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
FN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 438  
ID ABM27555 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 439  
ID ABM13156 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 440  
ID ABO31859 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003068731-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 441  
ID ABM14071 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 442  
ID ABM08276 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 443  
ID AB040146 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 444  
ID ABM74581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 445  
ID ABM33776 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 446  
ID ABM20235 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 447  
ID AB048727 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 448  
ID AB022540 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 449  
ID ABR72792 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 450  
ID AB015434 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 451  
ID ABR85149 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 452  
ID AB015129 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 453  
ID AB017264 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 454  
ID ABM17553 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 455  
ID ADA06520 standard; protein; 720 AA.  
DE Human secreted/transmembrane PRO polypeptide #65.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 456  
ID ADA39213 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 457  
ID ABR85454 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 458  
ID ABM77020 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 459  
ID ABO28199 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 460

ID ABM22980 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 461  
ID ABM30300 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 462  
ID ABM21760 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 463  
ID ABM21455 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 464  
ID ABM14986 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 465  
ID ABM31825 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 466  
ID ABM31215 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 467  
ID ABM31691 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 468  
ID ABM75191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 469  
ID ABM33471 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 470  
ID ABO46226 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 471  
ID ADA82605 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 472  
ID ADB95611 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 473  
ID ADB96239 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 474  
ID ABM31825 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 475  
ID ABM31215 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 476  
ID ADB85913 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 477  
ID ABM32130 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 478  
ID ABM32435 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068713-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 479  
ID AD68290 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
FN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 480  
ID AD68097 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
FN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 481  
ID ABM31520 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 482  
ID ABM30910 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 483  
ID ADB90914 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 484  
ID ADC57111 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
FN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 485  
ID ADC55075 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
FN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 486  
ID ADC11942 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
FN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 487  
ID ADC06994 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
FN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 488

ID ADC5364 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
FN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 489  
ID ADC17173 standard; protein; 720 AA.  
DE Mammalian PRO polypeptide (SeqID 38).  
FN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 490  
ID ADC07419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
FN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 491  
ID ADC11409 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
FN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 492  
ID ADC14871 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 493  
ID ADC52366 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 494  
ID ADC14531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 495  
ID ADD08063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 496  
ID ADC81888 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
FN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 497  
ID ADD07530 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 498  
ID ADG62421 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 499  
ID ADD05643 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 500  
ID ADD08601 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 501  
ID ADD06850 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 502  
ID ADC83097 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 503  
ID ADD55204 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 504  
ID .ADD36042 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 505  
ID ADD56162 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 506  
ID ADD54600 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 507  
ID AD26754 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 508  
ID ADE26221 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 509  
ID ADF67158 standard; protein; 720 AA.  
DE Human PRO1344 amino acid sequence SEQ ID NO:231.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 510  
ID ADG01043 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 511  
ID ADG08596 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 512  
ID ADG02638 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 513  
ID ADG01345 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 514  
ID ADF95520 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 515  
ID ADF95217 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 516  
ID ADG12335 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 517  
ID ADH24070 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 518  
ID ADH34096 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 519  
ID ADH29929 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 520  
ID ADH23900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 521  
ID ADH08995 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 522  
ID ADH85304 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 523  
ID ADH24580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 524  
ID ADH37436 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 525  
ID ADH02025 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 526  
ID ADH37606 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 cDNA.

PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 527  
ID ADH85644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 528  
ID ADH24240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 529  
ID ADH38534 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 530  
ID ADH83655 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 531  
ID ADH29463 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 532  
ID ADH27579 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 533  
ID ADH37776 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 534  
ID ADH37953 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 535  
ID ADH57373 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180920-A1.



PD 25-SEP-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 536  
ID ADH53515 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 537  
ID ADH53685 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 538  
ID ADH52021 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 539  
ID ADH49876 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 540  
ID ADI25386 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 541  
ID ADH90179 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 542  
ID ADI25556 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 543  
ID ADH97730 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 544  
ID ADI35412 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.

Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 545  
ID ADI03578 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 546  
ID ADI11935 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 547  
ID ADH90009 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 548  
ID ADH99904 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 549  
ID ADH98410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 550  
ID ADI11085 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 551  
ID ADI11595 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 552  
ID ADH98240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 553  
ID ADH98580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 7; Length 720;  
RESULT 554  
ID ADI35412 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.

RESULT 554	ID ADH97900 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181674-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 555	ID ADI01285 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003190669-A1.	PD 09-OCT-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 556	ID ADI03408 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181654-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 557	ID ADI04803 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181657-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 558	ID ADH78257 standard; protein; 720 AA.	DE Human PRO polypeptide #19.	PN US2003181668-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 559	ID ADI19601 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181676-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 560	ID ADH90349 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181699-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 561	ID ADI03068 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181653-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 562	ID ADH7917 standard; protein; 720 AA.	DE Human PRO polypeptide #19.	PN US2003181666-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 563	ID ADH79474 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003191290-A1.	PD 09-OCT-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 564	ID ADI01285 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003190669-A1.	PD 09-OCT-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 565	ID ADI01980 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181652-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 566	ID ADI03238 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181655-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 567	ID ADI11425 standard; protein; 720 AA.	DE Human PRO polypeptide #19.	PN US2003181681-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 568	ID ADI02327 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181650-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 569	ID ADI11765 standard; protein; 720 AA.	DE Human PRO polypeptide #19.	PN US2003181685-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 570	ID ADI05402 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003190716-A1.	PD 09-OCT-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 571	ID ADH79474 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003191290-A1.	PD 09-OCT-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;	Length 720;
	Best Local Similarity	100.0%;	Pred. No. 0;							
RESULT 572	ID ADI19431 standard; protein; 720 AA.	DE Novel human secreted and transmembrane protein PRO1344.	PN US2003181666-A1.	PD 25-SEP-2003.	PA (GETH ) GENENTECH INC.	Query Match	100.0%;	Score 720;	DB 7;</	

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 573  
ID ADI05232 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 574  
ID ADH79644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 575  
ID ADI01470 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 576  
ID ADI01640 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 577  
ID ADI01810 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 578  
ID ADH79814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 579  
ID ADI04632 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 580  
ID ADI07768 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 581  
ID ADH78087 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 582  
ID ADI25726 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 583  
ID ADI25896 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 584  
ID ADK65408 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 585  
ID ADH98750 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 586  
ID ADH79991 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 587  
ID ADL32776 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 588  
ID ADM30310 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 589  
ID ADL93722 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 590  
ID ADC52176 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003130483-A1.

PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 591  
ID ADE74307 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 592  
ID ADE74919 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 593  
ID ADF5357 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 594  
ID ADG11607 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 595  
ID ADF96132 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 596  
ID ADG04403 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 597  
ID ADG00563 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 598  
ID ADH06608 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 599  
ID ADH06438 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 600

ID ADG68859 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 601  
ID ADH27749 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 602  
ID ADH25090 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 603  
ID ADH33722 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 604  
ID ADG82819 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 605  
ID ADH02365 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 606  
ID ADH07972 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 607  
ID ADG6369 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 608  
ID ADH39190 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 609  
ID ADH26100 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 610  
ID ADG83930 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 611  
ID ADH19477 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 612  
ID ADG85474 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 613  
ID ADH06268 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 614  
ID ADH30098 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 615  
ID ADH24410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 616  
ID ADH33069 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 617  
ID ADG69539 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 618  
ID ADH07802 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 619  
ID ADG85814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 620  
ID ADH39360 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 621  
ID ADH33552 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 622  
ID ADH33892 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 623  
ID ADH01102 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 624  
ID ADG69709 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 625  
ID ADH20970 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 626  
ID ADH02195 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 627  
ID ADG69199 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180847-A1.  
PD 25-SEP-2003.

Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 637				
ID ADH25798 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003180911-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 638				
ID ADH38364 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003180922-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 639				
ID ADH57203 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003181642-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 640				
ID ADH52191 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003180921-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 641				
ID ADH49557 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003180857-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 642				
ID ADH90519 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003181700-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 643				
ID ADH11255 standard; protein; 720 AA.				
DE Human PRO polypeptide #19.				
PN US2003181683-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 644				
ID ADH38920 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003190698-A1.				
PD 09-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 645				
ID ADI02150 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003190699-A1.				
PD 09-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 646				
ID ADI02150 standard; protein; 720 AA.				
DE Novel human secreted and transmembrane protein PRO1344.				
PN US2003190699-A1.				
PD 09-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 720;	DB 8;	Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 646  
ID ADH9689 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 647  
ID ADJ54808 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 648  
ID ADJ98564 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 649  
ID ADJ98734 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 650  
ID ADH7893 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 651  
ID ADJ99127 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 652  
ID ADJ99297 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 653  
ID ADJ99915 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 654  
ID ADH79063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 655  
ID ADK00923 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 656  
ID ADK1444 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 657  
ID ADJ64579 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 658  
ID ADM31475 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 659  
ID ADM35522 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 660  
ID ADM40327 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 661  
ID ADM80893 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 662  
ID ADN37935 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 663  
ID AAB70531 standard; protein; 567 AA.  
DE Human PRO1 protein sequence SEQ ID NO:2.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 77.2%; Score 556; DB 4; Length 567;  
Best Local Similarity 100.0%; Pred. No. 0;



ID AAY88280 standard; protein; 720 AA.  
DE Human TANGO 215 protein.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 71.9%; Score 518; DB 3; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 665  
ID AAB70532 standard; protein; 720 AA.  
DE Human PRO2 protein sequence SEQ ID NO:4.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 71.9%; Score 518; DB 4; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 666  
ID AAU00401 standard; protein; 720 AA.  
DE Human secreted protein, POLY13.  
PN WO200119856-A2.  
PD 22-MAR-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 71.9%; Score 518; DB 4; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 667  
ID ADH89028 standard; protein; 720 AA.  
DE Human POLYX polypeptide #13.  
PN US200318958-A1.  
PD 23-OCT-2003.  
PA (SHIM/) SHIMKETS R. A.  
PA (FERN/) FERNANDES E.  
PA (HERR/) HERRMANN J L.  
PA (LIUX/) LIU X.  
PA (YANG/) YANG M.  
PA (BOLD/) BOLDOG F L.  
PA (SMT/) SMITHSON G.  
PA (RAS/) RASTELI L.  
Query Match 71.9%; Score 518; DB 8; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 668  
ID AAM41706 standard; protein; 499 AA.  
DE Human polypeptide SEQ ID NO 6637.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSBO INC.  
Query Match 61.9%; Score 446; DB 4; Length 499;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 669  
ID AAB85891 standard; protein; 737 AA.  
DE Human serine protease-like protein (hC-PLACE100992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.9%; Score 446; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 670  
ID AAB93670 standard; protein; 737 AA.  
DE Human protein sequence SEQ ID NO:13202.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.9%; Score 446; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 671  
ID ADJ69990 standard; protein; 737 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.  
PN WO200308768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 61.9%; Score 446; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 672  
ID ADN04640 standard; protein; 737 AA.

DE Antiporiatic protein sequence #505.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 61.9%; Score 446; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 673  
ID ADS85034 standard; protein; 737 AA.  
DE Human atopic dermatitis-related protein sequence SeqID36.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 61.9%; Score 446; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 674  
ID ADS85022 standard; protein; 737 AA.  
DE Human atopic dermatitis-related protein sequence SeqID24.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 61.9%; Score 446; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 675  
ID AAB85893 standard; protein; 762 AA.  
DE Human serine protease-like protein (hC-PLACE100992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.9%; Score 446; DB 4; Length 762;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 676  
ID ADL06662 standard; protein; 417 AA.  
DE Human 3T3 cell conversion promoter FP938.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIDIE GENE TECHN DEV CO LTD.  
Query Match 53.6%; Score 386; DB 7; Length 417;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 677  
ID AAE19180 standard; protein; 649 AA.  
DE Human protease, PRTS-17 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 52.1%; Score 375; DB 5; Length 649;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 678  
ID AAM39920 standard; protein; 359 AA.  
DE Human polypeptide SEQ ID NO 3065.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSBO INC.  
Query Match 49.9%; Score 359; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 679  
ID AAM39957 standard; protein; 359 AA.  
DE Human polypeptide SEQ ID NO 3102.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSBO INC.  
Query Match 49.9%; Score 359; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 680  
ID AAB49533 standard; protein; 570 AA.  
DE Clone HPEY75.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 49.3%; Score 355; DB 3; Length 570;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 681

ID AAE20817 standard; protein; 455 AA.  
DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:79.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.5%; Score 277; DB 5; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
RESULT 682  
ID ABG64652 standard; protein; 455 AA.  
DE Human albumin fusion protein #1327.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.5%; Score 277; DB 5; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
RESULT 683  
ID ADL77919 standard; protein; 455 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 38.5%; Score 277; DB 8; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
RESULT 684  
ID ADRA1485 standard; protein; 551 AA.  
DE Human CD-like molecule HSKDR41, SEQ ID NO:264.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.5%; Score 277; DB 5; Length 551;  
Best Local Similarity 100.0%; Pred. No. 5.4e-261;  
RESULT 685  
ID AAE20797 standard; protein; 323 AA.  
DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:59.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.3%; Score 276; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3.2e-260;  
RESULT 686  
ID ABG64653 standard; protein; 323 AA.  
DE Human albumin fusion protein #1328.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.3%; Score 276; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3.2e-260;  
RESULT 687  
ID ADL77920 standard; protein; 323 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 38.3%; Score 276; DB 8; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3.2e-260;  
RESULT 688  
ID AAM24485 standard; protein; 234 AA.  
DE Human EST encoded protein SEQ ID NO: 2010.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 25.4%; Score 183; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-169;  
RESULT 689  
ID AAM41743 standard; protein; 146 AA.  
DE Human polypeptide SEQ ID NO 6674.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.8%; Score 114; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2.2e-102;

RESULT 690  
ID AAB0927 standard; protein; 719 AA.  
DE Murine TANGO 215 protein.  
PN WO2000018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 8.5%; Score 61; DB 3; Length 719;  
Best Local Similarity 100.0%; Pred. No. 5.2e-50;  
RESULT 691  
ID AAB85892 standard; protein; 720 AA.  
DE Mouse serine protease-like protein (MC-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 8.5%; Score 61; DB 4; Length 720;  
Best Local Similarity 100.0%; Pred. No. 5.2e-50;  
RESULT 692  
ID AAY11743 standard; protein; 103 AA.  
DE Human 5' EST secreted protein SEQ ID No: 343.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 5.3%; Score 38; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 2.5e-28;  
RESULT 693  
ID AAY11763 standard; protein; 34 AA.  
DE Human 5' EST secreted protein SEQ ID No: 363.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 2.1%; Score 15; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 694  
ID AAB49539 standard; peptide; 12 AA.  
DE Clone HPEY75 peptide fragment.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.7%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
RESULT 695  
ID AAY72114 standard; peptide; 12 AA.  
DE Human serine protease epidermal growth factor (EGF)-like domain.  
PN WO200068247-A2.  
PD 16-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.7%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
RESULT 696  
ID AAR93594 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS14 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU-) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 697  
ID AAR76945 standard; peptide; 30 AA.  
DE UK t-PA hybrid CS13 (residues 276-306).  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU-) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 698  
ID AAR93590 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS20 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU-) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 699

ID AAR93593 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS11 residues 276-306.  
PN WO9509908-A1.  
PA (SUDU) SUDITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 700  
ID AAR93598 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS18 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUDU) SUDITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 701  
ID AAY82896 standard; protein; 101 AA.  
DE CUB domain from murine BMP-1.  
PN WO200009691-A2.  
PD 24-FEB-2000.  
PA (UROG-) UROGENESYS INC.  
PA (APAR/) APAR D E.  
PA (HUSE/) HUBERT R S.  
PA (LEON/) LEONG K.  
PA (RAIT/) RAITANO A B.  
PA (SAFE/) SAFERAN D C.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 1.2%; Score 9; DB 3; Length 101;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
RESULT 702  
ID AAY27043 standard; protein; 110 AA.  
DE Amino acid sequence of human Bmp-1 CUB1 domain.  
PN WO937757-A1.  
PD 29-JUL-1999.  
PA (TUDA) TULANE EDUCATIONAL FUND.  
PA (INIM) INST NAT SANTE & RECH MEDICALE.  
Query Match 1.2%; Score 9; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
RESULT 703  
ID ABM84572 standard; protein; 622 AA.  
DE Human diagnostic and therapeutic protease SEQ ID NO:4821.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.2%; Score 9; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 704  
ID ABM80969 standard; protein; 622 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81651, SEQ:2500.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GENTH) GENEENTECH INC.  
Query Match 1.2%; Score 9; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 705  
ID AAP80618 standard; protein; 730 AA.  
DE Human Bone Morphogenic Protein-1 of lambda UZOS-1.  
PN WO8800205-A.  
PD 14-JAN-1988.  
PA (GENV) GENETICS INST INC.  
Query Match 1.2%; Score 9; DB 1; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 706  
ID AAM13669 standard; protein; 730 AA.  
DE C-proteinase encoded by clone pcP-1.  
PN WO9706242-A1.  
PD 20-FEB-1997.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Query Match 1.2%; Score 9; DB 2; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 707  
ID ADP65217 standard; protein; 730 AA.  
DE Human bone morphogenetic protein 1, isoform 1, precursor, PCP.  
PN WO2004009834-A2.

PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 1.2%; Score 9; DB 7; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 708  
ID ABM80967 standard; protein; 730 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO3042, SEQ:2496.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GENTH) GENEENTECH INC.  
Query Match 1.2%; Score 9; DB 8; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 709  
ID AAW75919 standard; protein; 788 AA.  
DE C-proteinase sequence used to cleave procollagens.  
PN US5807981-A.  
PD 15-SEP-1998.  
PA (FIBR-) FIBROGEN INC.  
Query Match 1.2%; Score 9; DB 2; Length 788;  
Best Local Similarity 100.0%; Pred. No. 33;  
RESULT 710  
ID ADH41541 standard; protein; 821 AA.  
DE Novel human protein NOV8e.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 711  
ID ADH41549 standard; protein; 821 AA.  
DE Novel human protein NOV8f.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 712  
ID ADH41533 standard; protein; 821 AA.  
DE Novel human protein NOV8a.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 713  
ID ADH41543 standard; protein; 821 AA.  
DE Novel human protein NOV8f.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 714  
ID ADH41545 standard; protein; 821 AA.  
DE Novel human protein NOV8g.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 715  
ID ADH41547 standard; protein; 821 AA.  
DE Novel human protein NOV8h.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 716  
ID ADM87216 standard; protein; 823 AA.  
DE Human protein SEQ ID NO:309.  
PN WO2004009834-A2.

PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 823;  
Pred. No. 34;  
RESULT 717  
ID ABM80968 standard; protein; 823 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide, PRO81650, SEQ.2498.  
PN W02004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 823;  
Pred. No. 34;  
RESULT 718  
ID ABG79188 standard; protein; 970 AA.  
DE Human colloid-like 2-like protein #2.  
PN W0200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 5; Length 970;  
Pred. No. 40;  
RESULT 719  
ID ADH41539 standard; protein; 970 AA.  
DE Novel human protein NOV8d.  
PN W02003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 970;  
Pred. No. 40;  
RESULT 720  
ID AAM13670 standard; protein; 986 AA.  
DE C-proteinase encoded by clone pcP-2.  
PN W09706242-A1.  
PD 20-FEB-1997.  
PA (UYU-) UNIV JEFFERSON THOMAS.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 2; Length 986;  
Pred. No. 41;  
RESULT 721  
ID ABB90755 standard; protein; 986 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 242.  
PN W0200210217-A2.  
PD 07-FEB-2002.  
PA (UYU-) UNIV JOHNS HOPKINS.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 5; Length 986;  
Pred. No. 41;  
RESULT 722  
ID ASU54462 standard; protein; 986 AA.  
DE Human tumour endothelial marker TEM 25.  
PN W0200283674-A2.  
PD 24-OCT-2002.  
PA (UYU-) UNIV JOHNS HOPKINS.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 6; Length 986;  
Pred. No. 41;  
RESULT 723  
ID ADH11578 standard; protein; 986 AA.  
DE Human bone morphogenic protein (BMP) polypeptide #6.  
PN US2003224501-A1.  
PD 04-DEC-2003.  
PA (YOUNG) YOUNG P E.  
PA (RUBEN) RUBEN S M.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 986;  
Pred. No. 41;  
RESULT 724  
ID ADQ16558 standard; protein; 986 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1377.  
PN W02004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 986;  
Pred. No. 41;  
RESULT 725  
ID ABG79187 standard; protein; 992 AA.  
DE Human colloid-like 2-like protein #1.  
PN W0200264791-A2.  
PD 22-AUG-2002.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 5; Length 992;  
Pred. No. 41;  
RESULT 726  
ID ADH41535 standard; protein; 992 AA.  
DE Novel human protein NOV8b.  
PN W02003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 992;  
Pred. No. 41;  
RESULT 727  
ID AAY32240 standard; protein; 1015 AA.  
DE Human colloid-like protein mtl1-2.  
PN W09951730-A2.  
PD 14-OCT-1999.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 3; Length 1015;  
Pred. No. 42;  
RESULT 728  
ID ADH41537 standard; protein; 1015 AA.  
DE Novel human protein NOV8c.  
PN W02003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 8; Length 1015;  
Pred. No. 42;  
RESULT 729  
ID ABB71111 standard; protein; 1464 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40125.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match  
Best Local Similarity 1.2%; Score 9; DB 4; Length 1464;  
Pred. No. 58;  
RESULT 730  
ID ABB77068 standard; peptide; 11 AA.  
DE AC2885 antibody light chain hypervariable region CDR1'.  
PN W0200216436-A2.  
PD 28-FEB-2002.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 5; Length 11;  
Pred. No. 64;  
RESULT 731  
ID ADH17699 standard; peptide; 11 AA.  
DE Human 15H12/19D12 CDR (complementarity determining region)-L1 peptide.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 11;  
Pred. No. 64;  
RESULT 732  
ID ADM41606 standard; peptide; 11 AA.  
DE Interleukin-1 receptor type 1 antibody light chain variable region CDR1.  
PN W02004022718-A2.  
PD 18-MAR-2004.  
PA (AMGE-) AMGEN INC.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 11;  
Pred. No. 64;  
RESULT 733  
ID AAE36602 standard; protein; 50 AA.  
DE Human epigen BGF-like domain.  
PN W02003014159-A1.  
PD 20-FEB-2003.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
PA (BIOM-) BIOMOLECULAR RES INST LTD.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 6; Length 50;  
Pred. No. 25;  
RESULT 734

ID AAY76087 standard; protein; 51 AA.  
DE MUTRI fragment (residues 53-103) mutRIa, SEQ ID NO:342.  
PN WO9955865-A1.  
PD 04-NOV-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 1.1%; Score 8; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 26;  
RESULT 735  
ID AAB56026 standard; protein; 51 AA.  
DE Skin cell protein, SEQ ID NO: 342.  
PN WO200069884-A2.  
PD 23-NOV-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 1.1%; Score 8; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 26;  
RESULT 736  
ID ABB72226 standard; protein; 51 AA.  
DE Murine protein isolated from skin cells SEQ ID NO: 342.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 1.1%; Score 8; DB 5; Length 51;  
Best Local Similarity 100.0%; Pred. No. 26;  
RESULT 737  
ID AAY56653 standard; protein; 88 AA.  
DE Partial peptide fragment of chimpanzee Vkapra CDNA clone 46-4.  
PN WO9953569-A1.  
PD 04-NOV-1999.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 1.1%; Score 8; DB 3; Length 88;  
Best Local Similarity 100.0%; Pred. No. 43;  
RESULT 738  
ID AAY79331 standard; protein; 94 AA.  
DE Human EGF repeat-containing protein EGF-Hy1.  
PN WO200017357-A1.  
PD 30-MAR-2000.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 3; Length 94;  
Best Local Similarity 100.0%; Pred. No. 45;  
RESULT 739  
ID ABO27159 standard; protein; 95 AA.  
DE Human germline light chain variable region gene segment #39.  
PN US2003039649-A1.  
PD 27-FEB-2003.  
PA (FOOT/) FOOT J.  
Query Match 1.1%; Score 8; DB 6; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 740  
ID ABO27158 standard; protein; 95 AA.  
DE Human germline light chain variable region gene segment #38.  
PN US2003039649-A1.  
PD 27-FEB-2003.  
PA (FOOT/) FOOT J.  
Query Match 1.1%; Score 8; DB 6; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 741  
ID ADF10204 standard; protein; 95 AA.  
DE Antibody light chain variable region VLK\_6-21.  
PN WO2003074679-A2.  
PD 12-SEP-2003.  
PA (XENC-) XENCOR.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 742  
ID ADF10103 standard; protein; 95 AA.  
DE VEGF antibody light chain variable region VLK\_6D-21.  
PN WO2003074679-A2.  
PD 12-SEP-2003.  
PA (XENC-) XENCOR.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 743  
ID ADF10102 standard; protein; 95 AA.

DE VEGF antibody light chain variable region VLK\_6-21.  
PN WO2003074679-A2.  
PD 12-SEP-2003.  
PA (XENC-) XENCOR.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 744  
ID ADF10000 standard; protein; 95 AA.  
DE Antibody light chain variable region VLK\_6-21.  
PN WO2003074679-A2.  
PD 12-SEP-2003.  
PA (XENC-) XENCOR.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 745  
ID ADF10001 standard; protein; 95 AA.  
DE Antibody light chain variable region VLK\_6D-21.  
PN WO2003074679-A2.  
PD 12-SEP-2003.  
PA (XENC-) XENCOR.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 746  
ID ADF10205 standard; protein; 95 AA.  
DE Antibody light chain variable region VLK\_6D-21.  
PN WO2003074679-A2.  
PD 12-SEP-2003.  
PA (XENC-) XENCOR.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 747  
ID ADF80278 standard; protein; 95 AA.  
DE Vkapra gene locus antibody amino acid sequence #38.  
PN WO2003048321-A2.  
PD 12-JUN-2003.  
PA (ALEX-) ALEXION PHARM INC.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 748  
ID ADF80279 standard; protein; 95 AA.  
DE Vkapra gene locus antibody amino acid sequence #39.  
PN WO2003048321-A2.  
PD 12-JUN-2003.  
PA (ALEX-) ALEXION PHARM INC.  
Query Match 1.1%; Score 8; DB 7; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 749  
ID ADO07347 standard; protein; 95 AA.  
DE Human antibody A26 light chain variable region.  
PN WO2004033658-A2.  
PD 22-APR-2004.  
PA (INTE-) INTEGRIS INC.  
Query Match 1.1%; Score 8; DB 8; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 750  
ID ADO07348 standard; protein; 95 AA.  
DE Human antibody A10 light chain variable region.  
PN WO2004033658-A2.  
PD 22-APR-2004.  
PA (INTE-) INTEGRIS INC.  
Query Match 1.1%; Score 8; DB 8; Length 95;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 751  
ID AAS35905 standard; protein; 96 AA.  
DE Human A10/A26 antibody light chain germline protein.  
PN EP1262193-A1.  
PD 04-DEC-2002.  
PA (PRIZ ) PRIZER PROD INC.  
Query Match 1.1%; Score 8; DB 6; Length 96;  
Best Local Similarity 100.0%; Pred. No. 46;  
RESULT 752  
ID ADO07305 standard; protein; 107 AA.  
DE Human proteolytic A26-UK1 light chain, used in catalytic antibody.

PN W02004033658-A2.  
PD 22-APR-2004.  
PA (INTE-) INTEGRIGEN INC.  
Query Match 1.1%; Score 8; DB 8; Length 107;  
Best Local Similarity 100.0%; Pred. No. 51;  
RESULT 753  
ID A0007307 standard; protein; 107 AA.  
DE Human proteolytic A10-JK1 light chain, used in catalytic antibody.  
PN W02004033658-A2.  
PD 22-APR-2004.  
PA (INTE-) INTEGRIGEN INC.  
Query Match 1.1%; Score 8; DB 8; Length 107;  
Best Local Similarity 100.0%; Pred. No. 51;  
RESULT 754  
ID ABB03399 standard; protein; 124 AA.  
DE Human musculoskeletal system related polypeptide SEQ ID NO 1346.  
PN W0200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.1%; Score 8; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 58;  
RESULT 755  
ID ABU12693 standard; protein; 124 AA.  
DE Novel human musculoskeletal system antigen #313.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 1.1%; Score 8; DB 6; Length 124;  
Best Local Similarity 100.0%; Pred. No. 58;  
RESULT 756  
ID ADJ28719 standard; protein; 124 AA.  
DE Human musculoskeletal system-associated protein - SEQ ID 1346.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.1%; Score 8; DB 8; Length 124;  
Best Local Similarity 100.0%; Pred. No. 58;  
RESULT 757  
ID ABB77064 standard; protein; 126 AA.  
DE AC2885 antibody light chain variable region.  
PN W0200216436-A2.  
PD 28-FEB-2002.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERN GES MBH.  
Query Match 1.1%; Score 8; DB 5; Length 126;  
Best Local Similarity 100.0%; Pred. No. 59;  
RESULT 758  
ID ADM41553 standard; protein; 126 AA.  
DE Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.  
PN W02004022718-A2.  
PD 18-MAR-2004.  
PA (AMGE-) AMGEN INC.  
Query Match 1.1%; Score 8; DB 8; Length 126;  
Best Local Similarity 100.0%; Pred. No. 59;  
RESULT 759  
ID ABB57370 standard; protein; 127 AA.  
DE Anti-TRAIL-R antibody related clone KMTR1 protein SEQ ID NO:35.  
PN W0200294880-A1.  
PD 28-NOV-2002.  
PA (KIRI ) KIRIN BEER KK.  
Query Match 1.1%; Score 8; DB 6; Length 127;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 760  
ID AAY56718 standard; protein; 128 AA.  
DE Amino acid sequence of chimpanzee Vkapaa cDNA clone 46-4.  
PN W03955369-A1.  
PD 04-NOV-1999.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 1.1%; Score 8; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 761

ID ADH17963 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain C (LCC) protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 762  
ID ADH17967 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain E (LCE) protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 763  
ID ADH17969 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain F (LCF) protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 764  
ID ADH17932 standard; protein; 128 AA.  
DE Human 15H12/19D12 light chain A (LCA) protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 765  
ID ADH17965 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain D (LCD) protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 766  
ID ADH17934 standard; protein; 128 AA.  
DE Human 15H12/19D12 light chain B (LCB) protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 767  
ID ADH17893 standard; protein; 128 AA.  
DE Human 15H12/19D12 light chain variable region protein.  
PN W02003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 128;  
Best Local Similarity 100.0%; Pred. No. 60;  
RESULT 768  
ID AAY7609 standard; protein; 152 AA.  
DE Murine TGF-alpha homologue mutRL, SEQ ID 187.  
PN W03955865-A1.  
PD 04-NOV-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 1.1%; Score 8; DB 3; Length 152;  
Best Local Similarity 100.0%; Pred. No. 70;  
RESULT 769  
ID AAB55948 standard; protein; 152 AA.  
DE Skin cell protein, SEQ ID NO: 187.  
PN W0200069884-A2.  
PD 23-NOV-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 1.1%; Score 8; DB 4; Length 152;  
Best Local Similarity 100.0%; Pred. No. 70;  
RESULT 770  
ID ABB72148 standard; protein; 152 AA.

Query Match	1.1%;	Score 8;	DB 6;	Length 596;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
RESULT 779				
ID ADG93413 standard; protein; 807 AA.				
DE Maize lipoxygenase (LOX) polypeptide #22.				
PN US2003166855-A1.				
PD 04-SEP-2003.				
PA (PION-) PIONEER HI-BRED INT INC.				
Query Match	1.1%;	Score 8;	DB 7;	Length 807;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;		
RESULT 780				
ID ADG93411 standard; protein; 807 AA.				
DE Maize lipoxygenase (LOX) polypeptide #21.				
PN US2003166855-A1.				
PD 04-SEP-2003.				
PA (PION-) PIONEER HI-BRED INT INC.				
Query Match	1.1%;	Score 8;	DB 7;	Length 807;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;		
RESULT 781				
ID ABB68935 standard; protein; 859 AA.				
DE Human polypeptide SEQ ID NO 982.				
PN WO200270539-A2.				
PD 12-SEP-2002.				
PA (HYSE-) HYSEQ INC.				
Query Match	1.1%;	Score 8;	DB 5;	Length 859;
Best Local Similarity	100.0%;	Pred. No. 3.4e+02;		
RESULT 782				
ID AAW43394 standard; protein; 1019 AA.				
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).				
PN SG42456-A1.				
PD 15-AUG-1997.				
PA (UYST-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 2;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 783				
ID AAY05750 standard; protein; 1019 AA.				
DE Horseshoe crab Factor C.				
PN WO9915676-A1.				
PD 01-APR-1999.				
PA (UYST-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 2;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 784				
ID AAW94302 standard; protein; 1019 AA.				
DE Horseshoe crab Factor C protein #2.				
PN US5858706-A.				
PD 12-JAN-1999.				
PA (UYST-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 2;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 785				
ID AAY42490 standard; protein; 1019 AA.				
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein				
PN US9985590-A.				
PD 16-NOV-1999.				
PA (UYST-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 3;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 786				
ID AAB60935 standard; protein; 1019 AA.				
DE Horseshoe crab recombinant Factor C #2.				
PN WO200127289-A2.				
PD 19-APR-2001.				
PA (UYST-) UNIV SINGAPORE NAT.				
Query Match	1.1%;	Score 8;	DB 4;	Length 1019;
Best Local Similarity	100.0%;	Pred. No. 4e+02;		
RESULT 787				
ID ABB72332 standard; protein; 1019 AA.				
DE Horseshoe crab Factor C.				
PN WO2003002976-A2.				
PD 09-JAN-2003.				
PA (WHIK ) BIONEER INC.				
Query Match	1.1%;	Score 8;	DB 6;	Length 1019;



Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 788  
ID AAB72334 standard; protein; 1019 AA.  
DE Horsehoe crab Factor C.  
PN W02003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK ) B10WHITTAKER INC.  
Query Match 1.1%; Score 8; DB 6; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 789  
ID AAW43393 standard; protein; 1083 AA.  
DE Singapore horsehoe crab factor C proenzyme (CrFC 26).  
PN SG42456-A1.  
PD 15-AUG-1997.  
PA (YYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 790  
ID AAY05749 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C.  
PN W0915676-A1.  
PD 01-APR-1999.  
PA (YYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 791  
ID AAW94301 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C protein #1.  
PN US5858706-A.  
PD 12-JAN-1999.  
PA (YYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 792  
ID AAY42489 standard; protein; 1083 AA.  
DE Horsehoe crab recombinant Factor C protein.  
PN US5985590-A.  
PD 16-NOV-1999.  
PA (YYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 3; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 793  
ID AAB60934 standard; protein; 1083 AA.  
DE Horsehoe crab recombinant Factor C #1.  
PN W0200127289-A2.  
PD 19-APR-2001.  
PA (YYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 4; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 794  
ID AAB72333 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C.  
PN W02003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK ) B10WHITTAKER INC.  
Query Match 1.1%; Score 8; DB 6; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 795  
ID AAB62022 standard; protein; 1238 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12858.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PBKE ) PB CORP NY.  
Query Match 1.1%; Score 8; DB 4; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 796  
ID AAB94754 standard; protein; 1316 AA.  
DE Human protein sequence SEQ ID NO:15811.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 1.1%; Score 8; DB 4; Length 1316;  
Best Local Similarity 100.0%; Pred. No. 5e+02;

RESULT 797  
ID ADF28695 standard; protein; 1484 AA.  
DE Neurological therapy-related protein - SED ID 605.  
PN W02003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 7; Length 1484;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
RESULT 798  
ID ADF28692 standard; protein; 1487 AA.  
DE Human peroxidase-like protein - SED ID 602.  
PN W02003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 7; Length 1487;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
RESULT 799  
ID ADS10671 standard; protein; 1507 AA.  
DE Human therapeutic protein - SEQ ID 908.  
PN W02004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 1.1%; Score 8; DB 8; Length 1507;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 800  
ID ADF28708 standard; protein; 1538 AA.  
DE Peroxidase-like protein - SED ID 618.  
PN W02003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 7; Length 1538;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 801  
ID ADS10672 standard; protein; 1538 AA.  
DE Human therapeutic protein - SEQ ID 909.  
PN W02004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 1.1%; Score 8; DB 8; Length 1538;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 802  
ID ADN39112 standard; protein; 3557 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:430.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.1%; Score 8; DB 7; Length 3557;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 803  
ID ADN39979 standard; protein; 3557 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C349.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.1%; Score 8; DB 7; Length 3557;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 804  
ID AAB37944 standard; protein; 3570 AA.  
DE Human CGSD-33 protein.  
PN W02003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.1%; Score 8; DB 7; Length 3570;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 805  
ID AAE20146 standard; protein; 3571 AA.  
DE Human C3b/C4b complement receptor-like protein.  
PN W0200210388-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 1.1%; Score 8; DB 5; Length 3571;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 806

ID ADL22512 standard; protein; 3571 AA.  
DE Human CNGH0004 antibody protein.  
PN WO2004003147-A2.  
PD 08-JAN-2004.  
PA (CENZ ) CENTOCOR INC.  
Query Match 1.1%; Score 8; DB 8; Length 3571;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 807  
ID AD075791 standard; peptide; 10 AA.  
DE Human 213P1F11 HLA motif bearing epitope #9890.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 1.0%; Score 7; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 56;  
RESULT 808  
ID AD077622 standard; peptide; 15 AA.  
DE Human 213P1F11 HLA motif bearing epitope #11721.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 1.0%; Score 7; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 81;  
RESULT 809  
ID AAR71665 standard; peptide; 30 AA.  
DE Modified urinary plasminogen activator residues 159-188.  
PN JP07039374-A.  
PD 10-FEB-1995.  
PA (SUMV ) SUMITOMO SEIYAKU KK.  
Query Match 1.0%; Score 7; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 810  
ID AAP78761 standard; protein; 43 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 4052.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 811  
ID AAM23655 standard; protein; 49 AA.  
DE Human EST encoded protein SEQ ID NO: 1380.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 812  
ID AOC3379 standard; protein; 49 AA.  
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3361.  
PN WO2003028271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 7; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 813  
ID AAM06451 standard; protein; 50 AA.  
DE Human foetal protein, SEQ ID NO: 182.  
PN WO200155339-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 814  
ID AAG51460 standard; protein; 54 AA.  
DE C glutamincum protein fragment SEQ ID NO: 5214.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 1.0%; Score 7; DB 4; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 815  
ID AAY02522 standard; protein; 56 AA.  
DE Clone selected after panning a NNK library of the invention.  
PN WO9920749-A1.  
PD 29-APR-1999.  
PA (MED-) MEDICAL RES COUNCIL.  
Query Match 1.0%; Score 7; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 816  
ID ABM71426 standard; protein; 59 AA.  
DE Staphylococcus aureus protein #666.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 817  
ID AAU46293 standard; protein; 62 AA.  
DE Propionibacterium acnes immunogenic protein #9189.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 818  
ID AAM44612 standard; protein; 62 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9488.  
PN WO200303515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 62;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 819  
ID ABB42063 standard; peptide; 63 AA.  
DE Peptide #9569 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 820  
ID AAM75756 standard; protein; 63 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36062.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 821  
ID AAM62944 standard; protein; 63 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35049.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 822  
ID ABG57494 standard; peptide; 63 AA.  
DE Human liver peptide, SEQ ID NO 36142.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;

Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 823  
ID AAB35189 standard; protein; 74 AA.  
DE Human deaminase-like ORF4162 protein, SEQ ID NO:8324.  
PN W0200190366-A2.  
PD 29-NOV-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.0%; Score 7; DB 5; Length 74;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 824  
ID AAB66472 standard; protein; 76 AA.  
DE Propionibacterium acnes immunogenic protein #27368.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 825  
ID AAB67610 standard; protein; 76 AA.  
DE Propionibacterium acnes immunogenic protein #28506.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 826  
ID AAB62991 standard; protein; 76 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27667.  
PN W0200303515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 827  
ID AAB64129 standard; protein; 76 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28805.  
PN W0200303515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 828  
ID AAB20816 standard; protein; 79 AA.  
DE Human gene 5 encoded secreted protein HSLG75, SEQ ID NO:78.  
PN W0200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 829  
ID AAB64651 standard; protein; 79 AA.  
DE Human albumin fusion protein #1326.  
PN W0200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 830  
ID AAB77918 standard; protein; 79 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1400.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C. A.  
PA (HASE/) HASELTINE W. A.  
Query Match 1.0%; Score 7; DB 8; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 831  
ID AAB64695 standard; protein; 81 AA.  
DE Propionibacterium acnes immunogenic polypeptide #29371.  
PN W0200303515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 81;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 832  
ID AAB05104 standard; protein; 83 AA.  
DE Bacterial polypeptide #1217.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 83;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 833  
ID AAG03800 standard; protein; 103 AA.  
DE Human secreted protein, SEQ ID NO: 7881.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match 1.0%; Score 7; DB 3; Length 103;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 834  
ID AAY64590 standard; peptide; 105 AA.  
DE Nonclassical cadherin extracellular domain SEQ ID NO:18.  
PN W09957149-A2.  
PD 11-NOV-1999.  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
Query Match 1.0%; Score 7; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 835  
ID AAB06753 standard; protein; 107 AA.  
DE Human ORFX protein sequence SEQ ID NO:13488.  
PN W0200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.0%; Score 7; DB 5; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 836  
ID AAB27656 standard; protein; 108 AA.  
DE Human protein AFP548753.  
PN W020016748-A2.  
PD 13-SEP-2001.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 837  
ID AAD32136 standard; protein; 108 AA.  
DE Mutant B licheniformis secreted polypeptide Seqid 106.  
PN W02003093453-A2.  
PD 13-NOV-2003.  
PA (NOVO-) NOVOTYMS AS.  
Query Match 1.0%; Score 7; DB 8; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 838  
ID AAB99113 standard; protein; 111 AA.  
DE Bovine zeta 2 prethrombin 2.  
PN W09855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 839  
ID AAB074597 standard; protein; 111 AA.  
DE Pseudomonas aeruginosa polypeptide #6772.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 111;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 840  
ID AAB99115 standard; protein; 116 AA.  
DE Human zeta 2 prethrombin 2.  
PN W09855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 841  
ID AAG26792 standard; protein: 117 AA.  
DE Zea mays protein fragment SEQ ID NO: 31379.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.2e+02; Length 117;  
RESULT 842  
ID AAG51373 standard; protein: 121 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65194.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Length 121;  
RESULT 843  
ID AAG26791 standard; protein: 121 AA.  
DE Zea mays protein fragment SEQ ID NO: 31378.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Length 121;  
RESULT 844  
ID ABO73690 standard; protein: 121 AA.  
DE Pseudomonas aeruginosa polypeptide #5865.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Length 121;  
RESULT 845  
ID AAG11631 standard; protein: 128 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10420.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Length 128;  
RESULT 846  
ID AAG51372 standard; protein: 128 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65193.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Length 128;  
RESULT 847  
ID AAG26790 standard; protein: 142 AA.  
DE Zea mays protein fragment SEQ ID NO: 31377.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Length 142;  
RESULT 848  
ID ABO63944 standard; protein: 142 AA.  
DE Klebsiella pneumoniae polypeptide seqid 10461.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Length 142;  
RESULT 849  
ID AAW41967 standard; protein: 144 AA.  
DE Flea serine protease SEQ ID NO: 81.  
PN WO9740058-A1.  
PD 30-OCT-1997.  
PA (HESK-) HESKA CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Length 144;  
RESULT 850  
ID AAB50629 standard; protein: 144 AA.  
DE Flea serine protease PFSF32-144 protein sequence #153.  
PN US6150125-A.  
PD 21-NOV-2000.  
PA (HESK-) HESKA CORP.  
Query Match  
1.0%; Score 7; DB 3; Length 144;  
Score 7; DB 4; Length 144;

Best Local Similarity 100.0%; Pred. No. 6.3e+02; Length 144;  
RESULT 851  
ID AAF64494 standard; protein: 148 AA.  
DE Propionibacterium acnes immunogenic protein #25390.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Length 148;  
RESULT 852  
ID AAM61013 standard; protein: 148 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25689.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.5e+02; Length 148;  
RESULT 853  
ID AAG51371 standard; protein: 151 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65192.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Length 151;  
RESULT 854  
ID AD145291 standard; protein: 164 AA.  
DE Rice isoprenoid biosynthesis-associated protein #111.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG/) LANGE B M.  
PA (GHAS/) GHASSEMIMAN M.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZERBOOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
PA (ZHUT/) ZHU T.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.1e+02; Length 164;  
RESULT 855  
ID AAY34950 standard; protein: 172 AA.  
DE Amino acid sequence of a Chlamydia pneumoniae protein.  
PN WO9927105-A2.  
PD 03-JUN-1999.  
PA (GEST) GENSET.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Length 172;  
RESULT 856  
ID ABO39246 standard; protein: 172 AA.  
DE Protein encoded by Prokaryotic essential gene #24773.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.4e+02; Length 172;  
RESULT 857  
ID AAG51370 standard; protein: 184 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65190.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Length 184;  
RESULT 858  
ID ADC97109 standard; protein: 187 AA.  
DE E. faecium protein sequence SEQ ID 6736.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
1.0%; Score 7; DB 7; Length 187;  
Score 7; DB 7; Length 187;

Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 859  
ID AAU25597 standard; protein: 194 AA.  
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #44.  
PN W0200162797-A2.  
PD 30-AUG-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 1.0%; Score 7; DB 4; Length 194;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
RESULT 860  
ID AAU29491 standard; protein: 200 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #112.  
PN W0200168858-A2.  
PD 20-SEP-2001.  
PA (PHAA) PHARMACIA & UPJOHN CO.  
Query Match 1.0%; Score 7; DB 4; Length 200;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 861  
ID AAG60779 standard; protein: 200 AA.  
DE Novel G protein coupled receptor (nGCPR-x) #112.  
PN US2002058306-A1.  
PD 16-MAY-2002.  
PA (VOGE/) VOGELI G.  
Query Match 1.0%; Score 7; DB 5; Length 200;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 862  
ID ABB65610 standard; protein: 202 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23622.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 202;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 863  
ID ABR09068 standard; protein: 202 AA.  
DE Human protein useful for treating neurological disease Seq 2574.  
PN RP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.0%; Score 7; DB 8; Length 202;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 864  
ID AAU45202 standard; protein: 209 AA.  
DE Propionibacterium acnes immunogenic protein #6098.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 865  
ID ABM41721 standard; protein: 209 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6397.  
PN W0200303515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 209;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 866  
ID AAY35451 standard; protein: 210 AA.  
DE Chlamydia pneumoniae transmembrane protein sequence.  
PN W09927105-A2.  
PD 03-JUN-1999.  
PA (GEST) GENSET.  
Query Match 1.0%; Score 7; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 867  
ID ABU27599 standard; protein: 210 AA.  
DE Protein encoded by Prokaryotic essential gene #13126.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 210;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 868  
ID ADS41665 standard; protein: 210 AA.  
DE Bacterial polypeptide #20095.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 210;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 869  
ID ABU49962 standard; protein: 211 AA.  
DE Protein encoded by Prokaryotic essential gene #35489.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 211;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 870  
ID AAU34556 standard; protein: 212 AA.  
DE E. coli cellular proliferation protein #137.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 871  
ID ABU31486 standard; protein: 212 AA.  
DE Protein encoded by Prokaryotic essential gene #17013.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 872  
ID ABU48063 standard; protein: 212 AA.  
DE Protein encoded by Prokaryotic essential gene #33590.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 873  
ID ABU15066 standard; protein: 212 AA.  
DE Protein encoded by Prokaryotic essential gene #593.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 874  
ID ABU45471 standard; protein: 212 AA.  
DE Protein encoded by Prokaryotic essential gene #30998.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 875  
ID ABB54972 standard; protein: 213 AA.  
DE Lactococcus lactis protein kdga.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 1.0%; Score 7; DB 5; Length 213;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 876  
ID ABU40559 standard; protein: 213 AA.  
DE Protein encoded by Prokaryotic essential gene #26086.  
PN W0200277183-A2.  
PD 03-OCT-2002.

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ID AAG33373 standard; protein; 230 AA.
DE Zea mays protein fragment SEQ ID NO: 40426.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 230;
Pred. No. 9.7e+02;
RESULT 887
ID ABW27062 standard; protein; 231 AA.
DE Protein encoded by Prokaryotic essential gene #12589.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 231;
Pred. No. 9.7e+02;
RESULT 888
ID AAW33655 standard; protein; 232 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #99
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 232;
Pred. No. 9.8e+02;
RESULT 889
ID ABW15506 standard; protein; 232 AA.
DE Protein encoded by Prokaryotic essential gene #1033.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 232;
Pred. No. 9.8e+02;
RESULT 890
ID AAW41957 standard; protein; 233 AA.
DE Flea serine protease SEQ ID NO:27.
PN WO9740058-A1.
PD 30-OCT-1997.
PA (HESK-) HESKA CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 2; Length 233;
Pred. No. 9.8e+02;
RESULT 891
ID AAG51368 standard; protein; 234 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65188.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 234;
Pred. No. 9.8e+02;
RESULT 892
ID AAG15808 standard; protein; 235 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16206.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 235;
Pred. No. 9.9e+02;
RESULT 893
ID AAG33372 standard; protein; 237 AA.
DE Zea mays protein fragment SEQ ID NO: 40425.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 237;
Pred. No. 1e+03;
RESULT 894
ID ABW49459 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #34986.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 239;
Pred. No. 1e+03;
RESULT 895
ID AAG33371 standard; protein; 241 AA.
DE Zea mays protein fragment SEQ ID NO: 40424.
PN EP1033405-A2.
PD 06-SEP-2000.

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Query Match 1.0%; Score 7; DB 3; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 RESULT 896  
 ID ABO77745 standard; protein; 245 AA.  
 DE Pseudomonas aeruginosa polypeptide #9920.  
 PN US651795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 1.0%; Score 7; DB 7; Length 245;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 RESULT 897  
 ID ADC73285 standard; protein; 254 AA.  
 DE Human 187H H protein - SEQ ID 11.  
 PN WO2003060765-A1.  
 PD 24-JUL-2003.  
 PA (AJIN) AJINOMOTO CO INC.  
 PA (UMEX/) UMEYAMA H.  
 Query Match 1.0%; Score 7; DB 7; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 898  
 ID ADK17097 standard; protein; 254 AA.  
 DE Nanorhacheum equitans cancer-associated (CA) protein #524.  
 PN WO2003093434-A2.  
 PD 13-NOV-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 1.0%; Score 7; DB 8; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 899  
 ID ADL05143 standard; protein; 255 AA.  
 DE M. catarrhalis protein #909.  
 PN US673910-B1.  
 PD 06-JAN-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 1.0%; Score 7; DB 8; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 900  
 ID AAU38252 standard; protein; 257 AA.  
 DE Salmonella typhi cellular proliferation protein #143.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 1.0%; Score 7; DB 4; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 901  
 ID ADA35762 standard; protein; 257 AA.  
 DE Actinobacter baumannii protein #2923.  
 PN US6562958-B1.  
 PD 13-MAY-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 1.0%; Score 7; DB 6; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 902  
 ID AAG18807 standard; protein; 258 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 16205.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 1.0%; Score 7; DB 3; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 903  
 ID AAM11545 standard; protein; 259 AA.  
 DE Human thrombin Asn99 mutant.  
 PN WO9641868-A2.  
 PD 27-DEC-1996.  
 PA (IMMO) IMMONO AG.  
 Query Match 1.0%; Score 7; DB 2; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 904  
 ID ABP60565 standard; protein; 259 AA.  
 DE Human thrombin variant W215A/E217A B-chain.  
 PN WO2002100337-A2.  
 PD 19-DEC-2002.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 1.0%; Score 7; DB 6; Length 259;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 905  
 ID ABP60563 standard; protein; 259 AA.  
 DE Human thrombin variant W215A B-chain.  
 PN WO2002100337-A2.  
 PD 19-DEC-2002.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 1.0%; Score 7; DB 6; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 906  
 ID AAW72891 standard; protein; 265 AA.  
 DE Mycobacterium tuberculosis antigen CFP29.  
 PN WO9844119-A1.  
 PD 08-OCT-1998.  
 PA (STAT-) STATENS SERUM INST.  
 Query Match 1.0%; Score 7; DB 2; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 907  
 ID AAY21908 standard; protein; 265 AA.  
 DE Amino acid sequence of antigen CFP29.  
 PN WO9924577-A1.  
 PD 20-MAY-1999.  
 PA (STAT-) STATENS SERUM INST.  
 Query Match 1.0%; Score 7; DB 2; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 908  
 ID AAM41956 standard; protein; 266 AA.  
 DE Flea serine protease SEQ ID NO:24.  
 PN WO9740058-A1.  
 PD 30-OCT-1997.  
 PA (HESK-) HESKA CORP.  
 Query Match 1.0%; Score 7; DB 2; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 909  
 ID AAO17669 standard; protein; 266 AA.  
 DE B tropicalis allergen B1oc 3 protein SEQ ID NO: 4.  
 PN WO200230968-A1.  
 PD 18-APR-2002.  
 PA (UYST-) UNIV SINGAPORE NAT.  
 Query Match 1.0%; Score 7; DB 5; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 910  
 ID AAO17668 standard; protein; 266 AA.  
 DE B tropicalis allergen B1oc 3 protein SEQ ID NO: 2.  
 PN WO200230968-A1.  
 PD 18-APR-2002.  
 PA (UYST-) UNIV SINGAPORE NAT.  
 Query Match 1.0%; Score 7; DB 5; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 911  
 ID AAB62510 standard; protein; 268 AA.  
 DE Flea serine protease PfSP2\_268.  
 PN US6204010-B1.  
 PD 20-MAR-2001.  
 PA (HESK-) HESKA CORP.  
 Query Match 1.0%; Score 7; DB 4; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 912  
 ID ADJ69394 standard; protein; 271 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1200.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match 1.0%; Score 7; DB 7; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 RESULT 913  
 ID ADQ21743 standard; protein; 271 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4563.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 1.0%; Score 7; DB 8; Length 271;



RESULT 923	ID AAR76035 standard; protein; 295 AA.
DE Mutant thrombin R233D.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 924	ID AAR74775 standard; protein; 295 AA.
DE Wild-type thrombin.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 925	ID AAR74780 standard; protein; 295 AA.
DE Mutant thrombin E229W.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 926	ID AAR76036 standard; protein; 295 AA.
DE Mutant thrombin R233F.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 927	ID AAR74777 standard; protein; 295 AA.
DE Mutant thrombin E229D.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 928	ID AAR76034 standard; protein; 295 AA.
DE Mutant thrombin R233N.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 929	ID AAR76040 standard; protein; 295 AA.
DE Mutant thrombin W50K.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 930	ID AAR76037 standard; protein; 295 AA.
DE Mutant thrombin W50C.	
PN WO9513385-A2.	
PD 18-MAY-1995.	
PA (GILE-) GILEAD SCI.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 931	ID AAW22892 standard; protein; 295 AA.
DE Human mature thrombin mutant Gly724Ala.	
PN DE19605126-A1.	
PD 14-AUG-1997.	
PA (BADI ) BASF AG.	
Query Match	1.0%; Score 7; DB 2; Length 295;
Best Local Similarity	100.0%; Pred. No. 1.2e+03;
RESULT 932	

ID AAB08633 standard; protein; 295 AA.  
 DE Amino acid sequence of a wild type human thrombin.  
 PN US6110721-A.  
 PD 29-AUG-2000.  
 PA (GILE-) GILEAD SCI INC.  
 Query Match 1.0%; Score 7; DB 3; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 933  
 ID AAB60562 standard; protein; 295 AA.  
 DE Human thrombin variant W215A.  
 PN WO2002100337-A2.  
 PD 19-DEC-2002.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 1.0%; Score 7; DB 6; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 934  
 ID AAB60564 standard; protein; 295 AA.  
 DE Human thrombin variant W215A/E217A.  
 PN WO2002100337-A2.  
 PD 19-DEC-2002.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 1.0%; Score 7; DB 6; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 935  
 ID ADS11062 standard; protein; 295 AA.  
 DE Human therapeutic protein - SEQ ID 1299.  
 PN WO2004080146-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC.  
 Query Match 1.0%; Score 7; DB 8; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 936  
 ID AAO17678 standard; protein; 296 AA.  
 DE B tropicallis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 40.  
 PN WO200230968-A1.  
 PD 18-APR-2002.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 1.0%; Score 7; DB 5; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 937  
 ID AAO17676 standard; protein; 296 AA.  
 DE B tropicallis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 38.  
 PN WO200230968-A1.  
 PD 18-APR-2002.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 1.0%; Score 7; DB 5; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 938  
 ID AAO17677 standard; protein; 296 AA.  
 DE B tropicallis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 39.  
 PN WO200230968-A1.  
 PD 18-APR-2002.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 1.0%; Score 7; DB 5; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 RESULT 939  
 ID AAW9107 standard; protein; 308 AA.  
 DE Bovine prethrombin 2.  
 PN WO9855130-A1.  
 PD 10-DEC-1998.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 1.0%; Score 7; DB 2; Length 308;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 940  
 ID AAW9109 standard; protein; 308 AA.  
 DE Human prethrombin 2.  
 PN WO9855130-A1.  
 PD 10-DEC-1998.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 1.0%; Score 7; DB 2; Length 308;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 941  
 ID AAB87820 standard; protein; 308 AA.

DE Mouse T2R26 amino acid sequence SEQ ID NO:155.  
 PN WO200118050-A2.  
 PD 15-MAR-2001.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 1.0%; Score 7; DB 4; Length 308;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 942  
 ID ADP29216 standard; protein; 308 AA.  
 DE Taste receptor modulation-related mouse T2R26 protein sequence SeqID155.  
 PN WO2004069191-A2.  
 PD 19-AUG-2004.  
 PA (SENO-) SENOMYX INC.  
 Query Match 1.0%; Score 7; DB 8; Length 308;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 943  
 ID ADC94558 standard; protein; 310 AA.  
 DE E. faecium protein sequence SEQ ID 4185.  
 PN US6583275-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 1.0%; Score 7; DB 7; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 944  
 ID ABR52886 standard; protein; 312 AA.  
 DE Protein sequence #SEQ ID 637.  
 PN EPI258494-A1.  
 PD 20-NOV-2002.  
 PA (CELL-) CELLZOME AG.  
 Query Match 1.0%; Score 7; DB 6; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 945  
 ID ADK62400 standard; protein; 312 AA.  
 DE Disease treating protein complex-derived protein #326.  
 PN EPI338608-A2.  
 PD 27-AUG-2003.  
 PA (CELL-) CELLZOME AG.  
 Query Match 1.0%; Score 7; DB 7; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 946  
 ID ADC73300 standard; protein; 313 AA.  
 DE Stereostucture-related IBTH protein.  
 PN WO2003060765-A1.  
 PD 24-JUL-2003.  
 PA (AJIN) AJINOMOTO CO INC.  
 Query Match 1.0%; Score 7; DB 7; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 947  
 ID AAB72885 standard; protein; 314 AA.  
 DE Murine ztrypl.  
 PN WO200112788-A2.  
 PD 22-FEB-2001.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Query Match 1.0%; Score 7; DB 4; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 948  
 ID ABU62253 standard; protein; 314 AA.  
 DE Mouse tryptase-like polypeptide Ztryp-1.  
 PN US6514741-B1.  
 PD 04-FEB-2003.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Query Match 1.0%; Score 7; DB 6; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 949  
 ID ABR62454 standard; protein; 314 AA.  
 DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIT) ELITLY & CO ELT.  
 Query Match 1.0%; Score 7; DB 7; Length 314;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 RESULT 950

ID ABR62456 standard; protein; 314 AA.  
DE Bovine Factor Xa activated recombinant prethrombin-2.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 951

ID ABR62453 standard; protein; 314 AA.  
DE Bovine thrombin.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 952

ID ABR62450 standard; protein; 314 AA.  
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 953

ID ADC17377 standard; protein; 314 AA.  
DE Mouse serine protease ztrypl.  
PN US2003119035-A1.  
PD 26-JUN-2003.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 954

ID ABP41695 standard; protein; 324 AA.  
DE Human ovarian antigen HNTB23, SEQ ID NO:2827.  
PN W0200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 324;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 955

ID ADS27176 standard; protein; 330 AA.  
DE Bacterial polypeptide #16209.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 956

ID ADS26796 standard; protein; 330 AA.  
DE Bacterial polypeptide #15829.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 957

ID AAB87793 standard; protein; 332 AA.  
DE Rat T2R13 amino acid sequence SEQ ID NO:101.  
PN W0200118050-A2.  
PD 15-MAR-2001.  
PA (PRGC ) UNIV CALIFORNIA.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 1.0%; Score 7; DB 4; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 958

ID ADR29162 standard; protein; 332 AA.  
DE Taste receptor modulation-related rat T2R13 protein sequence SeqID101.  
PN W02004069191-A2.  
PD 19-AUG-2004.  
PA (SENO-) SENOMYX INC.  
Query Match 1.0%; Score 7; DB 8; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 959

ID ADS26428 standard; protein; 332 AA.  
DE Bacterial polypeptide #15461.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 960

ID ADJ49544 standard; protein; 336 AA.  
DE Oil-associated gene related protein #1044.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 336;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 961

ID ADJ49561 standard; protein; 338 AA.  
DE Oil-associated gene related protein #1061.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 338;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 962

ID ADC31358 standard; protein; 357 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1440.  
PN W02003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 7; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 963

ID ADR09339 standard; protein; 357 AA.  
DE Human protein useful for treating neurological disease Seq 2845.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.0%; Score 7; DB 8; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 964

ID ABR62452 standard; protein; 362 AA.  
DE Bovine recombinant prethrombin-2, expressed in CHO cells.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 362;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 965

ID AAY38815 standard; protein; 375 AA.  
DE Neisseria meningitidis strain A antigen encoded by ORF146.  
PN W09924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.

Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 375;  
RESULT 966  
ID AAY38814 standard; protein; 375 AA.  
DE Neisseria meningitidis antigen encoded by ORF146.  
PN W09924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 375;  
RESULT 967  
ID AAY38817 standard; protein; 375 AA.  
DE Neisseria gonorrhoeae antigenic protein encoded by ORF146.  
PN W09924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 375;  
RESULT 968  
ID AAY75445 standard; protein; 375 AA.  
DE Neisseria gonorrhoeae ORF 706 protein sequence SEQ ID NO:2364.  
PN W09957280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 375;  
RESULT 969  
ID AAY75446 standard; protein; 375 AA.  
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2366.  
PN W09957280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 375;  
RESULT 970  
ID AAY75447 standard; protein; 375 AA.  
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2368.  
PN W09957280-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 375;  
RESULT 971  
ID AAY72957 standard; protein; 375 AA.  
DE Neisseria meningitidis virulence protein #47.  
PN W0200185772-A2.  
PD 15-NOV-2001.  
PA (MICR-) MICROSCIENCE LTD.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 5; Length 375;  
RESULT 972  
ID AAR41797 standard; protein; 376 AA.  
DE CD4/thrombin fusion protein.  
PN W09318162-A1.  
PD 16-SEP-1993.  
PA (CREA-) CREGEN INC.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 376;  
RESULT 973  
ID AAY42789 standard; protein; 376 AA.  
DE Human CD4/thrombin fusion protein.  
PN US5961973-A.  
PD 05-OCT-1999.  
PA (CREA/) CREMA R.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 376;  
RESULT 974  
ID AAU10703 standard; protein; 376 AA.  
DE Human CD4-thrombin fusion protein.  
PN US6287561-B1.  
PD 11-SEP-2001.  
PA (CREA/) CREMA R.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 5; Length 376;  
RESULT 975  
ID AAG21667 standard; protein; 398 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24304.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 398;  
RESULT 976  
ID AB080228 standard; protein; 399 AA.  
DE Pseudomonas aeruginosa polypeptide #12403.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 399;  
RESULT 977  
ID AAY38816 standard; protein; 409 AA.  
DE Neisseria gonorrhoeae antigen encoded by partial ORF146.  
PN W09924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 409;  
RESULT 978  
ID ABP80460 standard; protein; 409 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 7450.  
PN W0200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 6; Length 409;  
RESULT 979  
ID ABP79601 standard; protein; 409 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 5732.  
PN W0200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 6; Length 409;  
RESULT 980  
ID ABP37254 standard; protein; 409 AA.  
DE Protein encoded by prokaryotic essential gene #22781.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 6; Length 409;  
RESULT 981  
ID ADD15316 standard; protein; 420 AA.  
DE Fruitfly odourant receptor protein (Seqid 68).  
PN W02003020913-A2.  
PD 13-MAR-2003.  
PA (SENT-) SENTIGEN CORP.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 420;  
RESULT 982  
ID AB065926 standard; protein; 422 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12443.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 422;  
RESULT 983  
ID AAB03444 standard; protein; 426 AA.  
DE Candida albicans essential growth protein #2.  
PN W0200034481-A2.  
PD 15-JUN-2000.  
PA (JANC) JANSSEN PHARM NV.

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Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 426;
RESULT 984
ID ABO61095 standard; protein; 437 AA.
DE Klebsiella pneumoniae polypeptide seqid 7612.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENC-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 7; Length 437;
RESULT 985
ID ABU34680 standard; protein; 443 AA.
DE Protein encoded by Prokaryotic essential gene #20207.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 443;
RESULT 986
ID ABU17062 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #2589.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 444;
RESULT 987
ID ADU34407 standard; protein; 448 AA.
DE Acinetobacter baumannii protein #1568.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENC-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 448;
RESULT 988
ID AAG21666 standard; protein; 452 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24303.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 452;
RESULT 989
ID AAB26435 standard; protein; 456 AA.
DE Drosophila melanogaster odorant receptor DOR28.
PN W0200050566-A2.
PD 31-AUG-2000.
PA (UYCO) UNIV COLUMBIA NEW YORK.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 456;
RESULT 990
ID ABB64797 standard; protein; 456 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21183.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 456;
RESULT 991
ID ADJ32828 standard; protein; 459 AA.
DE Human prethrombin protein.
PN US200323414-A1.
PD 18-DEC-2003.
PA (MOOR/) MOORE M D.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 459;
RESULT 992
ID ABG33733 standard; protein; 461 AA.
DE Protein encoded by Prokaryotic essential gene #19260.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 461;
RESULT 993
ID ABU36990 standard; protein; 461 AA.
DE Protein encoded by Prokaryotic essential gene #22517.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 461;
RESULT 994
ID ABB60460 standard; protein; 463 AA.
DE Human cell cycle and proliferation protein CCYPR-8, SEQ ID NO:8.
PN W0200107471-A2.
PD 01-FEB-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 4; Length 463;
RESULT 995
ID ADP23764 standard; protein; 463 AA.
DE PRO polypeptide SEQ ID NO:942.
PN W02004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 463;
RESULT 996
ID ABW73357 standard; protein; 465 AA.
DE Staphylococcus aureus protein #2597.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 465;
RESULT 997
ID ADJ50012 standard; protein; 465 AA.
DE Oil-associated gene related protein #1512.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDENUX J R.
PA (ROGE/) ROGERS J A.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 465;
RESULT 998
ID ADM21085 standard; protein; 467 AA.
DE Bacterial polypeptide #3738.
PN US2003234675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 1.0%; Score 7; DB 8; Length 467;
RESULT 999
ID AAG21665 standard; protein; 469 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24302.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 1.0%; Score 7; DB 3; Length 469;
RESULT 1000
ID ABW72219 standard; protein; 469 AA.
DE Staphylococcus aureus protein #1459.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 1.0%; Score 7; DB 6; Length 469;
RESULT 1001
ID ADK41715 standard; protein; 470 AA.
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DE Soybean amino acid transporter protein.  
 PN W02003066879-A2.  
 PD 14-AUG-2003.  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 Query Match 1.0%; Score 7; DB 7; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 RESULT 1002  
 ID AAY20047 standard; protein; 481 AA.  
 DE B. burgdorferi antigenic protein, t352.aa.  
 PN W09859071-A1.  
 PD 30-DEC-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 Query Match 1.0%; Score 7; DB 2; Length 481;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 RESULT 1003  
 ID AAM68866 standard; protein; 492 AA.  
 DE Photophadus luminescens protein sequence #1963.  
 PN W0200294867-A2.  
 PD 28-NOV-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Query Match 1.0%; Score 7; DB 6; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 RESULT 1004  
 ID ABO84661 standard; protein; 494 AA.  
 DE Mouse cancer-associated protein MP20-004.1.  
 PN W02004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 1.0%; Score 7; DB 8; Length 494;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 RESULT 1005  
 ID AAM72030 standard; protein; 497 AA.  
 DE HSV-2 strain SBS Contig ID 103 ORF#8 protein.  
 PN W09820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 Query Match 1.0%; Score 7; DB 2; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1006  
 ID AAM72132 standard; protein; 497 AA.  
 DE HSV-2 strain SBS Contig ID 16 ORF#8 protein.  
 PN W09820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 Query Match 1.0%; Score 7; DB 2; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1007  
 ID AAY20046 standard; protein; 497 AA.  
 DE B. burgdorferi antigenic protein, f352.aa.  
 PN W09859071-A1.  
 PD 30-DEC-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 Query Match 1.0%; Score 7; DB 2; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1008  
 ID ABP27287 standard; protein; 497 AA.  
 DE Streptococcus polypeptide SEQ ID NO 3750.  
 PN W0200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Query Match 1.0%; Score 7; DB 5; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1009  
 ID ABO23531 standard; protein; 497 AA.  
 DE Borrelia burgdorferi outlier protein #1.  
 PN US200303963-A1.  
 PD 27-FEB-2003.  
 PA (BRAH/) BRAHMACHARI S K.  
 PA (RAMA/) RAMACHANDRAN S.

PA (NAND/) NANDI T.  
 PA (BHIM/) BHIMARAO C.  
 Query Match 1.0%; Score 7; DB 7; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1010  
 ID AAU16169 standard; protein; 498 AA.  
 DE Human novel secreted protein, Seq ID 1122.  
 PN W0200155322-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.0%; Score 7; DB 4; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1011  
 ID ABUS5238 standard; protein; 498 AA.  
 DE Human novel polypeptide #325.  
 PN US2002132753-A1.  
 PD 19-SEP-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 1.0%; Score 7; DB 6; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1012  
 ID ADS41994 standard; protein; 500 AA.  
 DE Bacterial polypeptide #20424.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 1.0%; Score 7; DB 8; Length 500;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1013  
 ID ABU01365 standard; protein; 502 AA.  
 DE S. pneumoniae type 4 strain protein from coding region #940.  
 PN W0200277021-A2.  
 PD 03-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Query Match 1.0%; Score 7; DB 6; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1014  
 ID ABP81378 standard; protein; 502 AA.  
 DE Streptococcus pneumoniae polypeptide SEQ ID NO 295.  
 PN W0200283855-A2.  
 PD 24-OCT-2002.  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 Query Match 1.0%; Score 7; DB 6; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1015  
 ID AAY00189 standard; protein; 503 AA.  
 DE Enterococcus faecalis antigenic polypeptide fragment EF094.  
 PN W09850554-A2.  
 PD 12-NOV-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.0%; Score 7; DB 2; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1016  
 ID ABP43408 standard; protein; 503 AA.  
 DE B. faecalis EF094 antigenic fragment.  
 PN US2002045737-A1.  
 PD 18-APR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 1.0%; Score 7; DB 5; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 RESULT 1017  
 ID ABUS8436 standard; protein; 503 AA.  
 DE E. faecalis novel protein #180.  
 PN US2003017495-A1.  
 PD 23-JAN-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.0%; Score 7; DB 6; Length 503;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1018  
ID ABU13687 standard; protein; 503 AA.  
DE Enterococcus faecalis EF040 polypeptide #180.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 503;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1019  
ID AAB68138 standard; protein; 504 AA.  
DE Amino acid sequence of a partial murine SPG4 polypeptide.  
PN FR278818-A1.  
PD 09-MAR-2001.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 1.0%; Score 7; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1020  
ID AAG29530 standard; protein; 508 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35152.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1021  
ID AUB54588 standard; protein; 509 AA.  
DE Human NOVX polypeptide #47.  
PN WO200281498-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.0%; Score 7; DB 6; Length 509;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1022  
ID ADS22207 standard; protein; 513 AA.  
DE Bacterial polypeptide #11240.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 513;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1023  
ID AAE20968 standard; protein; 517 AA.  
DE Staphylococcus aureus von Willebrand factor binding protein (vwb).  
PN WO200228892-A1.  
PD 11-APR-2002.  
PA (BIOS-) BIOSAPRO AB.  
Query Match 1.0%; Score 7; DB 5; Length 517;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1024  
ID ABUS5877 standard; protein; 518 AA.  
DE Mouse notch ligand jagged 2 protein.  
PN WO20027204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 1.0%; Score 7; DB 6; Length 518;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1025  
ID AAE34033 standard; protein; 518 AA.  
DE Murine notch ligand jagged 2 protein.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 1.0%; Score 7; DB 6; Length 518;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1026  
ID ABO75124 standard; protein; 525 AA.  
DE Pseudomonas aeruginosa polypeptide #7299.  
PN US6551795-B1.

PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1027  
ID ADO26850 standard; protein; 525 AA.  
DE Human receptors and membrane-associated protein, REMAP-40.  
PN WO2004044159-A2.  
PD 27-MAY-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.0%; Score 7; DB 8; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1028  
ID ABB58809 standard; protein; 542 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3219.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 542;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1029  
ID ADN21059 standard; protein; 543 AA.  
DE Bacterial polypeptide #3712.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1030  
ID AUV37798 standard; protein; 553 AA.  
DE Streptococcus pneumoniae cellular proliferation protein #227.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1031  
ID AAM01018 standard; protein; 553 AA.  
DE CFE 17 protein sequence.  
PN WO200149721-A2.  
PD 12-JUL-2001.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 1.0%; Score 7; DB 4; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1032  
ID ABU00989 standard; protein; 553 AA.  
DE S. pneumoniae type 4 strain protein from coding region #558.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 6; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1033  
ID ABU45930 standard; protein; 553 AA.  
DE Protein encoded by prokaryotic essential gene #31457.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1034  
ID ADK48791 standard; protein; 553 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 5306.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 8; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;



RESULT 1035  
ID AAG29529 standard; protein; 555 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35151.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1036  
ID AAU08803 standard; protein; 556 AA.  
DE Human phosphatidyl glycerol phosphate (PGP) synthase.  
PN W0200164895-A2.  
PD 07-SEP-2001.  
PA (MIL-) MILLENNIUM PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1037  
ID ADC14217 standard; protein; 556 AA.  
DE Human enzyme ENZM-23.  
PN W02003042357-A2.  
PD 22-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1038  
ID ADJ57901 standard; protein; 556 AA.  
DE Human 27411 GGP synthase protein.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MIL-) MILLENNIUM PHARM INC.  
Query Match 1.0%; Score 7; DB 8; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1039  
ID ABP61060 standard; protein; 557 AA.  
DE Lactobacillus rhamnosus HN001 polypeptide SEQ ID NO 120.  
PN W0200244383-A1.  
PD 06-JUN-2002.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (VIAL-) VIALACTIA BIOSCIENCE NZ LTD.  
Query Match 1.0%; Score 7; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1040  
ID ADR95837 standard; protein; 558 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4472.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 8; Length 558;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1041  
ID ABP75529 standard; protein; 563 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 713.  
PN W0200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 6; Length 563;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1042  
ID ABU18645 standard; protein; 573 AA.  
DE Protein encoded by prokaryotic essential gene #4172.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 573;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1043  
ID AAR35763 standard; protein; 579 AA.  
DE Prothrombin (PT).  
PN W09309804-A1.  
PD 27-MAY-1993.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1044  
ID AAW11544 standard; protein; 579 AA.  
DE Human prothrombin Aen419 mutant.  
PN W09641868-A2.  
PD 27-DEC-1996.  
PA (IMMO) IMMUNO AG.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1045  
ID AAW11546 standard; protein; 579 AA.  
DE Human prothrombin mutant (generic sequence).  
PN W09641868-A2.  
PD 27-DEC-1996.  
PA (IMMO) IMMUNO AG.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1046  
ID AAW99108 standard; protein; 579 AA.  
DE Human prothrombin.  
PN W09855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1047  
ID ADI33974 standard; protein; 579 AA.  
DE Human meizothrombin analogue mature protein.  
PN W02004007714-A1.  
PD 22-JAN-2004.  
PA (ASAH) ASAH KASEI KK.  
Query Match 1.0%; Score 7; DB 8; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1048  
ID AAM99106 standard; protein; 582 AA.  
DE Bovine prothrombin.  
PN W09855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1049  
ID AAG29528 standard; protein; 582 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35150.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1050  
ID ABR62449 standard; protein; 583 AA.  
DE Bovine recombinant prothrombin, expressed in Escherichia coli.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (BLIT) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 583;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1051  
ID ADS28808 standard; protein; 588 AA.  
DE Bacterial polypeptide #17841.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 588;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1052  
ID ABB66001 standard; protein; 603 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24795.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 603;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1053  
ID AAR38741 standard; protein; 615 AA.  
DE Human prothrombin.  
PN W09313208-A1.  
PD 08-JUL-1993.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 2; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1054  
ID AAR90377 standard; protein; 615 AA.  
DE Human prothrombin.  
PN US5476777-A.  
PD 19-DEC-1995.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 2; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1055  
ID AAR96216 standard; protein; 615 AA.  
DE Human prothrombin.  
PN US5502034-A.  
PD 26-MAR-1996.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 2; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1056  
ID AAB68137 standard; protein; 616 AA.  
DE Amino acid sequence of the human SPG4 polypeptide.  
PN FR2798138-A1.  
PD 09-MAR-2001.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 1.0%; Score 7; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1057  
ID AAM1543 standard; protein; 622 AA.  
DE Human preprothrombin (wild-type).  
PN W09641868-A2.  
PD 27-DEC-1996.  
PA (IMMO ) IMMO AG.  
Query Match 1.0%; Score 7; DB 2; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1058  
ID AAY4956 standard; protein; 622 AA.  
DE Platelet membrane glycoprotein IIa beta subunit protein sequence.  
PN W09950454-A2.  
PD 07-OCT-1999.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 1.0%; Score 7; DB 2; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1059  
ID AAG74671 standard; protein; 622 AA.  
DE Human F2 protein.  
PN W02003016494-A2.  
PD 27-FEB-2003.  
PA (VITI ) VITIVITY INC.  
Query Match 1.0%; Score 7; DB 6; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1060  
ID ADB88551 standard; protein; 622 AA.  
DE Human Factor 2, F2, protein, SEQ ID 2.  
PN W02003029493-A1.  
PD 10-APR-2003.  
PA (VITI ) VITIVITY INC.  
Query Match 1.0%; Score 7; DB 7; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1061  
ID ADL18196 standard; protein; 622 AA.  
DE Human coagulation factor II protein SEQ ID NO:116.  
PN W02003014381-A1.  
PD 20-FEB-2003.  
PA (AARA ) AARAM BIOSYSTEMS INC.  
Query Match 1.0%; Score 7; DB 7; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

RESULT 1062  
ID ADI33975 standard; protein; 622 AA.  
DE Human meizothrombin analogue full-length protein.  
PN W02004007714-A1.  
PD 22-JAN-2004.  
PA (ASAH ) ASAH KASEI KK.  
Query Match 1.0%; Score 7; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1063  
ID ADQ30580 standard; protein; 622 AA.  
DE Pancreas cancer marker - prothrombin precursor.  
PN W02004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO ) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 1.0%; Score 7; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1064  
ID ABR62455 standard; protein; 625 AA.  
DE Bovine preprothrombin.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 625;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1065  
ID ABR62451 standard; protein; 635 AA.  
DE Bovine recombinant prothrombin, expressed in CHO cells.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 635;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1066  
ID ADL27332 standard; peptide; 638 AA.  
DE Amino acid sequence of prethrombin (G4S)3scFvalphaHA.  
PN W02004019878-A2.  
PD 11-MAR-2004.  
PA (COMP ) COMPOUND THERAPEUTICS INC.  
PA (AFEV ) AFEV N B.  
Query Match 1.0%; Score 7; DB 8; Length 638;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1067  
ID ADL27333 standard; peptide; 638 AA.  
DE Amino acid sequence of scHA(G4S)3prethrombin.  
PN W02004019878-A2.  
PD 11-MAR-2004.  
PA (COMP ) COMPOUND THERAPEUTICS INC.  
PA (AFEV ) AFEV N B.  
Query Match 1.0%; Score 7; DB 8; Length 638;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1068  
ID ABB93056 standard; protein; 658 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2267.  
PN W0200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 1.0%; Score 7; DB 5; Length 658;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1069  
ID ABB58511 standard; protein; 683 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2325.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PERE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 683;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1070  
ID AAG30915 standard; protein; 684 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37042.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 684;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Query Match  
RESULT 1071  
ID ABB03731 standard; protein: 696 AA.  
DE Novel human diagnostic protein #3722.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.7e+03; Length 696;  
RESULT 1072  
ID ABB22196 standard; protein: 713 AA.  
DE Protein encoded by Prokaryotic essential gene #7723.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 6; Length 713;  
RESULT 1073  
ID ABB68587 standard; protein: 716 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32553.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 716;  
RESULT 1074  
ID AAB70937 standard; protein: 763 AA.  
DE S. pombe potassium transporter Ttkp protein.  
PN DE19941768-A1.  
PD 15-MAR-2001.  
PA (LICH-) LICHTENBERG-FRATE H.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 763;  
RESULT 1075  
ID ABB70253 standard; protein: 776 AA.  
DE C. neoformans amino acid sequence SEQ ID NO:3297.  
PN W02003052076-A2.  
PD 26-JUN-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 776;  
RESULT 1076  
ID ADS1498 standard; protein: 783 AA.  
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 553.  
PN W02004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA-) UNIV IOWA RES FOUND.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 8; Length 783;  
RESULT 1077  
ID ADI45247 standard; protein: 784 AA.  
DE Rice isoprenoid biosynthesis-associated protein #89.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG-) LANGE B M.  
PA (GHAS-) GHASSEMIAN M.  
PA (BRIG-) BRIGGS S P.  
PA (COOP-) COOPER B.  
PA (GLAZ-) GLAZEBROOK J.  
PA (GOLF-) GOLF S A.  
PA (KATA-) KATAGIRI F.  
PA (KREP-) KREPS J.  
PA (MOUT-) MOUTHAMER T.  
PA (PROV-) PROVART N.  
PA (RICK-) RICKES D.  
PA (ZHUT-) ZHU T.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 8; Length 784;  
RESULT 1078  
ID ABB58512 standard; protein: 787 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2328.  
PN W0200171042-A2.  
PD 27-SEP-2001.

PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 787;  
RESULT 1079  
ID AAG0377 standard; protein: 799 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4131.  
PN EPI108790-A2.  
PD 20-JUN-2001.  
PA (KYOM-) KYOMA HAKKO KOGYO KK.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 799;  
RESULT 1080  
ID ADL65785 standard; protein: 799 AA.  
DE C. glutamicum RXA-associated protein #71.  
PN DE10154177-A1.  
PD 08-MAY-2003.  
PA (BADT-) BASF AG.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 799;  
RESULT 1081  
ID ABO69076 standard; protein: 805 AA.  
DE Pseudomonas aeruginosa polypeptide #1251.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 805;  
RESULT 1082  
ID AAB47019 standard; protein: 808 AA.  
DE A. thaliana DGD1.  
PN CA2307960-A1.  
PD 06-NOV-2000.  
PA (UNMS-) UNIV MICHIGAN STATE.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 808;  
RESULT 1083  
ID ABB92279 standard; protein: 808 AA.  
DE Herbicidially active polypeptide SEQ ID NO 1490.  
PN W0200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 5; Length 808;  
RESULT 1084  
ID ADB95044 standard; protein: 808 AA.  
DE A. thaliana protein 21878 #SEQ ID 42.  
PN W0200308440-A2.  
PD 30-JAN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 808;  
RESULT 1085  
ID ADJ63822 standard; protein: 808 AA.  
DE Plant lipid metabolism protein PK239 SEQ ID NO:24.  
PN W02004013304-A2.  
PD 12-FEB-2004.  
PA (BADT-) BASF PLANT SCI GMEH.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 8; Length 808;  
RESULT 1086  
ID AAM07872 standard; protein: 859 AA.  
DE Aluminum resistance gene ALR1.  
PN W09634959-A1.  
PD 07-NOV-1996.  
PA (AUCC-) AUCCLAND UNISERVICES LTD.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 859;  
RESULT 1087  
ID ADB08613 standard; protein: 892 AA.  
DE Novel protein (useful for identifying genetic disorders) #768.  
PN W02003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.

Query Match 1.0%; Score 7; DB 7; Length 892;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1088  
ID ADE31112 standard; protein; 912 AA.  
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 244.  
PN WO2003062376-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 912;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
RESULT 1089  
ID ABB65063 standard; protein; 921 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21981.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 921;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
RESULT 1090  
ID ABB62769 standard; protein; 984 AA.  
DE Protein fragment #6 of S. roseosporus biosynthetic gene cluster.  
PN WO200259322-A2.  
PD 01-AUG-2002.  
PA (MIAO/) MIAO V P W.  
PA (BRJA/) BRIAN P.  
PA (BALU/) BALUTZ R H.  
PA (SILV/) SILVA C J.  
Query Match 1.0%; Score 7; DB 5; Length 984;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
RESULT 1091  
ID ADJ72180 standard; protein; 984 AA.  
DE Streptomyces roseosporus daptomycin biosynthesis gene cluster protein #6.  
PN WO2003014297-A2.  
PD 20-FEB-2003.  
PA (CUBI-) CUBIST PHARM INC.  
Query Match 1.0%; Score 7; DB 7; Length 984;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
RESULT 1092  
ID ADM57327 standard; protein; 995 AA.  
DE Recombinant protein production method related polypeptide SEQ ID NO: 8.  
PN WO2004027067-A2.  
PD 01-APR-2004.  
PA (CYMO-) CYMAP AS.  
Query Match 1.0%; Score 7; DB 8; Length 995;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
RESULT 1093  
ID ABB93966 standard; protein; 1047 AA.  
DE Herbicidially active polypeptide SEQ ID NO 3177.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match 1.0%; Score 7; DB 5; Length 1047;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
RESULT 1094  
ID ABM83005 standard; protein; 1061 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3254.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.0%; Score 7; DB 8; Length 1061;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1095  
ID AAY00188 standard; protein; 1074 AA.  
DE Enterococcus faecalis protein EF094.  
PN WO9850554-A2.  
PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 2; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1096  
ID AAY00206 standard; protein; 1074 AA.  
DE Enterococcus faecalis protein EF102.  
PN WO9850554-A2.

PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 2; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1097  
ID ABB43425 standard; protein; 1074 AA.  
DE E faecalis EF102 protein.  
PN US2002045737-A1.  
PD 18-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1098  
ID ABB43407 standard; protein; 1074 AA.  
DE E faecalis EF094 protein.  
PN US2002045737-A1.  
PD 18-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1099  
ID ABU88435 standard; protein; 1074 AA.  
DE E. faecalis novel protein #179.  
PN US2003017495-A1.  
PD 23-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1100  
ID ABU88453 standard; protein; 1074 AA.  
DE E. faecalis novel protein #197.  
PN US2003017495-A1.  
PD 23-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1101  
ID ABU13686 standard; protein; 1074 AA.  
DE Enterococcus faecalis EF040 polypeptide #179.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1102  
ID ABU13704 standard; protein; 1074 AA.  
DE Enterococcus faecalis EF040 polypeptide #197.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1103  
ID ADH87879 standard; protein; 1096 AA.  
DE Enterococcus faecalis polypeptide #2359.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 1.0%; Score 7; DB 7; Length 1096;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1104  
ID AAE37912 standard; protein; 1104 AA.  
DE Human CGDD-1 protein.  
PN WO2003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 1104;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1105  
ID AAY9613 standard; protein; 1140 AA.  
DE Streptococcus pneumoniae UvrA-like protein.  
PN GB2345288-A.

PD 05-JUL-2000.  
PA (GLAXO) GLAXO GROUP LTD.  
Query Match 1.0%; Score 7; DB 3; Length 1140;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
RESULT 1106  
ID ADR88899 standard; protein; 1158 AA.  
DE Anopheles chloester-containing protein (TEP) 16 sequence.  
PN EP1452184-A1.  
PD 01-SEP-2004.  
PA (EMBL-) EMBL.  
Query Match 1.0%; Score 7; DB 8; Length 1158;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
RESULT 1107  
ID ABB66758 standard; protein; 1240 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 27066.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 1240;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1108  
ID ADR88898 standard; protein; 1340 AA.  
DE Anopheles chloester-containing protein (TEP) 1 sequence.  
PN EP1452184-A1.  
PD 01-SEP-2004.  
PA (EMBL-) EMBL.  
Query Match 1.0%; Score 7; DB 8; Length 1340;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1109  
ID AAY77195 standard; protein; 1346 AA.  
DE S. venezuelae macrolide biosynthetic enzyme PIKATV, SEQ ID NO:37.  
PN W020000620-A2.  
PD 06-JAN-2000.  
PA (MINT) UNIV MINNESOTA.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1110  
ID AAY77203 standard; protein; 1346 AA.  
DE S. venezuelae pik (macrolide biosynthesis) gene cluster protein #4.  
PN W020000620-A2.  
PD 06-JAN-2000.  
PA (MINT) UNIV MINNESOTA.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1111  
ID AAB18640 standard; protein; 1346 AA.  
DE Amino acid sequence of narbonolide synthase subunit 4 (PICATV).  
PN US6117659-A.  
PD 12-SEP-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1112  
ID AAY67204 standard; protein; 1346 AA.  
DE Narbonolide synthase subunit 4 (PICATV) protein sequence.  
PN W09961599-A2.  
PD 02-DEC-1999.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1113  
ID ABG71664 standard; protein; 1346 AA.  
DE S. venezuelae narbonolide synthase subunit 4, PICATV.  
PN W0200297062-A2.  
PD 05-DEC-2002.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 6; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1114  
ID ADA09403 standard; protein; 1346 AA.  
DE S. venezuelae narbonolide synthase subunit 4 (PICATV).  
PN US6509455-B1.  
PD 21-JAN-2003.

PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 6; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1115  
ID ADH53447 standard; protein; 1346 AA.  
DE Streptomyces venezuelae narbonolide synthase subunit 4 protein, PICATV.  
PN US2003162262-A1.  
PD 28-AUG-2003.  
PA (ASHL/) ASHLEY G.  
PA (BETL/) BETLACH M. C.  
PA (BETL/) BETLACH M.  
PA (MCDA/) MCDANIEL R.  
PA (TANG/) TANG L.  
Query Match 1.0%; Score 7; DB 7; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1116  
ID ADJ1922 standard; protein; 1346 AA.  
DE Streptomyces macrolide biosynthetic protein - PIKIV.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER/) SHERMAN D H.  
PA (LIU/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 1.0%; Score 7; DB 8; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1117  
ID ABR53267 standard; protein; 1522 AA.  
DE Protein sequence #SEQ ID 1399.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Query Match 1.0%; Score 7; DB 6; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1118  
ID ADK63630 standard; protein; 1522 AA.  
DE Disease treating protein complex-derived protein #838.  
PN EP1338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZOME AG.  
Query Match 1.0%; Score 7; DB 7; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1119  
ID ADM35845 standard; protein; 1522 AA.  
DE Yeast Okazaki fragment endonuclease Dna2.  
PN KR2002072712-A.  
PD 18-SEP-2002.  
PA (SEORY/) SEO Y S.  
Query Match 1.0%; Score 7; DB 7; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1120  
ID ADS43628 standard; protein; 1522 AA.  
DE Bacterial polypeptide #22058.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1121  
ID ABP28343 standard; protein; 1631 AA.  
DE Streptococcus polypeptide SEQ ID NO 5862.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GRNO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 5; Length 1631;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
RESULT 1122  
ID ADG71666 standard; protein; 1666 AA.

DE Chlamydomonas reinhardtii PRB1 protein, SEQ ID NO:1.  
PN JP2003265186-A.  
PD 24-SEP-2003.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
PA (UYTY ) UNIV TOKYO.  
Query Match 1.0%; Score 7; DB 7; Length 166;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
RESULT 1123  
ID ABM65038 standard; protein; 1862 AA.  
DE Human diagnostic and therapeutic protein SEQ ID NO:5287.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.0%; Score 7; DB 8; Length 1862;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
RESULT 1124  
ID ABB62819 standard; protein; 1963 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15249.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 1963;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
RESULT 1125  
ID AD059382 standard; protein; 2910 AA.  
DE Human cancer-associated (CA) protein sequence SEQ ID NO:18.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.0%; Score 7; DB 8; Length 2910;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1126  
ID ADU56630 standard; protein; 2911 AA.  
DE Lung cancer-associated polypeptide #223.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.0%; Score 7; DB 6; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1127  
ID ABO07259 standard; protein; 2911 AA.  
DE Human p53 modifying protein, SEQ ID 219.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.0%; Score 7; DB 6; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1128  
ID ADJ68615 standard; protein; 2911 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID421.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.0%; Score 7; DB 7; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1129  
ID ADN38844 standard; protein; 2911 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:162.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.0%; Score 7; DB 7; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1130  
ID ADQ18204 standard; protein; 2911 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1021.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.0%; Score 7; DB 8; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1131

ID ABG06402 standard; protein; 2912 AA.  
DE Novel human diagnostic protein #6393.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 4; Length 2912;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1132  
ID AAE20788 standard; protein; 3095 AA.  
DE Rat C3b/C4b complement receptor like protein.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 1.0%; Score 7; DB 5; Length 3095;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
RESULT 1133  
ID AAB23749 standard; protein; 3972 AA.  
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:3.  
PN WO200050605-A1.  
PD 31-AUG-2000.  
PA (KITA ) KITASATO INST.  
Query Match 1.0%; Score 7; DB 3; Length 3972;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
RESULT 1134  
ID AAG65264 standard; protein; 3972 AA.  
DE Streptomyces avermitilis protein SEQ ID NO: 4.  
PN WO200162939-A1.  
PD 30-AUG-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (KITA ) KITASATO INST.  
Query Match 1.0%; Score 7; DB 4; Length 3972;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
RESULT 1135  
ID AAG65268 standard; protein; 3972 AA.  
DE Streptomyces avermitilis protein derivative SEQ ID NO: 8.  
PN WO200162939-A1.  
PD 30-AUG-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (KITA ) KITASATO INST.  
Query Match 1.0%; Score 7; DB 4; Length 3972;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
RESULT 1136  
ID ABB59051 standard; protein; 4547 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3945.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 4547;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
RESULT 1137  
ID ABB65885 standard; protein; 4899 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24447.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 4899;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
RESULT 1138  
ID ADJ91934 standard; protein; 11877 AA.  
DE Streptomyces venezuelae pik gene cluster protein.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER/) SHERMAN D H.  
PA (LITU/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 1.0%; Score 7; DB 8; Length 11877;  
Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
RESULT 1139  
ID AAY77180 standard; protein; 12199 AA.  
DE S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.  
PN WO200000620-A2.  
PD 06-JAN-2000.

PA (MINU ) UNIV MINNESOTA.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 3; Length 12199;  
RESULT 1140  
ID AAR74921 standard; peptide; 8 AA.  
DE Human 193P1E1B protein activator residues 173-180.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 2; Length 8;  
RESULT 1141  
ID ADD99639 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2631.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1142  
ID ADD97076 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 70.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1143  
ID ADD99119 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2111.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1144  
ID ADD99105 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2097.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1145  
ID ADD99567 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2559.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1146  
ID ADD98332 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 1524.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1147  
ID ADD99106 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2058.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1148  
ID ADD97325 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 319.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1149  
ID ADD99783 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2775.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1150  
ID ADD99689 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2681.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1151  
ID ADD98760 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 1752.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1152  
ID ADD99217 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2209.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1153  
ID ADD97053 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 47.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1154  
ID ADD98456 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 1448.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1155  
ID ADD99266 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2258.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1156  
ID ADD97623 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 617.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;  
RESULT 1157  
ID ADD97659 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 653.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 0.8%; Score 6; DB 7; Length 9;



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Best Local Similarity 100.0%; Pred. No. 1.8e+06;
RESULT 1158
ID ADD99515 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2507.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1159
ID ADD9936 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2928.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1160
ID ADD97875 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 869.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1161
ID ADD9933 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2227.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1162
ID ADD9945 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2447.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1163
ID ADD98169 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 1161.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1164
ID ADD99017 standard; peptide; 9 AA.
DE Human 193P1E1B protein peptide fragment 2009.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1165
ID ADO73283 standard; peptide; 9 AA.
DE Human 213P1F11 HLA motif bearing epitope #7382.
PN US200401915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GENW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1166
ID ADO73127 standard; peptide; 9 AA.
DE Human 213P1F11 HLA motif bearing epitope #7226.
PN US200401915-A1.
PD 29-JAN-2004.
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GENW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1167
ID ADP51254 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #1448.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GENW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1168
ID ADP5203 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2227.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GENW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1169
ID ADP52487 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #2561.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GENW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1170
ID ADP49875 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #70.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
PA (GENW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;
RESULT 1171
ID ADP50967 standard; peptide; 9 AA.
DE Human 193P1E1B epitope #1161.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALLITA-EID P M.
PA (FARI/) FARI S.
PA (HUBERT/) HUBERT R S.
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PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1172  
ID ADP52437 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2631.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1173  
ID ADP51917 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2111.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1174  
ID ADP52734 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2928.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1175  
ID ADP52064 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2258.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1176  
ID ADP52313 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2507.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1177  
ID ADP50125 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #319.  
PN US2004102407-A1.

PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1178  
ID ADP51815 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2009.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1179  
ID ADP51903 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2097.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1180  
ID ADP51330 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #1524.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1181  
ID ADP52581 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2775.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1182  
ID ADP52015 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2209.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1183  
ID ADP50125 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #319.  
PN US2004102407-A1.

Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1183  
ID ADP50423 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #617.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1184  
ID ADP50675 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #869.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1185  
ID ADP52365 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2559.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1186  
ID ADP51558 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #1752.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1187  
ID ADP52253 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2447.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1188  
ID ADP49853 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #47.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1189  
ID ADP50459 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #653.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1190  
ID ADP51904 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2098.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1191  
ID AAR59476 standard; peptide; 10 AA.  
DE Neuropeptide for controlling muscle contraction.  
PN JP06100590-A.  
PD 12-APR-1994.  
PA (SUNR ) SUNTORY LTD.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1192  
ID ADP97214 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 208.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1193  
ID ADP98893 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1885.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1194  
ID ADE00146 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3137.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1195  
ID ADP97235 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 229.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1196  
ID ADP97235 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 229.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;

ID ADE00128 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3119.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1197  
ID ADE00321 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3312.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1198  
ID ADE98389 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1381.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1199  
ID ADE00477 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3468.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1200  
ID ADE98046 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1038.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1201  
ID ADE00260 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3251.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1202  
ID ADD97458 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 452.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1203  
ID ADD97779 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 773.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1204  
ID ADD97789 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 783.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1205  
ID ADE00572 standard; peptide; 10 AA.

DE Human 193P1E1B protein peptide fragment 3563.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1206  
ID ADD98579 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1571.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1207  
ID ADD98038 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1030.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1208  
ID ADE00277 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3268.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1209  
ID ADE00419 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3410.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1210  
ID ADE00145 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3136.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1211  
ID ADD97471 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 465.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1212  
ID ADD98312 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1304.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1213  
ID ADE00322 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3313.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1214  
ID ADD97241 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 235.

PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 7; Length 10;  
RESULT 1215  
ID ADD97805 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 799.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 7; Length 10;  
RESULT 1216  
ID ADD97809 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 803.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 7; Length 10;  
RESULT 1217  
ID ADN14200 standard; peptide; 10 AA.  
DE HIV B cell epitope #58.  
PN US2003049253-A1.  
PD 13-MAR-2003.  
PA (UIFO/) LI P Q.  
PA (CHUY/) CHU Y.  
PA (QITU/) QIU J.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 7; Length 10;  
RESULT 1218  
ID ADP53057 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3251.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1219  
ID ADP53216 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3410.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1220  
ID ADP52943 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3137.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1221  
ID ADP53074 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3268.

PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1222  
ID ADP53118 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3312.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1223  
ID ADP50605 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #799.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1224  
ID ADP52942 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3136.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1225  
ID ADP50579 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #773.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 8; Length 10;  
RESULT 1226  
ID ADP52925 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3119.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.

Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1227  
ID ADP50014 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #208.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1228  
ID ADP51691 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #1885.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1229  
ID ADP50035 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #229.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1230  
ID ADP53274 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #3468.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1231  
ID ADP50589 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #783.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1232  
ID ADP50609 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #803.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.

PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1233  
ID ADP53369 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #3563.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1234  
ID ADP50836 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #1030.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1235  
ID ADP51110 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #1304.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1236  
ID ADP50271 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #465.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1237  
ID ADP51377 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #1571.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWV/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1238  
ID ADP50609 standard; peptide: 10 AA.  
DE Human 193P1E1B epitope #803.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.

ID ADP53119 standard; peptide; 10 AA.  
DE Human 193PIE1B eptiope #313.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1239  
ID ADP50041 standard; peptide; 10 AA.  
DE Human 193PIE1B eptiope #235.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1240  
ID ADP50258 standard; peptide; 10 AA.  
DE Human 193PIE1B eptiope #452.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1241  
ID ADP51187 standard; peptide; 10 AA.  
DE Human 193PIE1B eptiope #1381.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1242  
ID ADP50844 standard; peptide; 10 AA.  
DE Human 193PIE1B eptiope #1038.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.3e+02; Length 10;  
RESULT 1243  
ID AAR74926 standard; peptide; 11 AA.  
DE Urea plasmidogen activator residues 173-182.  
PN WO5059908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1244

ID AAR74924 standard; peptide; 11 AA.  
DE Urea plasmidogen activator residues 173-183.  
PN WO5059908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1245  
ID AAB68774 standard; peptide; 11 AA.  
DE Saccharopolyspora polyspora module 1 PKS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1246  
ID AAB68770 standard; peptide; 11 AA.  
DE Rat FAS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1247  
ID AAB68775 standard; peptide; 11 AA.  
DE Streptomyces venezuelae module 1 PKS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1248  
ID AAB68771 standard; peptide; 11 AA.  
DE Human FAS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1249  
ID AAB68772 standard; peptide; 11 AA.  
DE Caenorhabditis elegans FAS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1250  
ID AAB10873 standard; peptide; 11 AA.  
DE Bovine uroplakin II protein fragment (1-11 amino acids).  
PN US6290959-B1.  
PD 18-SEP-2001.  
PA (UTNY) UNIV NEW YORK STATE.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 5.8e+02; Length 11;  
RESULT 1251  
ID AAR74922 standard; peptide; 12 AA.  
DE Urea plasmidogen activator residues 173-183.  
PN WO5059908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Length 12;  
RESULT 1252  
ID AAW88589 standard; protein; 12 AA.  
DE Secreted protein encoded by gene 56 clone HE20F09.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 6.2e+02; Length 12;  
RESULT 1253  
ID ABB50356 standard; protein; 12 AA.



DE Human secreted protein encoded by gene 56 SEQ ID NO:304.  
PN W0200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1254  
ID ABR38980 standard; peptide: 12 AA.  
DE Human topoisomerase II alpha inhibitory protein. fragment #SEQ ID 6.  
PN W02003002737-A1.  
PD 09-JAN-2003.  
PA (RIKE) RIKEN KK.  
Query Match 0.8%; Score 6; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1255  
ID ABO44613 standard; protein: 12 AA.  
DE Novel human secreted protein #56.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1256  
ID ABO26093 standard; protein: 12 AA.  
DE Human protein from novel secreted protein gene 56.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1257  
ID AAB01945 standard; peptide: 13 AA.  
DE Human Endothelinase 2 repetitive peptide sequence.  
PN W0200136604-A2.  
PD 25-MAY-2001.  
PA (CORV-) CORVAS INT INC.  
Query Match 0.8%; Score 6; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1258  
ID MAG98215 standard; peptide: 14 AA.  
DE Human SNP associated peptide SEQ ID NO. 857.  
PN W0200148245-A2.  
PD 05-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1259  
ID AAB56899 standard; peptide: 14 AA.  
DE Human SNP related amino acid sequence SEQ ID NO:1464.  
PN W0200138586-A2.  
PD 31-MAY-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1260  
ID ABG67423 standard; peptide: 14 AA.  
DE Human ADP1 tryptic digest peptide #132.  
PN W0200246767-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
Query Match 0.8%; Score 6; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1261  
ID ADA23531 standard; peptide: 14 AA.  
DE Alzheimer's disease-associated protein isoform tryptic peptide #140.  
PN US2003064411-A1.  
PD 03-APR-2003.  
PA (HERA/) HERATH H M A C.  
PA (PARE/) PAREKH R B.  
PA (ROHL/) ROHLFF C.  
Query Match 0.8%; Score 6; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1262

ID ADN14199 standard; peptide: 14 AA.  
DE HIV B cell epitope #57.  
PN US2003049253-A1.  
PD 13-MAR-2003.  
PA (LIFQ/) LI F Q.  
PA (CHUY/) CHU Y.  
PA (QIUJ/) QIU J.  
Query Match 0.8%; Score 6; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1263  
ID ADO34385 standard; peptide: 14 AA.  
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 162.  
PN W02004043403-A2.  
PD 27-MAY-2004.  
PA (UABR-) UAB RES FOUND.  
Query Match 0.8%; Score 6; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1264  
ID ADO34421 standard; peptide: 14 AA.  
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 198.  
PN W02004043403-A2.  
PD 27-MAY-2004.  
PA (UABR-) UAB RES FOUND.  
Query Match 0.8%; Score 6; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1265  
ID AAG78745 standard; peptide: 15 AA.  
DE Human ribose phosphate glycine amide synthetase 12 N-terminus.  
PN W0200173065-A1.  
PD 04-OCT-2001.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 0.8%; Score 6; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1266  
ID ADE00866 standard; peptide: 15 AA.  
DE Human 193P1B1B protein peptide fragment 3857.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1267  
ID ADE00911 standard; peptide: 15 AA.  
DE Human 193P1B1B protein peptide fragment 3902.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1268  
ID ADE01040 standard; peptide: 15 AA.  
DE Human 193P1B1B protein peptide fragment 4031.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1269  
ID ADE00912 standard; peptide: 15 AA.  
DE Human 193P1B1B protein peptide fragment 3903.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1270  
ID ADE00664 standard; peptide: 15 AA.  
DE Human 193P1B1B protein peptide fragment 3655.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1271

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RESULT 1271
ID ADE00810 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 3801.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1272
ID ADE00966 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 3957.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1273
ID ADE01108 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 4099.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1274
ID ADE01070 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 4061.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1275
ID ADE00825 standard; peptide; 15 AA.
DE Human 193P1E1B protein peptide fragment 3816.
PN WO2003050255-A2.
PD 19-JUN-2003.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1276
ID ADP53709 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3903.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1277
ID ADP53622 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3816.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1278
ID ADP53837 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #4031.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1279
ID ADP53663 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3857.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1280
ID ADP53763 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3957.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1281
ID ADP53461 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #3655.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1282
ID ADP53905 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #4099.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1283
ID ADP53867 standard; peptide; 15 AA.
DE Human 193P1E1B epitope #4061.
PN US2004102407-A1.
PD 27-MAY-2004.
PA (RAIT/) RAITANO A B.
PA (CHAL/) CHALILITA-EID P M.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Length 15;
RESULT 1284
ID ADP53607 standard; peptide; 15 AA.
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DE Human 193P1E1B epitope #3801.  
 PN US2004102407-A1.  
 PD 27-MAY-2004.  
 PA (RAIT/) RAITANO A B.  
 PA (CHAL/) CHALLITA-EID P M.  
 PA (FARI/) FARI S M.  
 PA (HUBE/) HUBERT R S.  
 PA (GEWM/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 Query Match 0.8%; Score 6; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 RESULT 1285  
 ID ADP53708 standard; peptide; 15 AA.  
 DE Human 193P1E1B epitope #3902.  
 PN US2004102407-A1.  
 PD 27-MAY-2004.  
 PA (RAIT/) RAITANO A B.  
 PA (CHAL/) CHALLITA-EID P M.  
 PA (FARI/) FARI S M.  
 PA (HUBE/) HUBERT R S.  
 PA (GEWM/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 Query Match 0.8%; Score 6; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 RESULT 1286  
 ID AAR83658 standard; peptide; 17 AA.  
 DE Insect haemolymph antibacterial polypeptide #8.  
 PN WO9523513-A1.  
 PD 08-SEP-1995.  
 PA (SLOK/) SLOAN KETTERING INST CANCER RES.  
 Query Match 0.8%; Score 6; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 RESULT 1287  
 ID AAR74918 standard; peptide; 18 AA.  
 DE Urea plasmidogen activator residues 163-180.  
 PN WO9509908-A1.  
 PD 13-APR-1995.  
 PA (SUMO/) SUMITOMO PHARM CO LTD.  
 Query Match 0.8%; Score 6; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 RESULT 1288  
 ID AAR95973 standard; peptide; 18 AA.  
 DE Wasp venom BrTx-1 subunit (b) N-terminal peptide.  
 PN WO9616171-A1.  
 PD 30-MAY-1996.  
 PA (ZENE/) ZENECA LTD.  
 PA (CSIR/) COMMONWEALTH SCI & IND RES ORG.  
 Query Match 0.8%; Score 6; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 9e+02;  
 RESULT 1289  
 ID ADI29454 standard; peptide; 19 AA.  
 DE ErbB ligand HB-BGF CcY/F motif peptide.  
 PN WO2004005320-A2.  
 PD 15-JAN-2004.  
 PA (UMOR/) UNIV MISSOURI.  
 Query Match 0.8%; Score 6; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 RESULT 1290  
 ID AAR83657 standard; peptide; 20 AA.  
 DE Insect haemolymph antibacterial polypeptide #7.  
 PN WO9523513-A1.  
 PD 08-SEP-1995.  
 PA (SLOK/) SLOAN KETTERING INST CANCER RES.  
 Query Match 0.8%; Score 6; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 RESULT 1291  
 ID ABU08144 standard; peptide; 20 AA.  
 DE Human IL-1 RI signal peptide.  
 PN GB2375604-A.  
 PD 20-NOV-2002.  
 PA (WARN/) WARNER LAMBERT CO.  
 Query Match 0.8%; Score 6; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;

RESULT 1292  
 ID ADG17865 standard; peptide; 20 AA.  
 DE Binding affinity measurement-related peptide Segid67.  
 PN WO2003089662-A1.  
 PD 30-OCT-2003.  
 PA (REGC/) UNIV CALIFORNIA.  
 Query Match 0.8%; Score 6; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 RESULT 1293  
 ID ADK52540 standard; peptide; 20 AA.  
 DE Fungal mycotoxin biosynthetic protein consensus sequence #2.  
 PN EPI329521-A1.  
 PD 23-JUL-2003.  
 PA (EVIA/) EVIALIS T.  
 Query Match 0.8%; Score 6; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 RESULT 1294  
 ID ADN14077 standard; peptide; 20 AA.  
 DE HIV helper T cell epitope #44.  
 PN US2003049253-A1.  
 PD 13-MAR-2003.  
 PA (LIFO/) LI F O.  
 PA (CHUY/) CHU Y.  
 PA (QIU/) QIU J.  
 Query Match 0.8%; Score 6; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 RESULT 1295  
 ID ADN14201 standard; peptide; 20 AA.  
 DE HIV B cell epitope #59.  
 PN US2003049253-A1.  
 PD 13-MAR-2003.  
 PA (LIFO/) LI F O.  
 PA (CHUY/) CHU Y.  
 PA (QIU/) QIU J.  
 Query Match 0.8%; Score 6; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
 RESULT 1296  
 ID AAB89179 standard; peptide; 21 AA.  
 DE HIV gp120 protein binding peptide #272.  
 PN WO200116182-A2.  
 PD 08-MAR-2001.  
 PA (USSH/) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 0.8%; Score 6; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 RESULT 1297  
 ID AAB89181 standard; peptide; 21 AA.  
 DE HIV gp120 protein binding peptide #274.  
 PN WO200116182-A2.  
 PD 08-MAR-2001.  
 PA (USSH/) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 0.8%; Score 6; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 RESULT 1298  
 ID AAB89180 standard; peptide; 21 AA.  
 DE HIV gp120 protein binding peptide #273.  
 PN WO200116182-A2.  
 PD 08-MAR-2001.  
 PA (USSH/) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 0.8%; Score 6; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 RESULT 1299  
 ID AAU89796 standard; peptide; 21 AA.  
 DE Insulin/insulin-like growth factor receptor-binding peptide #1752.  
 PN WO200172771-A2.  
 PD 04-OCT-2001.  
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
 PA (NOVO/) NOVO NORDISK AS.  
 Query Match 0.8%; Score 6; DB 5; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 RESULT 1300  
 ID AAU89556 standard; peptide; 21 AA.  
 DE Insulin/insulin-like growth factor receptor-binding peptide #1512.  
 PN WO200172771-A2.

PD 04-OCT-2001.  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 0.8%; Score 6; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1301  
ID AAM18205 standard; protein; 22 AA.  
DE Peptide #4639 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1302  
ID AAM47407 standard; peptide; 22 AA.  
DE Peptide #37 for illustrating method of anticipating protein interaction.  
PN WO200167299-A1.  
PD 13-SEP-2001.  
PA (DAUC) DAICHI PHARM CO LTD.  
PA (FUT) FUJITSU LTD.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1303  
ID ABB31987 standard; peptide; 22 AA.  
DE Peptide #4638 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1304  
ID ABB2530 standard; protein; 22 AA.  
DE Protein #4529 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1305  
ID AAM70365 standard; protein; 22 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30671.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1306  
ID AAM57939 standard; protein; 22 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30044.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1307  
ID AAG52060 standard; peptide; 22 AA.  
DE Human liver peptide; SEQ ID NO 30708.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1308  
ID AAM05822 standard; protein; 22 AA.  
DE Peptide #4504 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1309  
ID AAG28549 standard; protein; 22 AA.  
DE Novel human diagnostic protein #28540.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1310  
ID AAG40009 standard; peptide; 22 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29674.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1311  
ID AAO20901 standard; peptide; 22 AA.  
DE Swine fever envelope protein E2 fragment #5.  
PN WO200232453-A1.  
PD 25-APR-2002.  
PA (UYOI) UNIV QINGHUA.  
PA (BEID-) BEIJING FEIKAI BIOTECH CO LTD.  
Query Match 0.8%; Score 6; DB 5; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1312  
ID AAM19926 standard; protein; 23 AA.  
DE Peptide #6360 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1313  
ID ABB39934 standard; peptide; 23 AA.  
DE Peptide #7440 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1314  
ID AAM33553 standard; protein; 23 AA.  
DE Peptide #7590 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1315  
ID ABB24479 standard; protein; 23 AA.  
DE Protein #6478 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1316  
ID AAM73351 standard; protein; 23 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33657.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1317  
ID AAM60679 standard; protein; 23 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32784.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1318  
ID AAG55067 standard; peptide; 23 AA.  
DE Human liver peptide; SEQ ID NO 33715.

PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1319  
ID ABG43204 standard; peptide; 23 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32869.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1320  
ID AAP93093 standard; peptide; 25 AA.  
DE CD4 anti-receptor peptide.  
PN W08909782-A.  
PD 19-OCT-1989.  
PA (USDC) US SEC OF COMMERCE.  
Query Match 0.8%; Score 6; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1321  
ID AAR74927 standard; peptide; 25 AA.  
DE Urea plasmidogen activator residues 163-186.  
PN W09509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1322  
ID AAR71483 standard; peptide; 25 AA.  
DE *Escherichia chaffeensis* P28 protein N-terminal signal peptide.  
PN W0200032745-A2.  
PD 08-JUN-2000.  
PA (RERE-) RES DEV FOUND.  
Query Match 0.8%; Score 6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1323  
ID AAR96113 standard; peptide; 25 AA.  
DE *Escherichia chaffeensis* P28 N-terminal signal peptide.  
PN W020022782-A2.  
PD 21-MAR-2002.  
PA (RERE-) RES DEV FOUND.  
Query Match 0.8%; Score 6; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1324  
ID ADR84080 standard; peptide; 26 AA.  
DE *S. Pyogenes* hyperimmune system reactive antigen SPO0287.4.  
PN W02004078907-A2.  
PD 16-SEP-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 0.8%; Score 6; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1325  
ID AAR11853 standard; peptide; 27 AA.  
DE Eel natrituretic peptide.  
PN JP03074400-A.  
PD 28-MAR-1991.  
PA (SMIB-) SMI BRYSTOL KK.  
PA (SUMU) SUMITOMO METAL IND LTD.  
Query Match 0.8%; Score 6; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1326  
ID AAB91306 standard; peptide; 27 AA.  
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:482.  
PN W0200069900-A2.  
PD 23-NOV-2000.  
PA (CONU-) CONJUCHEM INC.  
Query Match 0.8%; Score 6; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1327  
ID AAB91315 standard; peptide; 27 AA.  
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:491.

PN W0200069900-A2.  
PD 23-NOV-2000.  
PA (CONU-) CONJUCHEM INC.  
Query Match 0.8%; Score 6; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1328  
ID AAB91325 standard; peptide; 27 AA.  
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:501.  
PN W0200069900-A2.  
PD 23-NOV-2000.  
PA (CONU-) CONJUCHEM INC.  
Query Match 0.8%; Score 6; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1329  
ID AAR6346 standard; peptide; 28 AA.  
DE Spacer oligopeptide D28.  
PN JP04190791-A.  
PD 09-JUL-1992.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1330  
ID AAR71663 standard; peptide; 29 AA.  
DE Modified urinary plasmidogen activator residues 159-188.  
PN JP07039374-A.  
PD 10-FEB-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1331  
ID AAR6347 standard; peptide; 30 AA.  
DE Spacer oligopeptide D30.  
PN JP04190791-A.  
PD 09-JUL-1992.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1332  
ID AAR42811 standard; peptide; 30 AA.  
DE U-PA (159-188).  
PN W09320194-A1.  
PD 14-OCT-1993.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1333  
ID AAR72872 standard; peptide; 30 AA.  
DE Urokinase peptide fragment from amino acids 159-188.  
PN JP07075580-A.  
PD 20-MAR-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1334  
ID AAR93589 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS19 residues 276-306.  
PN W09509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1335  
ID AAR93591 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS21 residues 276-306.  
PN W09509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1336  
ID AAR76947 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS16 residues 276-306.  
PN W09509908-A1.

PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1337  
ID AAR76946 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS15 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1338  
ID AAR93592 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS12 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1339  
ID AAR71666 standard; peptide; 30 AA.  
DE Modified urinary plasminogen activator residues 159-188.  
PN JF07039374-A.  
PD 10-FEB-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1340  
ID AAR72874 standard; peptide; 31 AA.  
DE t-PA peptide fragment from amino acids 276-306.  
PN JF07075580-A.  
PD 20-MAR-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1341  
ID AAR71904 standard; peptide; 31 AA.  
DE Wild type tissue plasminogen activator residues 276-306.  
PN JF07039374-A.  
PD 10-FEB-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1342  
ID AAM05988 standard; protein; 31 AA.  
DE Peptide #4670 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1343  
ID AAR24949 standard; peptide; 32 AA.  
DE Urokinase fragment.  
PN JF04144682-A.  
PD 19-MAY-1992.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1344  
ID AAM16011 standard; protein; 33 AA.  
DE Peptide #2445 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1345  
ID ABB35004 standard; peptide; 33 AA.  
DE Peptide #2510 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1346  
ID AAM28512 standard; protein; 33 AA.  
DE Peptide #2549 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1347  
ID ABB20416 standard; protein; 33 AA.  
DE Protein #2415 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1348  
ID AAM68189 standard; protein; 33 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28495.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1349  
ID AAO00415 standard; protein; 33 AA.  
DE Human polypeptide SEQ ID NO 14307.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1350  
ID AAM55815 standard; protein; 33 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27920.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1351  
ID ABB49840 standard; peptide; 33 AA.  
DE Human liver peptide, SEQ ID NO 28488.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1352  
ID AAM03745 standard; protein; 33 AA.  
DE Peptide #2427 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1353  
ID ABB72758 standard; peptide; 33 AA.  
DE Anticancer peptide derived from human thrombin.  
PN WO2003013569-A2.  
PD 20-FEB-2003.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 0.8%; Score 6; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1354  
ID ABB72759 standard; peptide; 33 AA.  
DE Anticancer peptide derived from human thrombin.  
PN WO2003013569-A2.  
PD 20-FEB-2003.  
PA (TEXA) UNIV TEXAS SYSTEM.

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Query Match          0.8%; Score 6; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
RESULT 1355
ID AAR74068 standard; peptide: 35 AA.
DE Superantigen peptide HIV Nef(31-65).
PN WO9511975-A2.
PD 04-MAY-1995.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1356
ID AAY3987 standard; peptide: 35 AA.
DE HIV Negative factor (Nef) protein residues 31-65.
PN US5968514-A.
PD 19-OCT-1999.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1357
ID ABU61264 standard; peptide: 35 AA.
DE Human A domain from APOBR2 #7.
PN WO200288171-A2.
PD 07-NOV-2002.
PA (MAXY-) MAXYGEN INC.
Query Match          0.8%; Score 6; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1358
ID ADP21486 standard; peptide: 35 AA.
DE Human LDL receptor A domain peptide SeqID 62.
PN WO2004044011-A2.
PD 27-MAY-2004.
PA (AVID-) AVIDIA RES INST.
Query Match          0.8%; Score 6; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1359
ID AAO02449 standard; protein: 36 AA.
DE Human polypeptide SEQ ID NO 16341.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match          0.8%; Score 6; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1360
ID AAR97691 standard; protein: 37 AA.
DE Rat PB65 WW domain-1.
PN WO9617061-A1.
PD 06-JUN-1996.
PA (UYRQ ) UNIV ROCKEFELLER.
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
Query Match          0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1361
ID AAM21577 standard; protein: 37 AA.
DE Alzheimer's disease protein encoded by DNA from plaemid pGCS1243.
PN WO9721807-A1.
PD 19-JUN-1997.
PA (KYOM ) KYOMA HAKKO KOGYO KK.
Query Match          0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1362
ID AAY46444 standard; protein: 37 AA.
DE Human prostate cancer-associated protein 141.
PN DE19811194-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match          0.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1363
ID AAB21981 standard; peptide: 37 AA.
DE F865/rat peptide containing a ww-domain #2.
PN WO200048621-A2.
PD 24-AUG-2000.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Query Match          0.8%; Score 6; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1364
ID AAR83566 standard; protein: 37 AA.
DE Colicin N 40-76 amino acid sequence SEQ ID NO:33.
PN WO2003057708-A2.
PD 17-JUL-2003.
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.
Query Match          0.8%; Score 6; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
RESULT 1365
ID AAR74067 standard; peptide: 38 AA.
DE Superantigen peptide HIV Nef(1-38).
PN WO9511975-A2.
PD 04-MAY-1995.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1366
ID AAY39972 standard; peptide: 38 AA.
DE HIV Negative factor (Nef) protein residues 1-38.
PN US5968514-A.
PD 19-OCT-1999.
PA (UYFL ) UNIV FLORIDA.
Query Match          0.8%; Score 6; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1367
ID AAB70442 standard; peptide: 38 AA.
DE L. lactis signal peptide SP310 mutant amino acid sequence SEQ:55.
PN WO200111060-A2.
PD 15-FEB-2001.
PA (BIOT-) BIOTEKNOLOGISK INST.
Query Match          0.8%; Score 6; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1368
ID ABO58270 standard; protein: 38 AA.
DE Human genome derived single exon protein #4504.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match          0.8%; Score 6; DB 8; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1369
ID AAR64211 standard; peptide: 39 AA.
DE Urinary plasminogen activator residues 150-188.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU ) SUMITOMO SRIYAKU KK.
Query Match          0.8%; Score 6; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1370
ID AAO11683 standard; protein: 39 AA.
DE Human polypeptide SEQ ID NO 25575.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match          0.8%; Score 6; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1371
ID AAE32936 standard; peptide: 39 AA.
DE Human albumin-CD4 fusion protein junction peptide.
PN WO200279232-A2.
PD 10-OCT-2002.
PA (LEXI-) LEXIGEN PHARM CORP.
Query Match          0.8%; Score 6; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
RESULT 1372
ID AAE32648 standard; peptide: 39 AA.
DE Albumin-CD4 fusion protein junction peptide.
PN WO200279415-A2.
PD 10-OCT-2002.
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PA (LEXI-) LEXIGEN PHARM CORP.  
Query Match 0.8%; Score 6; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1373  
ID ADF75022 standard; peptide; 39 AA.  
DE Human serum albumin-CD4 fusion protein junction sequence.  
PN US2003166877-A1.  
PD 04-SEP-2003.  
PA (LEXI-) LEXIGEN PHARM CORP.  
Query Match 0.8%; Score 6; DB 7; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1374  
ID AAP71494 standard; protein; 40 AA.  
DE Antigenic peptide cross-reactive with HTLV-III env protein 3'ORF.  
PN W08702988-A1.  
PD 21-MAY-1987.  
PA (HARD) HARVARD COLLEGE.  
Query Match 0.8%; Score 6; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1375  
ID AAY48263 standard; protein; 40 AA.  
DE Human prostate cancer-associated protein 49.  
PN DE1981193-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 0.8%; Score 6; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1376  
ID AAB09340 standard; protein; 40 AA.  
DE Hepatitis GB virus protein sequence SEQ ID NO:467.  
PN US6051374-A.  
PD 18-APR-2000.  
PA (ABBO) ABBOTT LAB.  
Query Match 0.8%; Score 6; DB 3; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1377  
ID AAE23150 standard; peptide; 40 AA.  
DE Influenza A virus subtype 16 haemagglutinin (HA) protein fragment #14.  
PN W0200224734-A2.  
PD 28-MAR-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 0.8%; Score 6; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1378  
ID AAB07101 standard; protein; 41 AA.  
DE Melanocyte-stimulating hormone inhibitor #6.  
PN EP389950-A.  
PD 03-OCT-1990.  
PA (LLOY) LION CORP.  
Query Match 0.8%; Score 6; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1379  
ID AAM24782 standard; peptide; 42 AA.  
DE Adhesin Pctr44 N-terminal peptide.  
PN W09716542-A1.  
PD 09-MAY-1997.  
PA (UYME) UNIV MELBOURNE.  
Query Match 0.8%; Score 6; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1380  
ID AAO02438 standard; protein; 42 AA.  
DE Human polypeptide SEQ ID NO 16330.  
PN W0200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1381  
ID ABO60596 standard; protein; 42 AA.  
DE Human genome derived single exon protein #6830.  
PN US2003194704-A1.  
PD 16-OCT-2003.

PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANTZ/) HANZEL D K.  
Query Match 0.8%; Score 6; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1382  
ID AAR58896 standard; protein; 43 AA.  
DE Human-223 cadherin-related molecule.  
PN W09414960-A2.  
PD 07-JUL-1994.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 0.8%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1383  
ID AAR87135 standard; peptide; 43 AA.  
DE Protocadherin clone HUMAN-223.  
PN W09600289-A1.  
PD 04-JAN-1996.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 0.8%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1384  
ID AAY21020 standard; protein; 43 AA.  
DE Human glial fibrillary acidic protein GFAP mutant fragment 29.  
PN W09845322-A2.  
PD 15-OCT-1998.  
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
Query Match 0.8%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1385  
ID AAY32350 standard; peptide; 43 AA.  
DE Human C1gRP EGF-2 peptide.  
PN W09355838-A1.  
PD 04-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 0.8%; Score 6; DB 3; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1386  
ID ABG77431 standard; protein; 43 AA.  
DE Selected Interacting Domain (SID) polypeptide #242.  
PN W0200259255-A2.  
PD 01-AUG-2002.  
PA (HYBR-) HYBRGENICS.  
Query Match 0.8%; Score 6; DB 5; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1387  
ID AAE30226 standard; peptide; 43 AA.  
DE Human LP288 YWTD Island 2 repeat peptide #1.  
PN W0200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 0.8%; Score 6; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1388  
ID ADR51552 standard; protein; 43 AA.  
DE DT-binding receptor region of HB-EGF from humans.  
PN W02004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1389  
ID ADR51550 standard; protein; 43 AA.  
DE DT-binding receptor region of HB-EGF from pigs.  
PN W02004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1390  
ID AAO01303 standard; protein; 44 AA.

DE Human polypeptide SEQ ID NO 15195.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1391  
ID ADR51549 standard; protein; 44 AA.  
DE DT-binding receptor region of HB-EGF from rabbits.  
PN WO2004069870-A2.  
PD 13-AUG-2004.  
PA (VYLR-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1392  
ID ADR51551 standard; protein; 44 AA.  
DE DT-binding receptor region of HB-EGF from monkeys.  
PN WO2004069870-A2.  
PD 13-AUG-2004.  
PA (VYLR-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1393  
ID AAR64212 standard; peptide; 45 AA.  
DE Urinary plasminogen activator residues 159-203.  
PN JF06327473-A.  
PD 29-NOV-1994.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1394  
ID AAY08546 standard; protein; 45 AA.  
DE C-terminal alpha-CTD protein fragment FTSH\_HELPY.  
PN WO9925733-A2.  
PD 27-MAY-1999.  
PA (YISS) YISSUM RES & DEV CO.  
Query Match 0.8%; Score 6; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1395  
ID AAG21119 standard; protein; 45 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23559.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 0.8%; Score 6; DB 3; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1396  
ID AAM14231 standard; protein; 45 AA.  
DE Peptide #665 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1397  
ID ABB31178 standard; peptide; 45 AA.  
DE Peptide #684 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1398  
ID AAM26641 standard; protein; 45 AA.  
DE Peptide #678 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 02-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1399  
ID AAB28006 standard; peptide; 45 AA.  
DE Human peptide #557 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.

PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1400  
ID ABB18643 standard; protein; 45 AA.  
DE Protein #642 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1401  
ID AAM66362 standard; protein; 45 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26668.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1402  
ID AAM53974 standard; protein; 45 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26079.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1403  
ID AAB48028 standard; peptide; 45 AA.  
DE Human liver peptide, SEQ ID No 26676.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1404  
ID AAM01963 standard; protein; 45 AA.  
DE Peptide #645 encoded by probe for measuring human breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1405  
ID AAB36010 standard; peptide; 45 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25675.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1406  
ID ADN05538 standard; protein; 45 AA.  
DE Antiparasitic protein sequence #935.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GERTH) GENENTECH INC.  
Query Match 0.8%; Score 6; DB 8; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1407  
ID ABB03327 standard; protein; 46 AA.  
DE Human musculoskeletal system related polypeptide SEQ ID NO 1274.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1408  
ID AAO01399 standard; protein; 46 AA.  
DE Human polypeptide SEQ ID NO 15291.  
PN WO200164835-A2.  
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1409  
ID AAO08005 standard; protein; 46 AA.  
DE Human polypeptide SEQ ID NO 21897.  
PN W0200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1410  
ID ADH32592 standard; protein; 46 AA.  
DE Yeast smorf387-encoded polypeptide, SEQ ID NO:1050.  
PN W0200268693-A2.  
PD 06-SEP-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 0.8%; Score 6; DB 5; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1411  
ID ADU12621 standard; protein; 46 AA.  
DE Novel human musculoskeletal system antigen #241.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 0.8%; Score 6; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1412  
ID ADJ28647 standard; protein; 46 AA.  
DE Human musculoskeletal system-associated protein - SEQ ID 1274.  
PN US2004099488-A1.  
PD 15-JUN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1413  
ID ADS07325 standard; protein; 46 AA.  
DE Staphylococcus epidermis polypeptide seqid 6620.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Query Match 0.8%; Score 6; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1414  
ID AAM28321 standard; protein; 47 AA.  
DE Staphylococcus aureus protein of unknown function.  
PN W09730070-A1.  
PD 21-AUG-1997.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 0.8%; Score 6; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1415  
ID AAG18782 standard; protein; 47 AA.  
DE Epi mays protein fragment SEQ ID NO: 20328.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 0.8%; Score 6; DB 3; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1416  
ID AAM47202 standard; peptide; 47 AA.  
DE Modular enzyme system related ACP-domain N-terminal peptide AYRAI\_3.  
PN W0200181564-A2.  
PD 01-NOV-2001.  
PA (ACTI-) ACTINODRUG PHARM GMBH.  
Query Match 0.8%; Score 6; DB 5; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1417  
ID ADD96929 standard; protein; 47 AA.  
DE Human 193p1E1B protein variant 1 fragment #2.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1418  
ID ADP49728 standard; peptide; 47 AA.  
DE Human 193p1E1Bv.1.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITRA-ERD P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1419  
ID AAB33113 standard; protein; 48 AA.  
DE Pinus radiata transcription factor protein sequence #240.  
PN W0200053724-A2.  
PD 14-SEP-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 0.8%; Score 6; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1420  
ID ABP43712 standard; protein; 48 AA.  
DE PRO566 protein.  
PN W0200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1421  
ID AAE36818 standard; protein; 48 AA.  
DE Human HB-EGF domain.  
PN W02003014159-A1.  
PD 20-FEB-2003.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
PA (BIOW-) BIOMOLECULAR RES INST LTD.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 0.8%; Score 6; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1422  
ID ADN48881 standard; peptide; 48 AA.  
DE Heparat-binding epidermal-growth factor (HB-EGF) peptide.  
PN US6727077-B1.  
PD 27-APR-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (GEOU) UNIV GEORGETOWN MEDICAL CENT.  
Query Match 0.8%; Score 6; DB 8; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1423  
ID ABB38598 standard; peptide; 49 AA.  
DE Peptide #6104 encoded by human foetal liver single exon probe.  
PN W0200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1424  
ID AAM32054 standard; protein; 49 AA.  
DE Peptide #6091 encoded by probe for measuring placental gene expression.  
PN W0200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1425  
ID AAM71762 standard; protein; 49 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32068.

PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1426  
ID AAM59226 standard; protein; 49 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31331.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1427  
ID ABG53447 standard; peptide; 49 AA.  
DE Human liver peptide, SEQ ID No 32095.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1428  
ID ABG41576 standard; peptide; 49 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31241.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1429  
ID ADK14940 standard; protein; 49 AA.  
DE Urinary specific protein #46.  
PN W02003057839-A2.  
PD 17-JUL-2003  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1430  
ID AAG04489 standard; protein; 50 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 535.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1431  
ID AAG37508 standard; protein; 50 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46130.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1432  
ID ABB22229 standard; protein; 50 AA.  
DE Protein #4228 encoded by probe for measuring heart cell gene expression.  
PN W0200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1433  
ID AAM70055 standard; protein; 50 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30361.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1434  
ID AAM40213 standard; protein; 50 AA.  
DE Propionibacterium acnes immunogenic protein #1109.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.

Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1435  
ID AAM57648 standard; protein; 50 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29753.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1436  
ID ABG51748 standard; peptide; 50 AA.  
DE Human liver peptide, SEQ ID No 30396.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1437  
ID AAM05532 standard; protein; 50 AA.  
DE Peptide #4214 encoded by probe for measuring breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1438  
ID ABG39686 standard; peptide; 50 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29351.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1439  
ID ABM36732 standard; protein; 50 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1408.  
PN W02003033515-A1.  
PD 24-APR-2003  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1440  
ID AAB36799 standard; protein; 50 AA.  
DE Human HB-EGF protein BGF-like domain.  
PN W02003014159-A1.  
PD 20-FEB-2003.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
PA (BIOM-) BIOMOLECULAR RES INST LTD.  
PA (HALT-) HALT INST MEDICAL RES WALTER & ELITZ.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1441  
ID AAM67925 standard; protein; 51 AA.  
DE Fragment of human secreted protein encoded by gene 3.  
PN W09842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1442  
ID AAG04488 standard; protein; 51 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 534.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1443  
ID AAG37507 standard; protein; 51 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46129.  
PN EP1033405-A2.  
PD 06-SEP-2000.

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Query Match
Best Local Similarity 0.8%; Score 6; DB 3; Length 51;
RESULT 1444
ID AAU5334 standard; protein; 51 AA.
DE Propionibacterium acnes immunogenic protein #14230.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 4; Length 51;
RESULT 1445
ID ABP11027 standard; protein; 51 AA.
DE Human ORFX protein sequence SEQ ID NO:22036.
PN W0200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 5; Length 51;
RESULT 1446
ID AAM49853 standard; protein; 51 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14529.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 6; Length 51;
RESULT 1447
ID AAM21562 standard; protein; 52 AA.
DE LFTO rat cholecystokinin-A receptor fragment, encoded by exon 1.
PN JF09065900-A.
PD 11-MAR-1997.
PA (SHIO) SHIONOGI & CO LTD.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 52;
RESULT 1448
ID AAR45144 standard; protein; 53 AA.
DE Plasmid pCDM8-D09 - D44 fragment D09.
PN W09324624-A1.
PD 09-DEC-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 53;
RESULT 1449
ID AAM91699 standard; protein; 53 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:19292.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 0.8%; Score 6; DB 4; Length 53;
RESULT 1450
ID AAM00082 standard; protein; 53 AA.
DE Sucrose transporter sequence #150.
PN W0200144476-A2.
PD 21-JUN-2001.
PA (BADT) BASF PLANT SCI GMBH.
Query Match
Best Local Similarity 0.8%; Score 6; DB 4; Length 53;
RESULT 1451
ID AAR64213 standard; peptide; 54 AA.
DE Urinary plasminogen activator residues 150-203.
PN JF06327473-A.
PD 29-NOV-1994.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 54;
RESULT 1452
ID AAU46238 standard; protein; 54 AA.
DE Propionibacterium acnes immunogenic protein #7134.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match
0.8%; Score 6; DB 4; Length 54;
RESULT 1453
ID AAM35847 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #523.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 6; Length 54;
RESULT 1456
ID AAM42757 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7433.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 6; Length 54;
RESULT 1455
ID AAM42757 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7433.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 6; Length 54;
RESULT 1456
ID AAM35847 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #523.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 0.8%; Score 6; DB 6; Length 54;
RESULT 1457
ID AAR45145 standard; protein; 55 AA.
DE Plasmid pCDM8-D09 - D44 fragment D11.
PN W09324624-A1.
PD 09-DEC-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 55;
RESULT 1458
ID AAR45146 standard; protein; 56 AA.
DE Plasmid pCDM8-D09 - D44 fragment D(1+11).
PN W09324624-A1.
PD 09-DEC-1993.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 56;
RESULT 1459
ID AAR64210 standard; peptide; 56 AA.
DE Tissue plasminogen activator residues 266-321.
PN JF06327473-A.
PD 29-NOV-1994.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 0.8%; Score 6; DB 2; Length 56;
RESULT 1460
ID AAG2118 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23558.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 0.8%; Score 6; DB 3; Length 56;
RESULT 1461
ID AAG5284 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70861.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 0.8%; Score 6; DB 3; Length 56;
RESULT 1462
ID AAG5284 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70861.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (SUMU) SUMITOMO SEIYAKU KK.
Query Match
Best Local Similarity 0.8%; Score 6; DB 3; Length 56;
RESULT 1462
ID AAG5284 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70861.
PN EPI033405-A2.
PD 06-SEP-2000.
PA (SUMU) SUMITOMO SEIYAKU KK.
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ID AAM14482 standard; protein; 56 AA.  
DE Peptide #916 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1463  
ID ABB3430 standard; peptide; 56 AA.  
DE Peptide #936 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1464  
ID AAM26895 standard; protein; 56 AA.  
DE Peptide #932 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1465  
ID ABB28255 standard; peptide; 56 AA.  
DE Human peptide #906 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1466  
ID ABB18889 standard; protein; 56 AA.  
DE Protein #888 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1467  
ID AAM6609 standard; protein; 56 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26915.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1468  
ID AAM54215 standard; protein; 56 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26320.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1469  
ID ABB48277 standard; peptide; 56 AA.  
DE Human liver peptide; SEQ ID NO 26925.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1470  
ID AAM02209 standard; protein; 56 AA.  
DE Peptide #891 encoded by probe for measuring human breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1471  
ID ABB05146 standard; protein; 56 AA.

DE Human ORFX protein sequence SEQ ID NO:10274.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 5; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1472  
ID ABB09648 standard; protein; 56 AA.  
DE Human ORFX protein sequence SEQ ID NO:19678.  
PN WO200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 5; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1473  
ID ABB36261 standard; peptide; 56 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25926.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1474  
ID ABB05586 standard; protein; 56 AA.  
DE M. tuberculosis and M. leprae marker protein #237.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP-) INST PASTEUR.  
Query Match 0.8%; Score 6; DB 5; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1475  
ID ABB47344 standard; protein; 56 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1222.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 0.8%; Score 6; DB 8; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1476  
ID AAG10655 standard; protein; 57 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9063.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 0.8%; Score 6; DB 3; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1477  
ID AAR45147 standard; protein; 58 AA.  
DE Plasmid pCDM8-D09 - D44 fragment D(14).  
PN WO9324624-A1.  
PD 09-DEC-1993.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1478  
ID AAO1116 standard; protein; 58 AA.  
DE Human polypeptide SEQ ID NO 25008.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1479  
ID AAO02406 standard; protein; 58 AA.  
DE Human polypeptide SEQ ID NO 16298.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1480  
ID AAB41904 standard; protein; 59 AA.  
DE Human ORFX ORF1668 polypeptide sequence SEQ ID NO:3336.  
PN WO200058473-A2.

PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 3; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1481  
ID AAB90620 standard; protein; 59 AA.  
DE Human secreted protein, SEQ ID NO: 163.  
PN W0200121658-A1.  
PD 29-MAR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1482  
ID AAG99892 standard; peptide; 59 AA.  
DE ERA binding domain polypeptide SEQ ID NO 334.  
PN W0200153458-A2.  
PD 26-JUL-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1483  
ID AAM96307 standard; protein; 59 AA.  
DE Human reproductive system related antigen SEQ ID NO: 4965.  
PN W0200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1484  
ID AAO11933 standard; protein; 59 AA.  
DE Human polypeptide SEQ ID NO 25825.  
PN W0200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1485  
ID AAU64191 standard; protein; 59 AA.  
DE Propionibacterium acnes immunogenic protein #25087.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1486  
ID AAU43121 standard; protein; 59 AA.  
DE Propionibacterium acnes immunogenic protein #4017.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1487  
ID AAU65216 standard; protein; 59 AA.  
DE Propionibacterium acnes immunogenic protein #26112.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 4; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1488  
ID AAM61735 standard; protein; 59 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #26411.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 6; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1489  
ID AAM39640 standard; protein; 59 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4316.  
PD W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 6; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1490  
ID AAM60710 standard; protein; 59 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25386.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 6; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1491  
ID AAB70853 standard; protein; 60 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 39351.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1492  
ID AAB41719 standard; peptide; 60 AA.  
DE Peptide #9225 encoded by human foetal liver single exon probe.  
PN W0200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1493  
ID AAM35515 standard; protein; 60 AA.  
DE Peptide #9552 encoded by probe for measuring placental gene expression.  
PN W0200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1494  
ID AAM75403 standard; protein; 60 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35709.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1495  
ID AAU52361 standard; protein; 60 AA.  
DE Propionibacterium acnes immunogenic protein #13257.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1496  
ID AAU63335 standard; protein; 60 AA.  
DE Propionibacterium acnes immunogenic protein #24231.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1497  
ID AAU61570 standard; protein; 60 AA.  
DE Propionibacterium acnes immunogenic protein #22466.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 0.8%; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1498  
ID AAM62593 standard; protein; 60 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34698.  
PN W0200157275-A2.  
PD 09-AUG-2001.



PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.88; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1499  
ID ABG57158 standard; peptide; 60 AA.  
DE Human liver peptide; SEQ ID No 35806.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PR (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.88; Score 6; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1500  
ID ABG44990 standard; peptide; 60 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34655.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PR (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.88; Score 6; DB 5; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 8, 2005, 16:06:48 ; Search time 18 Seconds  
(without alignments)  
3848.671 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 720

Sequence: 1 MEIGCWTLQGLFPLQLLIS.....LSTAFKVLPEKDIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	178	24.7	181	2 T08805	hypothetical prote
2	9	1.2	232	2 E70372	hypothetical prote
3	9	1.2	276	2 T29125	ketocycl reductase
4	9	1.2	730	1 BMH01	procollagen C-endo
5	9	1.2	823	1 A58788	procollagen C-endo
6	9	1.2	986	1 B58788	procollagen C-endo
7	9	1.2	991	2 I49540	procollagen C-endo
8	9	1.2	1464	2 S58984	development protei
9	9	1.2	2531	2 T31070	notch homolog - se
10	9	1.1	114	2 S00996	Ig kappa chain pre
11	8	1.1	158	2 G70323	conserved hypochet
12	8	1.1	235	2 D42696	chrombin (EC 3.4.2
13	8	1.1	235	2 H42696	chrombin (EC 3.4.2
14	8	1.1	236	2 C42696	chrombin (EC 3.4.2
15	8	1.1	240	2 AB0338	probable membrane
16	8	1.1	302	2 T25020	hypothetical prote
17	8	1.1	395	2 A82283	vibriolectin-spect
18	8	1.1	407	1 KFB07	coagulation factor
19	8	1.1	486	2 T38174	probable GCS1/GLO3
20	8	1.1	737	2 AG2156	hypothetical prote
21	8	1.1	1019	2 A38738	coagulation factor
22	8	1.1	1070	2 T31069	collid-BMP-1 like
23	7	1.0	59	2 B89983	hypothetical prote
24	7	1.0	75	2 A86487	unknown protein [l
25	7	1.0	91	2 E96528	protein F27015.6 [l
26	7	1.0	114	2 D72600	hypothetical prote
27	7	1.0	143	2 A85072	hypothetical prote
28	7	1.0	167	2 S05364	hypothetical prote
29	7	1.0	168	2 D86534	CT066 hypothetical

30	7	1.0	168	2 D72089	ct066 hypothetical
31	7	1.0	171	2 E81580	conserved hypotet
32	7	1.0	173	2 T45501	hypothetical prote
33	7	1.0	178	2 F86271	protein F16A14.6 [l
34	7	1.0	191	2 G75299	cellulium resistan
35	7	1.0	193	2 G64241	hypothetical prote
36	7	1.0	196	2 JC4257	beta A4-crystallin
37	7	1.0	201	1 S16262	auxin-binding prot
38	7	1.0	209	2 S27494	nods protein - Bra
39	7	1.0	211	2 AC0268	probable exported
40	7	1.0	212	2 AE0652	probable outer mem
41	7	1.0	212	2 S07797	ycid protein precu
42	7	1.0	212	2 C85706	probable outer mem
43	7	1.0	212	2 D90848	probable outer mem
44	7	1.0	213	2 B86828	hypothetical prote
45	7	1.0	215	2 T50589	probable TetR-fami
46	7	1.0	227	2 D69296	conserved hypochet
47	7	1.0	231	2 A86592	low calcium respon
48	7	1.0	231	2 H72031	type III secretion
49	7	1.0	232	2 C83139	outer membrane pro
50	7	1.0	235	2 E42696	thrombin (EC 3.4.2
51	7	1.0	236	2 F84273	hypothetical prote
52	7	1.0	239	2 G42696	thrombin (EC 3.4.2
53	7	1.0	239	2 B82123	chemotaxis protein
54	7	1.0	243	2 A56338	venom proteinase (
55	7	1.0	247	2 G86011	glycerophosphodies
56	7	1.0	247	2 G91165	probable chaperone
57	7	1.0	250	2 A10206	hypothetical prote
58	7	1.0	255	2 S07553	N-acetyl-muramoyl-L
59	7	1.0	259	2 A12835	hypothetical prote
60	7	1.0	259	2 D97613	hypothetical prote
61	7	1.0	260	2 A36402	corticotropin / li
62	7	1.0	263	2 S05433	corticotropin / li
63	7	1.0	265	2 E70520	hypothetical prote
64	7	1.0	270	2 S04380	opacity protein P.
65	7	1.0	271	2 T50620	hypothetical prote
66	7	1.0	307	2 B82343	D-isomer specific
67	7	1.0	312	2 S67052	conserved hypochet
68	7	1.0	315	2 A87249	transcription regu
69	7	1.0	333	2 A84055	probable membrane
70	7	1.0	336	2 G87202	hypothetical prote
71	7	1.0	337	2 D72690	queuine tRNA-ribos
72	7	1.0	339	2 AG2041	probable threonine
73	7	1.0	349	2 C72630	hypothetical prote
74	7	1.0	350	2 T25172	MSS2 protei
75	7	1.0	351	2 S67649	NADH2 dehydrogenas
76	7	1.0	355	2 T13831	NADH2 dehydrogenas
77	7	1.0	355	2 T13830	NADH2 dehydrogenas
78	7	1.0	355	2 T14016	NADH2 dehydrogenas
79	7	1.0	355	2 T11734	NADH2 dehydrogenas
80	7	1.0	355	2 T14009	NADH2 dehydrogenas
81	7	1.0	355	2 T14012	NADH2 dehydrogenas
82	7	1.0	355	2 T14011	NADH2 dehydrogenas
83	7	1.0	355	2 T11737	NADH2 dehydrogenas
84	7	1.0	355	2 T13989	NADH2 dehydrogenas
85	7	1.0	355	2 T14010	NADH2 dehydrogenas
86	7	1.0	355	2 T11752	NADH2 dehydrogenas
87	7	1.0	355	2 T11760	NADH2 dehydrogenas
88	7	1.0	355	2 T14013	NADH2 dehydrogenas
89	7	1.0	355	2 T11733	NADH2 dehydrogenas
90	7	1.0	355	2 T11762	NADH2 dehydrogenas
91	7	1.0	355	2 T14014	NADH2 dehydrogenas
92	7	1.0	355	2 T11754	NADH2 dehydrogenas
93	7	1.0	355	2 T13988	NADH2 dehydrogenas
94	7	1.0	355	2 T14008	NADH2 dehydrogenas
95	7	1.0	355	2 T11739	NADH2 dehydrogenas
96	7	1.0	355	2 T13977	NADH2 dehydrogenas
97	7	1.0	355	2 T13894	NADH2 dehydrogenas
98	7	1.0	355	2 T12118	NADH2 dehydrogenas
99	7	1.0	355	2 T14028	NADH2 dehydrogenas
100	7	1.0	355	2 T14048	NADH2 dehydrogenas
101	7	1.0	355	2 T11603	NADH2 dehydrogenas
102	7	1.0	355	2 T11604	NADH2 dehydrogenas

ct066 hypothetical  
conserved hypotet  
hypothetical prote  
protein F16A14.6 [l  
cellulium resistan  
hypothetical prote  
beta A4-crystallin  
auxin-binding prot  
nods protein - Bra  
probable exported  
probable outer mem  
ycid protein precu  
probable outer mem  
hypothetical prote  
probable TetR-fami  
conserved hypochet  
low calcium respon  
type III secretion  
outer membrane pro  
thrombin (EC 3.4.2  
hypothetical prote  
thrombin (EC 3.4.2  
chemotaxis protein  
venom proteinase (

103	7	1.0	355	2	T11602	NADH2 dehydrogenas	176	6	0.8	27	2	A33431	atrial natriuretic
104	7	1.0	355	2	T11601	NADH2 dehydrogenas	177	6	0.8	35	2	D82224	hypothetical prote
105	7	1.0	355	2	T12109	NADH2 dehydrogenas	178	6	0.8	40	2	E82433	hypothetical prote
106	7	1.0	355	2	T12107	NADH2 dehydrogenas	179	6	0.8	48	2	G81543	hypothetical prote
107	7	1.0	355	2	T12119	NADH2 dehydrogenas	180	6	0.8	53	2	G82813	hypothetical prote
108	7	1.0	355	2	A48358	ORF355 - Bradyrhiz	181	6	0.8	54	2	A95210	conserved hypochet
109	7	1.0	359	2	A28700	mandelate racemase	182	6	0.8	54	2	H81814	probable small sec
110	7	1.0	372	2	A83260	hypothetical prote	183	6	0.8	55	1	FECLCU	ferredoxin 2[Fe-4
111	7	1.0	375	2	A81227	conserved hypochet	184	6	0.8	55	2	T07197	hypothetical prote
112	7	1.0	375	2	F81599	probable integral	185	6	0.8	56	2	E87173	conserved hypochet
113	7	1.0	387	1	S75050	IMP dehydrogenase	186	6	0.8	57	2	S66318	protein kinase AK5
114	7	1.0	387	2	AC1813	IMP dehydrogenase	187	6	0.8	57	2	S66316	protein kinase AK3
115	7	1.0	398	2	E83438	probable transpor	188	6	0.8	59	2	A83209	hypothetical prote
116	7	1.0	413	2	F69383	coenzyme F390 synt	189	6	0.8	62	2	G59147	conotoxin Im5.1 pr
117	7	1.0	437	2	TS0237	hypothetical 48k p	190	6	0.8	64	2	T08457	probable outer env
118	7	1.0	439	2	T49289	kinesin heavy chai	191	6	0.8	64	2	H75204	ferredoxin PA83048
119	7	1.0	459	2	T08594	probable sulfate a	192	6	0.8	67	2	D98068	degenerate transpo
120	7	1.0	461	2	D70561	hypothetical prote	193	6	0.8	67	2	AC1954	hypothetical prote
121	7	1.0	472	2	T27755	hypothetical prote	194	6	0.8	68	2	T00189	hypothetical prote
122	7	1.0	479	2	H90042	hypothetical prote	195	6	0.8	69	2	A95993	hypothetical prote
123	7	1.0	489	2	S69027	ammonium transport	196	6	0.8	69	2	AE2949	ribosomal protein
124	7	1.0	492	2	T23349	hypothetical prote	197	6	0.8	70	1	R5EC31	50S ribosomal subu
125	7	1.0	492	2	S46225	ammonium transport	198	6	0.8	70	2	G91236	50S ribosomal subu
126	7	1.0	493	2	A33809	carthage matrix p	199	6	0.8	70	2	G82588	hypothetical prote
127	7	1.0	494	1	A29079	lymphocyte surface	200	6	0.8	70	2	G82588	CD4 receptor - hum
128	7	1.0	497	2	S43609	rofa protein - Str	201	6	0.8	71	2	H86751	probable p12 prote
129	7	1.0	497	2	H70168	hypothetical prote	202	6	0.8	71	2	H86751	conserved hypochet
130	7	1.0	505	2	C90869	hypothetical prote	203	6	0.8	73	2	H83304	hypothetical prote
131	7	1.0	529	2	T18595	hypothetical prote	204	6	0.8	73	2	F97136	hypothetical 8.1K
132	7	1.0	532	2	A72694	hypothetical prote	205	6	0.8	75	2	UQ1429	hypothetical prote
133	7	1.0	544	2	S06602	modulo antigen - f	206	6	0.8	75	2	D82592	hypothetical prote
134	7	1.0	553	2	D95071	metallo-beta-lacta	207	6	0.8	77	2	T06954	hypothetical prote
135	7	1.0	553	2	B97939	conserved hypochet	208	6	0.8	77	2	AC2101	lipoprotein [impor
136	7	1.0	556	2	S02154	NADH2 dehydrogenas	209	6	0.8	78	2	A42506	F-ORF-B protein -
137	7	1.0	561	2	C75543	6-aminohexanoate-c	210	6	0.8	79	2	D69309	conserved hypochet
138	7	1.0	580	2	D84772	probable sugar tra	211	6	0.8	80	2	E97949	hypothetical prote
139	7	1.0	581	2	T38864	probable regulator	212	6	0.8	80	2	S27162	heparin-binding ep
140	7	1.0	582	2	F71431	hypothetical prote	213	6	0.8	84	2	G64217	ribosomal protein
141	7	1.0	583	2	T25690	hypothetical prote	214	6	0.8	85	2	G64217	auxin-induced prot
142	7	1.0	585	2	T18736	hypothetical prote	215	6	0.8	85	2	T12211	hypothetical prote
143	7	1.0	617	2	S10511	thrombin (BC 3.4.2	216	6	0.8	86	2	E90660	hypothetical prote
144	7	1.0	617	2	D90487	maltoase ABC transp	217	6	0.8	86	2	C85511	damage-inducible p
145	7	1.0	618	2	A35827	thrombin (BC 3.4.2	218	6	0.8	86	2	G64747	DNA-damage-inducib
146	7	1.0	622	1	TBHU	thrombin (BC 3.4.2	219	6	0.8	87	2	T10462	hypothetical prote
147	7	1.0	625	1	TBBO	thrombin (BC 3.4.2	220	6	0.8	87	2	T50008	hypothetical prote
148	7	1.0	658	1	T04831	probable serine/th	221	6	0.8	88	2	B82860	hypothetical prote
149	7	1.0	678	2	D87607	hypothetical prote	222	6	0.8	88	2	C97251	probable membrane
150	7	1.0	684	2	H96646	hypothetical prote	223	6	0.8	88	2	AB1901	hypothetical prote
151	7	1.0	684	2	T02149	hypothetical prote	224	6	0.8	91	2	C81922	hypothetical prote
152	7	1.0	707	2	JC2218	procollagen C-endo	225	6	0.8	91	2	AE0710	conserved hypochet
153	7	1.0	709	2	T43109	cytolysin B transp	226	6	0.8	92	2	F36905	conserved hypochet
154	7	1.0	746	2	C95110	complete protein	227	6	0.8	94	2	T44722	hypothetical prote
155	7	1.0	783	2	B83232	conserved hypochet	228	6	0.8	95	2	C83517	hypothetical prote
156	7	1.0	790	2	G02678	cadherin-14 - huma	229	6	0.8	98	2	B82463	hypothetical prote
157	7	1.0	791	2	H96839	hypothetical prote	230	6	0.8	98	2	T44883	hypothetical prote
158	7	1.0	825	2	T06036	hypothetical prote	231	6	0.8	98	2	S03386	antigen (clone 22)
159	7	1.0	833	2	S50225	potassium transpor	232	6	0.8	99	2	S44658	ZK353.2 protein -
160	7	1.0	841	2	T38703	hypothetical prote	233	6	0.8	100	2	C71012	hypothetical prote
161	7	1.0	856	2	T16543	hypothetical prote	234	6	0.8	102	2	D84024	transcription regu
162	7	1.0	859	2	S66827	aluminum resistan	235	6	0.8	104	2	I40195	transposase - Bact
163	7	1.0	903	2	B88221	protein T0113.2 [i	236	6	0.8	104	2	F45681	orf 61.2 - phage T
164	7	1.0	980	2	T24336	hypothetical prote	237	6	0.8	105	2	C69068	divalent cation to
165	7	1.0	995	2	A88483	protein C05D1.1 [	238	6	0.8	106	2	D90392	conserved hypochet
166	7	1.0	1048	2	T31653	hypothetical prote	239	6	0.8	107	2	G71517	probable L21 ribos
167	7	1.0	1100	2	JC8033	leukocyte formin p	240	6	0.8	108	2	G84552	similar to gibbere
168	7	1.0	1240	2	T04893	hypothetical prote	241	6	0.8	108	2	A28667	hypothetical prote
169	7	1.0	1346	2	T17412	polyketide synthas	242	6	0.8	109	2	B53291	tetracenomycin-bio
170	7	1.0	1522	2	S48902	probable purine nu	243	6	0.8	109	2	T47985	hypothetical prote
171	7	1.0	1742	2	T49451	kinesin-like prote	244	6	0.8	109	2	T44129	hypothetical prote
172	7	1.0	1822	2	T50207	probable protein c	245	6	0.8	113	2	T45195	hypothetical prote
173	7	1.0	1852	2	T18552	saframycin Mxi syn	246	6	0.8	113	2	T26771	hypothetical prote
174	7	1.0	2907	2	A57278	fibrillin-2 precur	247	6	0.8	114	2	H72705	hypothetical prote
175	7	1.0	2918	2	A54105	fibrillin-2 precur	248	6	0.8	116	2	D96530	probable ribosomal

249	6	0.8	117	2	I51573	gene wnt-2 protein	322	159	2	A72709	hypothetical prote
250	6	0.8	117	2	H90021	50S ribosomal prot	323	159	2	D86743	hypothetical prote
251	6	0.8	117	2	C72511	hypothetical prote	324	159	2	D86286	Similar to gb - Ar
252	6	0.8	118	2	H71564	hypothetical prote	325	160	2	H55545	APA-III adhesin -
253	6	0.8	118	2	T14660	hypothetical prote	326	160	2	T35987	probable ribosome-
254	6	0.8	118	2	JC5793	elongin B - fruit	327	160	2	AC0835	Sara (tmRNA)-bindi
255	6	0.8	119	2	F70941	hypothetical prote	328	160	2	AE0135	Sara-binding prote
256	6	0.8	122	2	H64217	ribosomal protein	329	160	2	T48148	hypothetical prote
257	6	0.8	122	2	S62831	ribosomal protein	330	161	2	T31531	hypothetical prote
258	6	0.8	123	2	E71163	hypothetical prote	331	161	2	E90372	conserved hypotet
259	6	0.8	123	2	S72389	hypothetical prote	332	162	2	H75071	transcription regu
260	6	0.8	123	2	S75382	hypothetical prote	333	162	2	C97657	pexB protein limpo
261	6	0.8	124	1	MNIV71	nonstructural prot	334	162	2	AC2881	DNA-binding protei
262	6	0.8	124	2	A81163	conserved hypotet	335	162	2	H70803	probable transcrip
263	6	0.8	124	2	F81942	probable regulator	336	162	2	AB1950	hypothetical prote
264	6	0.8	126	2	T47297	hypothetical prote	337	162	2	H71093	hypothetical prote
265	6	0.8	127	2	T14956	hypothetical prote	338	163	2	B97290	3-isopropylmalate
266	6	0.8	127	2	F69377	molybdenum-pterin-	339	164	2	A45512	cold-regulated pro
267	6	0.8	127	2	T05261	cold-regulated pro	340	164	2	JC4675	transcription fact
268	6	0.8	129	2	T06188	probable DNA-dirc	341	165	2	AB0851	hypothetical prote
269	6	0.8	129	2	S52792	Ig kappa chain V r	342	165	2	S70217	slpE protein - Sal
270	6	0.8	129	2	C69488	LSU ribosomal prot	343	165	2	A57357	slcA protein - Sal
271	6	0.8	129	2	E75602	hypothetical prote	344	165	2	H86948	probable transcrip
272	6	0.8	130	2	S57896	polyketide synthas	345	166	2	I39546	hypothetical prote
273	6	0.8	130	2	T35906	probable quinone b	346	167	2	E71391	NADH2 dehydrogenas
274	6	0.8	130	2	H83992	hypothetical prote	347	167	2	AD0601	DNA protection dur
275	6	0.8	131	2	T49455	hypothetical prote	348	167	2	B90740	global regulator p
276	6	0.8	131	2	T29078	hypothetical prote	349	167	2	A46401	DNA-binding protei
277	6	0.8	132	2	T50416	40S ribosomal prot	350	167	2	D85590	global regulator,
278	6	0.8	132	2	H87626	hypothetical prote	351	167	2	AG0306	probable DNA-bindi
279	6	0.8	133	2	E71062	hypothetical prote	352	167	2	S11411	hypothetical prote
280	6	0.8	133	2	F81748	conserved hypotet	353	168	2	A69708	signal peptidase I
281	6	0.8	133	2	H81191	hypothetical prote	354	169	2	B48489	nitrate reductase
282	6	0.8	134	2	E71945	hypothetical prote	355	170	2	A88638	protein F58F6.3 [i
283	6	0.8	134	2	F64561	conserved hypotet	356	171	2	S76982	hypothetical prote
284	6	0.8	134	2	B72651	hypothetical prote	357	171	2	T41924	hypothetical prote
285	6	0.8	136	2	E69376	hypothetical prote	358	172	2	AG3532	D-lactate dehydrog
286	6	0.8	136	2	E90394	ferric uptake regu	359	172	2	G82151	peptidoglycan-asso
287	6	0.8	137	2	A83852	hypothetical prote	360	172	2	G69087	conserved hypotet
288	6	0.8	138	2	D83824	transcription regu	361	172	2	AE2283	hypothetical prote
289	6	0.8	138	2	T29558	hypothetical prote	362	172	2	D71136	hypothetical prote
290	6	0.8	139	2	G90414	conserved hypotet	363	173	2	H70113	ribosomal protein
291	6	0.8	140	2	E81659	conserved hypotet	364	174	2	E69038	heat shock protein
292	6	0.8	141	2	T33271	hypothetical prote	365	175	2	T07877	self-pruning prote
293	6	0.8	141	2	S55247	hemoglobin alpha-A	366	175	2	AC3014	Mut7/nudix family
294	6	0.8	141	2	I39720	ORF10 - Agrobacter	367	175	2	G86458	unknown protein, 7
295	6	0.8	141	2	G72661	hypothetical prote	368	176	2	A34690	DNA-binding protei
296	6	0.8	143	2	S50549	hypothetical prote	369	176	2	AE0866	conserved hypotet
297	6	0.8	143	2	B72627	hypothetical prote	370	177	2	S45878	hypothetical prote
298	6	0.8	144	2	T49457	hypothetical prote	371	177	2	E95222	conserved hypotet
299	6	0.8	145	2	C64447	hypothetical prote	372	177	2	D75309	protein-tyrosine p
300	6	0.8	145	2	F84251	hypothetical prote	373	177	2	E98086	conserved hypotet
301	6	0.8	146	2	H64340	hypothetical prote	374	178	2	A95367	probable NADH2 deh
302	6	0.8	147	2	S01655	alpha-amylase/tryr	375	178	2	B42845	3-hydroxybutyrate
303	6	0.8	147	2	T35980	probable peptide t	376	178	2	H84789	hypothetical prote
304	6	0.8	149	2	T35846	probable integral	377	178	2	A86836	hypothetical prote
305	6	0.8	149	2	T49200	hypothetical prote	378	178	2	S26481	calcium-binding pr
306	6	0.8	150	2	AC1720	transcription regu	379	179	2	G75462	ribonuclease H - D
307	6	0.8	151	2	C71503	probable rRNA meth	380	179	2	G90003	ATP synthase delta
308	6	0.8	151	2	B87624	transcription regu	381	180	2	FC1305	genome polyprotein
309	6	0.8	151	2	A97008	transcription regu	382	180	2	FC1304	genome polyprotein
310	6	0.8	152	2	D98270	hypothetical prote	383	180	2	FC1303	genome polyprotein
311	6	0.8	153	2	T06564	alpha-amylase/tryr	384	180	2	T23339	hypothetical prote
312	6	0.8	153	2	C98238	hypothetical 16.4K	385	182	2	T39915	meiotic recombinat
313	6	0.8	153	2	AH3047	conserved hypotet	386	182	2	A72361	hypothetical prote
314	6	0.8	153	2	AB1907	hypothetical prote	387	183	2	E69432	hypothetical prote
315	6	0.8	154	2	E83634	hypothetical prote	388	183	2	T07677	pirotil-specific pr
316	6	0.8	155	2	B90143	hypothetical prote	389	184	2	T09609	uroplakin II - hum
317	6	0.8	155	2	A82884	conserved hypotet	390	184	2	A54135	uroplakin II precu
318	6	0.8	156	2	G69233	N-terminal acetyl	391	184	2	JC7839	uroplakin II prote
319	6	0.8	157	2	T28321	ORF MSV160 hypothe	392	184	2	E87506	hypothetical prote
320	6	0.8	158	2	D82499	hypothetical prote	393	185	2	F70479	flavodoxin - Aquif
321	6	0.8	159	2	B70635	hypothetical prote	394	185	2	B81732	general stress pro

395	2	E71469	probable general s	468	208	2	D87565	conserved hypothet
396	2	A49713	uroplakin II precu	469	209	2	A99460	conserved hypothet
397	1	R5B98E	ribosomal protein	470	209	2	C87521	hypothetical prote
398	2	T41601	hypothetical prote	471	209	2	T07779	dehydrin homolog C
399	2	G75022	hypothetical prote	472	210	2	G95858	probable 3-octapre
400	2	B83084	hypothetical transcr	473	210	2	D84238	hypothetical prote
401	2	S70580	bplJ protein - Bor	474	210	2	H75361	leu/phe-tRNA-prote
402	1	XM6CFD	3-octaprenyl-4-hyd	475	211	1	ZKBP74	transcription regu
403	2	AB0801	probable decarboxy	476	211	2	T47580	ribosomal protein
404	2	C91028	3-octaprenyl-4-hyd	477	211	2	S45464	hypothetical prote
405	2	D85872	3-octaprenyl-4-hyd	478	212	1	QQLJZR	nef protein - huma
406	2	D71658	3-octaprenyl-4-hyd	479	212	2	S37973	DNA-directed RNA p
407	2	T51064	hypothetical prote	480	214	2	E46681	glutathione transf
408	2	AB0361	probable iron-sulp	481	214	2	T14920	hypothetical prote
409	2	AE0338	probable 3-octapre	482	215	2	C46681	glutathione transf
410	2	A97800	hypothetical prote	483	215	2	AD0455	thiamine-phosphate
411	2	C64574	hypothetical prote	484	215	2	T45985	hypothetical prote
412	2	A45816	MHC class II histo	485	215	2	T16383	hypothetical prote
413	2	H72099	phenylacrylate dec	486	216	1	C64081	L-fucose-phospha
414	2	H86523	phenylacrylate dec	487	216	2	D86564	YagE family (impor
415	2	E75021	probable transcrip	488	216	2	G72060	YagE family - Chla
416	2	T30325	hypothetical prote	489	216	2	G72509	hypothetical prote
417	1	HSU010	histone H1-0 - hum	490	216	2	D82407	outer membrane pro
418	2	C82041	general secretion	491	217	2	F85571	probable carboxyla
419	2	D98190	decarboxylase (imp	492	218	2	H90720	probable carboxyla
420	2	AE3096	phenylacrylic acid	493	218	2	F64806	YbgJ protein - Esc
421	2	AC3629	3-octaprenyl-4-hyd	494	218	2	B64806	YbgJ protein - Esc
422	1	R5MUL9	ribosomal protein	495	218	2	B64595	endonuclease III -
423	2	E95411	probable decarboxy	496	218	2	C71918	endonuclease III -
424	2	B70761	probable lipoprote	497	218	2	A70601	hypothetical prote
425	2	D87309	hypothetical prote	498	218	2	T50440	hypothetical prote
426	2	H75188	hypothetical prote	499	218	2	AG3301	glycerone kinase (
427	2	E81391	probable transcrip	500	218	2	H87666	conserved hypothet
428	2	AC1890	hypothetical prote	501	218	2	E75389	hypothetical prote
429	2	A46681	glutathione transf	502	218	2	G69374	hypothetical cytos
430	2	G75575	hypothetical prote	503	218	2	AI3612	14-3-3 protein hom
431	2	B95349	Probable decarboxy	504	220	2	S20581	hypothetical prote
432	2	C36885	bo-type ubiquinol	505	220	2	T26991	hypothetical prote
433	2	AD2419	SOS function regul	506	221	2	B70890	hypothetical prote
434	2	C69271	hypothetical prote	507	221	2	AI1232	oligopeptide ABC t
435	2	H81731	CDP-diacylglycerol	508	222	2	AC1495	ribulose-5-phospha
436	2	C71469	probable glycerol-	509	222	2	T35145	glutamate transpor
437	2	T37025	probable sigma fac	510	222	2	AH0991	cell division ATP-
438	2	AD2197	hypothetical prote	511	222	2	A81408	hypothetical prote
439	2	D72573	hypothetical prote	512	223	2	AG1166	hypothetical prote
440	2	S74809	lexA protein - Syn	513	223	2	C81397	phosphoribosylform
441	2	AH0223	probable glycosida	514	223	2	T34828	potassium uptake p
442	2	C38129	bo-type ubiquinol	515	223	2	D75040	hypothetical prote
443	2	S03246	nef protein (clone	516	223	2	T31703	hypothetical prote
444	2	G71172	hypothetical prote	517	224	1	R58P11	ribosomal protein
445	2	XMBS71	regulatory protein	518	224	2	C86571	L4 ribosomal prote
446	2	ASLJH3	nef protein - huma	519	224	2	H72055	ribosomal protein
447	2	D85764	probable oxidoredu	520	224	2	C81417	probable transcrip
448	2	G64914	dimethylsulfoxide	521	224	2	T21101	hypothetical prote
449	2	G90915	probable oxidoredu	522	225	2	B97580	conserved hypothet
450	2	T01744	ribosomal protein	523	225	2	AH2800	hypothetical prote
451	2	S43467	nef protein - huma	524	225	2	T29632	hypothetical prote
452	2	D69036	conserved hypothet	525	226	2	A35968	tox regulon transc
453	2	C82325	maf protein VC0418	526	227	2	T22144	hypothetical prote
454	2	JC7975	HIV accessory prot	527	227	2	A87361	flagellar hook ass
455	2	ASLJ12	nef protein - huma	528	227	2	T41133	hypothetical prote
456	2	ASLJFV	nef protein - huma	529	228	2	AB0438	conserved hypothet
457	2	ASLJVL	nef protein - huma	530	228	2	B82087	probable smp prote
458	2	A86609	glycerol-3-P phosp	531	229	2	S70599	cytochrome-c oxida
459	2	B72016	CDP-diacylglycerol	532	229	2	S14207	cytochrome-c oxida
460	2	S03245	nef protein (clone	533	229	2	C90912	probable antitermi
461	2	S33986	nef protein - huma	534	229	2	F90972	antiterminator lim
462	2	S03244	nef protein (clone	535	229	2	C85920	antiterminator lim
463	2	A39268	heterochromatin pr	536	229	2	T48348	lysine decarboxyla
464	2	A38432	heparin-binding EG	537	230	1	MNIV16	nonstructural prot
465	2	A41914	diphtheria toxin re	538	230	1	MNIV45	nonstructural prot
466	2	A41636	GTP-binding protei	539	230	1	MNIV46	nonstructural prot
467	2	E64357	ribosomal protein	540	230	1	MNIV47	nonstructural prot

541	6	0.8	230	1	MNIVA8	nonstructural prot	614	257	2	JQ0064	MERS protein - mou
542	6	0.8	230	2	A45575	nonstructural prot	615	257	2	T00780	myb-related protei
543	6	0.8	230	2	G70504	probable cmk prot	616	257	2	T33292	hypothetical prote
544	6	0.8	231	2	S57271	14-3-3 protein hom	617	258	2	T07389	14-3-3 protein tft
545	6	0.8	231	2	D49934	phosphoglycolate p	618	258	2	T04131	14-3-3 protein, is
546	6	0.8	231	2	B69858	hypothetical prote	619	258	2	AF0016	probable biotin bi
547	6	0.8	231	2	A13283	transcription regu	620	258	2	AH2615	hypothetical prote
548	6	0.8	232	2	AG2525	hypothetical prote	621	258	2	G86764	hypothetical prote
549	6	0.8	233	2	I55654	MHC class II prote	622	258	2	T31647	hypothetical prote
550	6	0.8	233	2	C82360	cell division ATP-	623	259	1	A47237	14-3-3 protein hom
551	6	0.8	233	2	A72786	probable transport	624	259	2	B69113	cell division inhi
552	6	0.8	233	2	H75359	hypothetical prote	625	259	2	G97397	ubiquitinone/menaqu
553	6	0.8	234	2	S61309	nitrate reductase	626	259	2	D81083	conserved hypotet
554	6	0.8	234	2	T07686	transcription fact	627	259	2	D81859	conserved hypotet
555	6	0.8	234	2	F95952	transable membrane-	628	260	1	S30927	14-3-3 protein hom
556	6	0.8	234	2	C97001	ABC transporter, A	629	260	2	T07388	14-3-3 protein tft
557	6	0.8	235	2	B98108	response regulator	630	260	2	T02051	14-3-3 protein hom
558	6	0.8	235	2	E95243	response regulator	631	260	2	S20580	14-3-3 protein hom
559	6	0.8	235	2	C75030	hypothetical prote	632	260	2	D69299	hypothetical prote
560	6	0.8	236	2	AH3230	hypothetical prote	633	260	2	T51079	related to chitina
561	6	0.8	236	2	E42600	probable octopine	634	261	1	S18911	14-3-3 protein hom
562	6	0.8	236	2	T10417	p25 protein - Orgy	635	261	2	S52110	sepiapterin reduct
563	6	0.8	236	2	T02432	ethylene-responsiv	636	261	2	A71192	probable glucosyl
564	6	0.8	237	2	E97712	transcription acti	637	261	2	S52899	14-3-3 protein hom
565	6	0.8	237	2	C70157	hypothetical prote	638	261	2	H83442	probable enoyl-CoA
566	6	0.8	238	2	I71907	MHC H2-IE-beta cel	639	261	2	H70100	conserved hypotet
567	6	0.8	238	2	T14629	hypothetical prote	640	261	2	D64166	hypothetical prote
568	6	0.8	239	2	A72623	hypothetical prote	641	262	2	H71390	cytochrome-c oxida
569	6	0.8	239	2	D81351	hypothetical prote	642	262	2	T04406	14-3-3b protein -
570	6	0.8	240	2	T24239	hypothetical prote	643	262	2	S57276	14-3-3 protein hom
571	6	0.8	241	2	I48657	I-E(b-beta) protei	644	262	2	T47002	hypothetical prote
572	6	0.8	241	2	T23823	hypothetical prote	645	262	2	AH0238	probable phosphate
573	6	0.8	241	2	H81536	hypothetical prote	646	262	2	T22148	hypothetical prote
574	6	0.8	242	2	B82815	conserved hypotet	647	263	2	F87043	ECF subfamily sigm
575	6	0.8	243	2	JX0162	lectin I - furze	648	263	2	T26031	hypothetical prote
576	6	0.8	244	2	C95901	probable short cha	649	263	2	T18930	hypothetical prote
577	6	0.8	244	2	S76160	hypothetical prote	650	264	1	HLMS81	H-2 class II histo
578	6	0.8	245	2	S28827	chlorophyll a/b-bi	651	264	1	HLMS8B	H-2 class II histo
579	6	0.8	246	1	S56439	ammonium transport	652	264	1	C64368	cell division inhi
580	6	0.8	246	2	T51631	probable transcrip	653	264	2	A30529	H-2 class II histo
581	6	0.8	246	2	AF1054	cytoQ protein [impo	654	264	2	I56056	MHC B-beta-f - mou
582	6	0.8	246	2	H86118	ammonium transport	655	264	2	A81668	conserved hypotet
583	6	0.8	247	2	H91277	ammonium transport	656	264	2	E71509	hypothetical prote
584	6	0.8	247	2	JT0555	MHC class II histo	657	264	2	T13116	protein gp30 - pha
585	6	0.8	247	2	S23474	rod-core linker po	658	264	2	D71037	hypothetical prote
586	6	0.8	247	2	H90419	hypothetical prote	659	265	2	T30246	NADH2 dehydrogenas
587	6	0.8	248	2	S53727	14-3-3 protein hom	660	265	2	T12599	NADH2 dehydrogenas
588	6	0.8	249	2	F87153	probable pseudouri	661	265	2	T12597	NADH2 dehydrogenas
589	6	0.8	249	2	H72200	conserved hypotet	662	265	2	T12601	NADH2 dehydrogenas
590	6	0.8	250	2	T06338	probable vacuolar	663	266	2	D83210	hypothetical prote
591	6	0.8	250	2	S58362	nucleolar protein	664	266	2	T40318	hypothetical prote
592	6	0.8	250	2	S61626	hypothetical prote	665	266	2	AB3571	nickel transport A
593	6	0.8	250	2	T46912	hypothetical prote	666	267	2	H85090	probable 14-3-3 pr
594	6	0.8	250	2	H95161	conserved hypotet	667	267	2	C86472	tryptophan (EC 3.4.21
595	6	0.8	250	2	G98027	conserved hypotet	668	267	2	S40006	hypothetical prote
596	6	0.8	250	2	E84708	probable signal pe	669	267	2	A98129	hypothetical prote
597	6	0.8	251	2	S47970	14-3-3 protein hom	670	267	2	AE3158	hypothetical prote
598	6	0.8	252	2	F84728	probable CCR4-asso	671	267	2	H90368	hypothetical prote
599	6	0.8	253	1	LDL01A	discooidin I chain	672	267	2	G84862	probable clathrin
600	6	0.8	253	1	LDL01C	discooidin I chain	673	268	2	H87708	exodeoxyribonuclea
601	6	0.8	253	2	AE0809	conserved hypotet	674	268	2	A64123	tryptophan synthas
602	6	0.8	253	2	E64025	hypothetical prote	675	268	2	S11224	transcription fact
603	6	0.8	254	2	T07387	14-3-3 protein tft	676	268	2	T04966	hypothetical prote
604	6	0.8	254	2	S55375	14-3-3 protein - p	677	268	2	T40606	hypothetical prote
605	6	0.8	254	2	T07103	14-3-3 protein hom	678	269	2	T36639	probable substrate
606	6	0.8	255	2	T04127	14-3-3 protein, is	679	269	2	AG3538	ubiquitinone/menaqu
607	6	0.8	255	2	T02050	14-3-3 protein hom	680	269	2	AE0466	probable haloacid
608	6	0.8	256	2	T04153	GF14-c protein - r	681	270	2	AB1308	conserved hypotet
609	6	0.8	256	2	T10109	tryptophan (EC 3.4.21	682	270	2	AB1680	conserved hypotet
610	6	0.8	256	2	T44452	amidase yedB [impo	683	270	2	F69362	probable carboxyla
611	6	0.8	256	2	D70565	probable pseudouri	684	271	2	A85552	probable carboxyla
612	6	0.8	256	2	AI0267	probable membrane	685	271	2	F90701	probable carboxyla
613	6	0.8	256	2	G71121	hypothetical prote	686	271	2	G64783	probable carboxyla



687	6	0.8	272	2	B75293	amino acid ABC tra	760	295	2	F83412	probable transcrip
688	6	0.8	272	2	AG2819	conserved hypotet	761	295	2	T32202	hypothetical prote
689	6	0.8	272	2	G97597	hypothetical prote	762	297	2	AD3225	ABC transporter, m
690	6	0.8	273	2	D81878	probable oxidoredu	763	297	2	T45990	probable regulator
691	6	0.8	273	2	H81140	oxidoreductase, sh	764	297	2	S50663	conserved hypotet
692	6	0.8	273	2	T49994	14-3-3-like protei	765	297	2	H90154	hypothetical prote
693	6	0.8	273	2	F82999	CysQ protein PA517	766	297	2	D83357	probable transcrip
694	6	0.8	273	2	A86280	F14L17.29 protein	767	297	2	T27525	hypothetical prote
695	6	0.8	273	2	AI3630	membrane protein n	768	298	2	AH0947	probable sugar kin
696	6	0.8	273	2	AC3573	oligopeptide trans	769	298	2	C55223	minor tail protein
697	6	0.8	273	2	G83403	conserved hypotet	770	298	2	A28260	chromosomal protei
698	6	0.8	273	2	C95924	probable response	771	299	2	A80269	conserved hypotet
699	6	0.8	274	2	G86977	probable methyltra	772	299	2	A87530	phosphorylase fami
700	6	0.8	274	2	H83707	bacitracin resista	773	299	2	S30861	hypothetical prote
701	6	0.8	274	2	D96840	hypothetical prote	774	300	1	S40827	probable sugar kin
702	6	0.8	274	2	H70247	hypothetical prote	775	300	2	F91229	probable kinase [i
703	6	0.8	275	2	S40007	trypsin (EC 3.4.21	776	300	2	E86076	probable kinase yi
704	6	0.8	275	2	S40005	trypsin (EC 3.4.21	777	301	2	AD0660	probable transcrip
705	6	0.8	275	2	E70693	probable ugpE prot	778	301	2	E86486	protein F28J9.4 [i
706	6	0.8	275	2	G83522	conserved hypotet	779	302	2	S69188	probable flavonol
707	6	0.8	276	2	JE0218	28k surface antige	780	302	2	AF3306	dipeptide transpor
708	6	0.8	276	2	E84373	hypothetical prote	781	302	2	E84421	probable phosphati
709	6	0.8	278	2	AE0210	4-deoxy-L-threo-5-	782	302	2	B70888	hypothetical prote
710	6	0.8	278	2	AD0146	probable ABC trans	783	302	2	PC4287	protein kinase (EC
711	6	0.8	279	1	S74824	glutamate racemase	784	303	2	D83082	probable permease
712	6	0.8	279	2	C70458	diaminopimelate ep	785	303	2	S77278	lipic acid synthe
713	6	0.8	279	2	B70328	hypothetical prote	786	303	2	T36509	probable molybdopt
714	6	0.8	280	2	T36066	hypothetical prote	787	303	2	B72218	hypothetical prote
715	6	0.8	280	2	B84498	En/Spm-like transp	788	304	2	F83987	heat-shock protein
716	6	0.8	280	2	H72504	hypothetical prote	789	304	2	D72316	ribosomal large su
717	6	0.8	281	2	T43945	ribosomal protein	790	304	2	A96642	hypothetical prote
718	6	0.8	281	2	T05522	hypothetical prote	791	304	2	S75441	hypothetical prote
719	6	0.8	281	2	JE0418	aminoglycoside-N-a	792	305	2	T23022	hypothetical prote
720	6	0.8	282	2	AC1728	hypothetical prote	793	305	2	T20585	hypothetical prote
721	6	0.8	282	2	AB1054	conserved hypotet	794	306	2	A48552	transfer protein t
722	6	0.8	284	2	D81075	conserved hypotet	795	307	2	B83723	hypothetical prote
723	6	0.8	284	2	S75817	hypothetical prote	796	307	2	H70214	antigen, P35 homol
724	6	0.8	284	2	T24479	hypothetical prote	797	307	2	S55596	hypothetical prote
725	6	0.8	284	2	F81431	ABC transporter AR	798	308	2	I40166	hypothetical prote
726	6	0.8	285	2	B83588	hypothetical prote	799	308	2	S77938	aspartate carbamoy
727	6	0.8	285	2	F70194	hypothetical prote	800	308	2	T05297	EBNA-IP protein -
728	6	0.8	285	2	AH0200	conserved hypotet	801	308	2	E90670	hypothetical prote
729	6	0.8	286	2	E97720	hflC protein (mpo	802	309	2	B84550	hypothetical prote
730	6	0.8	286	2	A71722	hflC protein (hflC	803	310	2	AE3398	N-acetyl-gamma-glu
731	6	0.8	286	2	B83343	hypothetical prote	804	311	2	G90407	homoserine kinase
732	6	0.8	286	2	E91277	probable oxidoredu	805	312	2	F82889	holliday junction
733	6	0.8	286	2	E86118	probable oxidoredu	806	312	2	T45834	hypothetical prote
734	6	0.8	287	2	S56436	hypothetical 29.7K	807	313	2	AI2202	hypothetical prote
735	6	0.8	287	2	E75202	diptide abc tran	808	314	2	C69286	hypothetical prote
736	6	0.8	287	2	S03787	probable dimethyls	809	314	2	E96759	probable tumor-rel
737	6	0.8	287	2	AF0970	conserved hypotet	810	314	2	D97318	ABC-type MDR trans
738	6	0.8	287	2	F65165	33.2 kD protein in	811	316	2	E70664	hypothetical prote
739	6	0.8	287	2	H86040	probable alpha hel	812	316	2	E97086	hypothetical prote
740	6	0.8	287	2	G91193	probable alpha hel	813	317	1	E87185	3',5'-cyclic-nucle
741	6	0.8	287	2	E69778	conserved hypotet	814	317	2	F82672	ATP sulfurylase, s
742	6	0.8	288	2	G64102	phosphatidate cyti	815	317	2	S72871	hypothetical prote
743	6	0.8	288	2	T22721	hypothetical prote	816	318	1	F70536	3',5'-cyclic-nucle
744	6	0.8	290	1	D47468	cytochrome-c oxida	817	318	2	C71168	hypothetical prote
745	6	0.8	290	2	E70141	oligopeptide trans	818	319	2	AC2536	hypothetical prote
746	6	0.8	290	2	T24747	hypothetical prote	819	320	2	T10281	hypothetical prote
747	6	0.8	290	2	D71546	probable DNA pol I	820	321	2	F97122	exopolysphatase
748	6	0.8	290	2	F81700	DNA polymerase III	821	321	2	T27463	hypothetical prote
749	6	0.8	291	2	S05508	photosystem II oxy	822	321	2	G72347	hypothetical prote
750	6	0.8	291	2	A97387	hypothetical prote	823	321	2	F81030	ABC transporter, p
751	6	0.8	291	2	AD2605	hypothetical prote	824	321	2	F81976	probable ferric en
752	6	0.8	292	2	S54533	ribosomal protein	825	321	2	A69088	conserved hypotet
753	6	0.8	292	2	T34529	hypothetical prote	826	322	2	G72421	iron(III) ABC tran
754	6	0.8	292	2	T52257	CCR4-associated fa	827	322	2	E64238	hypothetical prote
755	6	0.8	292	2	H70513	hypothetical prote	828	322	2	E70306	conserved hypotet
756	6	0.8	293	1	D69300	4-hydroxybenzoate	829	322	2	AF2725	transcription regu
757	6	0.8	293	2	T41928	hypothetical prote	830	322	2	B97507	probable transcrip
758	6	0.8	293	2	T31618	hypothetical prote	831	323	2	T22492	hypothetical prote
759	6	0.8	293	2	B75570	conserved hypotet	832	323	2	T47447	sulfotransferase-1

833	6	0.8	323	2	E83454	flagellar motor sw	906	6	0.8	344	2	C75203	hypothetical prote
834	6	0.8	324	2	T07832	probable steroid s	907	6	0.8	345	2	T17065	NADH2 dehydrogenas
835	6	0.8	324	2	F86788	transcription regu	908	6	0.8	345	2	JC1174	amidase (EC 3.5.1.1.
836	6	0.8	325	1	A45470	hydroxymethylgluta	909	6	0.8	345	2	S73729	MG307 homolog H08
837	6	0.8	325	2	T11610	probable cinnamyl-	910	6	0.8	345	2	A88251	hypothetical prote
838	6	0.8	325	2	T07833	probable steroid s	911	6	0.8	345	2	AB3035	conserved hypothet
839	6	0.8	325	2	T57009	3-Hydroxy-3-methyl	912	6	0.8	346	2	JC7523	catabolite control
840	6	0.8	325	2	G90040	uroporphyrin-III C	913	6	0.8	346	2	C96739	hypothetical prote
841	6	0.8	325	2	T23426	hypothetical prote	914	6	0.8	346	2	D42087	al-phenomone recep
842	6	0.8	326	2	T03928	probable peroxidase	915	6	0.8	346	2	S64693	pheromone receptor
843	6	0.8	326	2	F86407	probable sulfotran	916	6	0.8	346	2	T46914	hypothetical prote
844	6	0.8	326	2	A84452	probable steroid s	917	6	0.8	347	2	T22555	hypothetical prote
845	6	0.8	326	2	A41732	heterogeneous ribo	918	6	0.8	347	2	D84798	probable mitochond
846	6	0.8	326	2	A49937	hypothetical prote	919	6	0.8	348	2	D84922	probable sugar tra
847	6	0.8	327	2	AB1822	pyruvate dehydroge	920	6	0.8	348	2	T31681	bacs protein - Bac
848	6	0.8	327	2	T19529	hypothetical prote	921	6	0.8	348	2	F96997	uncharacterized co
849	6	0.8	328	2	T27911	hypothetical prote	922	6	0.8	348	2	T25366	hypothetical prote
850	6	0.8	328	2	T50104	hypothetical prote	923	6	0.8	351	2	G96923	NADH-dependent fla
851	6	0.8	328	2	E95307	hypothetical prote	924	6	0.8	351	2	T01845	hypothetical prote
852	6	0.8	328	2	E95404	probable ABC trans	925	6	0.8	352	2	A39042	fatty-acid synthas
853	6	0.8	329	2	T47448	sulfotransferase-1	926	6	0.8	352	2	E83519	quinolinate synthe
854	6	0.8	329	2	C97264	UDP-galactose 4-ep	927	6	0.8	353	2	S74379	probable ATPase -
855	6	0.8	329	2	AD1170	lipote-protein li	928	6	0.8	353	2	F84252	phycocyanin alpha
856	6	0.8	329	2	AF1527	lipote-protein li	929	6	0.8	353	2	H71223	probable dolichol-
857	6	0.8	329	2	T09897	hypothetical prote	930	6	0.8	354	2	C81986	probable O-sialogl
858	6	0.8	329	2	H85520	probable Lyser-like	931	6	0.8	354	2	C81040	O-sialoglycoprotei
859	6	0.8	330	2	G88115	protein F53C3.1 (i	932	6	0.8	355	2	C86592	aminopeptidase P (
860	6	0.8	330	2	F72428	oligopeptide ABC t	933	6	0.8	355	2	B72032	proline dipeptidas
861	6	0.8	330	2	A95074	ABC transporter, A	934	6	0.8	356	2	T36961	probable zinc-cont
862	6	0.8	330	2	E97941	hypothetical prote	935	6	0.8	356	2	H84934	UDP-N-acetylurama
863	6	0.8	331	2	S70212	hypothetical prote	936	6	0.8	356	2	H72214	hypothetical prote
864	6	0.8	331	2	B87359	riboflavin biosynt	937	6	0.8	356	2	AC1888	hypothetical prote
865	6	0.8	331	2	E82170	peptide ABC transp	938	6	0.8	357	2	E64233	membrane transport
866	6	0.8	332	2	T47703	Ca-dependent solut	939	6	0.8	358	2	T45934	hypothetical prote
867	6	0.8	332	2	A11355	low-affinity inorg	940	6	0.8	358	2	JQ0596	hypothetical prote
868	6	0.8	332	2	AB1726	hypothetical prote	941	6	0.8	359	2	T36443	probable penicilli
869	6	0.8	333	1	H64400	hypothetical prote	942	6	0.8	359	2	T29647	hypothetical prote
870	6	0.8	333	2	A84523	probable steroid s	943	6	0.8	360	2	D83255	3-isopropylmalate
871	6	0.8	333	2	A41881	collagenase PrtC (	944	6	0.8	361	1	SYEBKR	chorismate synthas
872	6	0.8	334	2	T19637	hypothetical prote	945	6	0.8	361	1	SYECKR	chorismate synthas
873	6	0.8	334	2	B87545	hypothetical prote	946	6	0.8	361	2	AF0804	chorismate synthas
874	6	0.8	334	2	AB3414	probable transcrip	947	6	0.8	361	2	E91030	chorismate synthas
875	6	0.8	335	2	G70369	sialoglycoproteina	948	6	0.8	361	2	F85874	chorismate synthas
876	6	0.8	335	2	F96999	hydrogenase format	949	6	0.8	361	2	F82115	chorismate synthas
877	6	0.8	335	2	H81677	conserved hypothet	950	6	0.8	361	2	JC6314	major porin protei
878	6	0.8	335	2	H91191	hypothetical prote	951	6	0.8	361	2	A43510	probable histidine
879	6	0.8	335	2	AB6039	probable LPS biosy	952	6	0.8	362	2	D72734	hypothetical prote
880	6	0.8	335	2	AB2193	hypothetical prote	953	6	0.8	362	2	G84526	glycosyltransferas
881	6	0.8	335	2	T33457	hypothetical prote	954	6	0.8	364	2	AB2993	hypothetical prote
882	6	0.8	335	2	E71215	hypothetical prote	955	6	0.8	364	2	H70776	ferredoxin-NADP re
883	6	0.8	336	2	S61299	lipopolysaccharide	956	6	0.8	365	1	A44974	hypothetical prote
884	6	0.8	336	2	C81073	ADP-heptose-LPS he	957	6	0.8	365	2	T23220	hypothetical prote
885	6	0.8	336	2	B81869	lipopolysaccharide	958	6	0.8	366	1	JN0146	translation releas
886	6	0.8	336	2	A97305	hypothetical prote	959	6	0.8	366	2	A64950	membrane-bound pen
887	6	0.8	337	2	AD0972	lipopolysaccharide	960	6	0.8	366	2	C85800	probable cyclochrom
888	6	0.8	339	2	AD0009	glycerol-3-phospha	961	6	0.8	366	2	G90951	probable cyclochrom
889	6	0.8	339	2	T46713	hypothetical prote	962	6	0.8	366	2	JE0105	testicular serine
890	6	0.8	339	2	E95962	probable taurine u	963	6	0.8	366	2	F87508	GTP-binding protei
891	6	0.8	339	2	E82211	conserved hypothet	964	6	0.8	367	2	S68680	stress-activated p
892	6	0.8	339	2	G82113	lipoprotein-34 Nlp	965	6	0.8	367	2	JE0104	testicular serine
893	6	0.8	339	2	F97121	probable membrane-	966	6	0.8	367	2	H83088	membrane-bound lyp
894	6	0.8	340	2	T35394	probable glycerol	967	6	0.8	368	2	G85587	hypothetical prote
895	6	0.8	340	2	T14774	hypothetical prote	968	6	0.8	368	2	F90737	hypothetical prote
896	6	0.8	341	2	T33221	hypothetical prote	969	6	0.8	368	2	H64815	ybhR protein - Esc
897	6	0.8	341	2	AB1394	galactosyltransfer	970	6	0.8	369	1	RDSPPX	ferredoxin-NADP re
898	6	0.8	341	2	AB1769	galactosyltransfer	971	6	0.8	369	2	F81674	conserved hypothet
899	6	0.8	342	2	H86893	elongation factor	972	6	0.8	369	2	S37314	cycH protein - Bra
900	6	0.8	342	2	A10043	conserved hypothet	973	6	0.8	369	2	H82404	hypothetical prote
901	6	0.8	342	2	AF1398	ATP binding protei	974	6	0.8	370	2	F95363	probable serine-py
902	6	0.8	342	2	AC1774	ATP binding protei	975	6	0.8	370	2	C96979	similar to spore g
903	6	0.8	342	2	C86811	hypothetical prote	976	6	0.8	370	2	AF1432	recF protein limpo
904	6	0.8	343	2	G72218	conserved hypothet	977	6	0.8	370	2	H72748	probable glycerol
905	6	0.8	344	1	S49978	aspartate-semialde	978	6	0.8	370	2	T33382	hypothetical prote

979	6	0.8	371	2	C70237	hypothetical prote	1052	393	2	AB1146	histidyl-tRNA synt
980	6	0.8	371	2	T18558	probable mitochond	1053	393	2	P91195	probable integrase
981	6	0.8	372	1	A55510	chorismate synthas	1054	393	2	G86042	probable integrase
982	6	0.8	372	1	D69442	conserved hypothet	1055	393	2	A55859	regulatory protein
983	6	0.8	372	2	S18953	fix23-1 protein -	1056	393	2	D96577	hypothetical prote
984	6	0.8	372	2	T09612	secreted glycoprot	1057	393	2	E97309	probable amidohydr
985	6	0.8	373	2	A82398	maltose/maltodextr	1058	394	2	JS0600	t-plasminogen acti
986	6	0.8	373	2	G90398	hypothetical prote	1059	394	2	T44463	integrase int [limp
987	6	0.8	373	2	E72216	alanine-tRNA ligas	1060	394	2	S26431	intermediate filam
988	6	0.8	374	2	G90338	hypothetical prote	1061	394	2	S39739	efflux protein hom
989	6	0.8	374	2	G89846	hypothetical prote	1062	395	1	Q08CTR	hypothetical 45.2K
990	6	0.8	375	2	S17253	alcohol dehydrogen	1063	395	2	F69148	hypothetical prote
991	6	0.8	375	2	D82585	imidazoleglycerolp	1064	395	2	T00574	probable protein k
992	6	0.8	375	2	A83802	NAD biosynthesis n	1065	395	2	A40270	cyclin E - human
993	6	0.8	375	2	C90746	probable enzyme (i	1066	395	2	A91129	hypothetical prote
994	6	0.8	375	2	G85596	probable enzyme yb	1067	395	2	H85973	hypothetical prote
995	6	0.8	375	2	C64824	probable RNA methy	1068	395	2	A83543	succinyl-diaminopi
996	6	0.8	376	1	F64705	conserved hypothet	1069	395	2	A95860	hypothetical prote
997	6	0.8	376	2	F71815	hypothetical prote	1070	395	2	B83313	probable type II s
998	6	0.8	376	2	AD1915	hypothetical prote	1071	396	2	AB2309	hypothetical prote
999	6	0.8	377	2	G85975	hypothetical prote	1072	397	2	AE2108	flagellar hook-ass
1000	6	0.8	379	2	T32778	hypothetical prote	1073	397	2	AE1142	penicillin-binding
1001	6	0.8	379	2	T21417	hypothetical prote	1074	398	2	C81729	Mtr/TnaB/Tyros per
1002	6	0.8	380	2	A55259	kappa opioid recep	1075	398	2	D83506	conserved hypothet
1003	6	0.8	380	2	T43016	DNA mismatch repai	1076	398	2	AH1500	penicillin-binding
1004	6	0.8	380	2	G86656	ABC transporter pe	1077	399	2	F82657	beta-ketoacyl-AACP
1005	6	0.8	380	2	A12185	hypothetical prote	1078	399	2	A31137	hemocyanin - giant
1006	6	0.8	381	2	A43769	fodrin alpha chain	1079	399	2	F89893	hypothetical prote
1007	6	0.8	381	2	S65212	hypothetical prote	1080	400	1	JC1428	ketol-acid reducto
1008	6	0.8	381	2	T34692	probable transmemb	1081	400	2	G64104	pantothenate metab
1009	6	0.8	382	2	E82249	mrp protein VCL037	1082	400	2	F86987	hypothetical prote
1010	6	0.8	382	2	G86791	hypothetical prote	1083	400	2	T04460	protein kinase AME
1011	6	0.8	382	2	T38092	hypothetical prote	1084	401	2	T25031	hypothetical prote
1012	6	0.8	382	2	A13175	conserved hypothet	1085	402	2	AD1417	drug-efflux transp
1013	6	0.8	383	1	A25978	alcohol dehydrogen	1086	402	2	S71137	ectin C1 - sea ur
1014	6	0.8	383	2	S32375	gene BCF2 protein	1087	402	2	T04348	endosperm specific
1015	6	0.8	383	2	B83205	hypothetical prote	1088	402	2	C83881	hypothetical prote
1016	6	0.8	383	2	T23041	hypothetical prote	1089	403	1	S23802	homeotic protein 1
1017	6	0.8	383	2	A71139	hypothetical prote	1090	403	1	S01828	probable high-affi
1018	6	0.8	384	2	G91130	N-acetylglactosam	1091	403	2	JQ0028	cytokeratin 19 - m
1019	6	0.8	385	2	T52483	hypothetical prote	1092	403	2	T45580	hypothetical prote
1020	6	0.8	385	2	T47535	hypothetical prote	1093	403	2	T27948	hypothetical prote
1021	6	0.8	385	2	T51127	GGPP synthase [limp	1094	403	2	JC5171	D-galactose-bindin
1022	6	0.8	385	2	AE2651	hypothetical prote	1095	404	2	T40532	ketol-acid reducto
1023	6	0.8	385	2	D97433	polyamine transpor	1096	404	2	G01507	LiM domain transcr
1024	6	0.8	386	1	S22315	snRNP-associated p	1097	404	2	A55444	integral membrane
1025	6	0.8	386	2	H71511	probable 2-compone	1098	404	2	B46189	orf within vasotoc
1026	6	0.8	386	2	T09598	cyclin 4, D-type -	1099	405	1	T00089	ABC transporter rg
1027	6	0.8	387	2	H71708	pol (A) POLYMERASE	1100	405	2	AB2995	conserved hypothet
1028	6	0.8	387	2	T38876	probable ribosomal	1101	405	2	AB0793	probable MR-MuE-fa
1029	6	0.8	387	2	F82815	voltage-gated pota	1102	406	1	I58187	homeotic protein 1
1030	6	0.8	387	2	C86640	multidrug efflux t	1103	406	1	I48186	homeotic protein 1
1031	6	0.8	387	2	S00867	colicin N - Escher	1104	406	1	I48637	homeotic protein 1
1032	6	0.8	387	2	T47013	hypothetical prote	1105	406	1	I50375	homeotic protein 1
1033	6	0.8	387	2	E83679	multidrug-efflux t	1106	406	2	G70639	hypothetical prote
1034	6	0.8	387	2	E97028	probable amidohydr	1107	406	2	B89942	conserved hypothet
1035	6	0.8	387	2	AD0237	probable membrane	1108	406	2	AC2721	MFS permease [limp
1036	6	0.8	387	2	H83714	FeA14.9 protein -	1109	407	2	G97502	probable mfs trans
1037	6	0.8	388	2	H83714	alanine racemase B	1110	407	2	E95214	hypothetical prote
1038	6	0.8	388	2	AG2663	mrp protein [impor	1111	408	2	H98290	hypothetical prote
1039	6	0.8	389	2	B86017	probable 3-oxoacyl	1112	408	2	JC1378	aryldialkylphospha
1040	6	0.8	389	2	B91171	probable 3-oxoacyl	1113	409	2	C95042	hypothetical prote
1041	6	0.8	389	2	C83202	alginate biosynthe	1114	410	2	T34717	probable transmemb
1042	6	0.8	390	2	F97445	mrp protein homolo	1115	410	2	S68515	hypothetical argini
1043	6	0.8	390	2	AB3384	N-acetylmuramoyl-L	1116	410	2	D84785	hypothetical prote
1044	6	0.8	391	2	F83269	fatty-acid oxidati	1117	410	2	S38238	hypothetical prote
1045	6	0.8	391	2	F88778	protein T20D3.3 [i	1118	411	2	H95048	3-oxoacyl-(acyl)-ca
1046	6	0.8	391	2	B70625	probable PPE prote	1119	411	2	PC2061	genome polypeptid
1047	6	0.8	392	2	F83610	probable fatty aci	1120	411	2	AB3485	florfenicol resist
1048	6	0.8	392	2	AB1505	histidyl-tRNA synt	1121	411	2	S40064	3-deoxy-manno-octu
1049	6	0.8	392	2	S72984	hypothetical prote	1122	412	2	H70915	probable pgk prote
1050	6	0.8	392	2	T34095	zinc finger protei	1123	412	2	H75484	hypothetical prote
1051	6	0.8	393	2	AB0035	cystathionine beta	1124	412	2		

1125	6	0.8	413	2	T43170	probable triacylgly	1198	6	0.8	431	2	T00698	methionyl aminopep
1126	6	0.8	413	2	S61305	cycH protein - Par	1199	6	0.8	431	2	JS0599	t-plasminogen acti
1127	6	0.8	413	2	A82726	conserved hypotet	1200	6	0.8	431	2	F86179	hypothetical prote
1128	6	0.8	413	2	T26915	hypothetical prote	1201	6	0.8	432	1	RWCQT4	T-cell surface gly
1129	6	0.8	414	2	H70667	probable oxidoredu	1202	6	0.8	432	1	RWCZT4	probable asparagin
1130	6	0.8	414	2	F97919	3-oxoacyl-lacyl-ca	1203	6	0.8	432	2	B71442	conserved hypotet
1131	6	0.8	414	2	E90572	hypothetical prote	1204	6	0.8	432	2	E89954	u-plasminogen acti
1132	6	0.8	414	2	E87316	periplasmic phosph	1205	6	0.8	432	1	JN0560	UDP-N-acetylmutamo
1133	6	0.8	414	2	E87292	pentapeptide repea	1206	6	0.8	433	1	UKBAY	F611.5 protein - A
1134	6	0.8	414	2	A29835	Sali protein - Esc	1207	6	0.8	433	2	D75480	nicotinate phospho
1135	6	0.8	414	2	A10277	probable phage-rel	1208	6	0.8	434	2	A86305	hypothetical prote
1136	6	0.8	415	2	I58144	corticotropin-rele	1209	6	0.8	435	2	H82501	hypothetical prote
1137	6	0.8	415	2	D81909	probable integral	1210	6	0.8	435	2	T47737	cellulose phospho
1138	6	0.8	415	2	D81107	conserved hypotet	1211	6	0.8	435	2	AB1786	probable 2-ketoglu
1139	6	0.8	415	2	T49072	hypothetical prote	1212	6	0.8	435	2	E83362	polynucleotide ade
1140	6	0.8	416	1	S06763	calreticulin precu	1213	6	0.8	436	2	G97701	cholecystokinin-A
1141	6	0.8	416	1	ACCH3N	nicotinic acetylch	1214	6	0.8	436	2	JC5599	hypothetical prote
1142	6	0.8	416	2	D71277	tyrosine-tRNA liga	1215	6	0.8	436	2	S74385	hypothetical prote
1143	6	0.8	417	2	D98078	conserved oxidase	1216	6	0.8	436	2	S48399	hypothetical prote
1144	6	0.8	417	2	G98200	sarcosine oxidase	1217	6	0.8	436	2	F86486	protein F2809.3 [I
1145	6	0.8	417	2	AB3086	sarcosine oxidase	1218	6	0.8	436	2	G97186	NADH2 dehydrogenas
1146	6	0.8	417	2	AE3056	sarcosine oxidase	1219	6	0.8	437	2	S34959	keratin 13, type I
1147	6	0.8	417	2	T05207	hypothetical prote	1220	6	0.8	437	2	A55682	transcription fact
1148	6	0.8	417	2	A97063	NAD(PAD)-dependent	1221	6	0.8	438	1	S11225	transforming prote
1149	6	0.8	418	2	H97437	cyclopropane-fatty	1222	6	0.8	438	2	JC1179	hypothetical prote
1150	6	0.8	418	2	AC2656	cyclopropane-fatty	1223	6	0.8	438	2	AF3215	transforming prote
1151	6	0.8	418	2	E96765	hypothetical prote	1224	6	0.8	438	2	AH2285	hypothetical prote
1152	6	0.8	418	2	H83126	probable secretion	1225	6	0.8	439	1	TVCTMC	transforming prote
1153	6	0.8	419	2	C84813	probable protein k	1226	6	0.8	439	1	TVMS	probable cytochrom
1154	6	0.8	419	2	D86785	diaminopimelate de	1227	6	0.8	439	2	T25494	transcription fact
1155	6	0.8	419	2	JC4123	pregnancy-specific	1228	6	0.8	440	1	A35875	TyA protein - years
1156	6	0.8	419	2	S75647	glutamate N-acetyl	1229	6	0.8	440	1	QOBYTY	phosphopyruvate hy
1157	6	0.8	419	2	B89788	hypothetical prote	1230	6	0.8	440	2	S43113	transcription fact
1158	6	0.8	419	2	F83673	PTS system, galact	1231	6	0.8	440	2	I48291	protein-tyrosine-p
1159	6	0.8	420	2	B98288	hypothetical prote	1232	6	0.8	440	2	I50213	TyA protein - years
1160	6	0.8	420	2	B95100	conserved hypotet	1233	6	0.8	440	2	S57044	TyA protein - years
1161	6	0.8	420	2	D97368	hypothetical prote	1234	6	0.8	440	2	A22671	TyA protein - years
1162	6	0.8	421	2	B84702	iron-containing al	1235	6	0.8	440	2	S57046	TyA protein - years
1163	6	0.8	422	2	H82236	xanthine permease	1236	6	0.8	440	2	S69837	TyA protein - years
1164	6	0.8	422	2	F89803	trNA adenyllyltrans	1237	6	0.8	440	2	S45866	TyA protein - years
1165	6	0.8	423	2	A13309	sarcosine oxidase	1238	6	0.8	440	2	S69964	TyA protein - years
1166	6	0.8	423	2	A99230	PTS system galacti	1239	6	0.8	440	2	SS0947	TyA protein - years
1167	6	0.8	423	2	AH1407	PTS system galacti	1240	6	0.8	440	2	SS1894	TyA protein - years
1168	6	0.8	423	2	AH1783	ragD protein - Bra	1241	6	0.8	440	2	S69840	TyA protein - years
1169	6	0.8	423	2	T31342	aconitate hydratase	1242	6	0.8	440	2	S69985	TyA protein - years
1170	6	0.8	424	2	C64362	probable secreted	1243	6	0.8	440	2	S69971	TyA protein - years
1171	6	0.8	424	2	T35535	cell wall-binding	1244	6	0.8	440	2	S69976	TyA protein - years
1172	6	0.8	424	2	AD2017	probable malate de	1245	6	0.8	440	2	SS3588	TyA protein - years
1173	6	0.8	426	2	A81933	malate oxidoreduct	1246	6	0.8	440	2	S70228	TyA protein - years
1174	6	0.8	426	2	C81173	serine/threonine-s	1247	6	0.8	440	2	S53553	TyA protein - years
1175	6	0.8	426	2	T52285	ubiquinol-cytochro	1248	6	0.8	440	2	S51249	TyA protein YD8557
1176	6	0.8	426	2	E70058	phosphotransferase	1249	6	0.8	440	2	S61577	TyA protein - years
1177	6	0.8	427	2	S55905	N-ethylmalamine ch	1250	6	0.8	440	2	S40909	branched-chain ami
1178	6	0.8	427	2	G69067	hypothetical prote	1251	6	0.8	440	2	D69596	conserved hypotet
1179	6	0.8	427	2	T29376	polymorphic outer	1252	6	0.8	440	2	D64186	probable proteinase
1180	6	0.8	427	2	A86493	transforming prote	1253	6	0.8	440	2	C97620	transcription fact
1181	6	0.8	428	1	TVHUEK	probable oxidoredu	1254	6	0.8	441	1	A53988	transcription fact
1182	6	0.8	428	2	D70989	glycine hydroxymet	1255	6	0.8	441	1	TVCHTE	transcription fact
1183	6	0.8	428	2	D70343	cholecystokinin ty	1256	6	0.8	441	1	TVHUEK	glucuronate 2-dehydr
1184	6	0.8	428	2	JN0692	flavoprotein, elec	1257	6	0.8	441	2	C38575	isochorismate synt
1185	6	0.8	428	2	F85482	flavoprotein (impo	1258	6	0.8	442	1	UKFG	probable cytochrom
1186	6	0.8	428	2	F90634	fixC protein - Esc	1259	6	0.8	442	1	E84264	hypothetical prote
1187	6	0.8	428	2	C64725	cytochrome-c3 hydr	1260	6	0.8	442	2	G84465	alpha-amyliase - Ae
1188	6	0.8	428	2	B75133	hypothetical prote	1261	6	0.8	443	2	G59102	NADH2 dehydrogenas
1189	6	0.8	428	2	T06290	protein-histidine	1262	6	0.8	443	2	P30010	cholecystokinin re
1190	6	0.8	429	2	G56273	carbon dioxide-fix	1263	6	0.8	443	2	I39538	probable helicase
1191	6	0.8	429	2	E70979	elk1 protein - mou	1264	6	0.8	444	2	A24685	hybrid cluster [4F
1192	6	0.8	429	2	JC4965	hypothetical prote	1265	6	0.8	445	2	H71243	hypothetical prote
1193	6	0.8	429	2	C84194	hypothetical prote	1266	6	0.8	446	2	T26762	hypothetical prote
1194	6	0.8	429	2	A70949	FMN oxidoreductase	1267	6	0.8	446	2	E75075	hydroxyproline-ric
1195	6	0.8	430	2	F87472	homoserine dehydro	1268	6	0.8	446	2	F86815	DNA repair protein
1196	6	0.8	431	1	UKGU		1269	6	0.8	446	2	T07907	
1197	6	0.8	431	2	F84077		1270	6	0.8	446	2	A75209	

1271	6	0.8	447	2	C86233	hypothetical prote	1344	6	0.8	471	2	E83173	hypothetical prote
1272	6	0.8	448	2	AE1919	hypothetical prote	1345	6	0.8	472	2	A84741	probable myrosinas
1273	6	0.8	449	2	AC1019	probable xanthine/	1346	6	0.8	473	2	T47436	protein kinase-lik
1274	6	0.8	449	2	T23126	hypothetical prote	1347	6	0.8	472	2	E98020	hypothetical prote
1275	6	0.8	450	2	C87463	hypothetical prote	1348	6	0.8	472	2	TS1559	probable flavonol
1276	6	0.8	450	2	T08701	hypothetical prote	1349	6	0.8	473	2	E86955	conserved hypothet
1277	6	0.8	451	2	A85836	PTS system galacti	1350	6	0.8	473	2	G70975	hypothetical prote
1278	6	0.8	451	2	C64976	gacC protein - Esc	1351	6	0.8	474	2	S30227	transposase - Clos
1279	6	0.8	451	2	G90990	PTS system galacti	1352	6	0.8	474	2	H82564	3-isopropylmalate
1280	6	0.8	451	2	T36217	plasmid transfer p	1353	6	0.8	474	2	T26694	hypothetical prote
1281	6	0.8	452	2	I49595	cytokerin 15 - m	1354	6	0.8	476	2	A70318	aldehyde dehydroge
1282	6	0.8	454	1	C69214	zinc metalloprotei	1355	6	0.8	476	2	T47606	UMP synthase - Ara
1283	6	0.8	454	2	F75580	probable sugar tra	1356	6	0.8	476	2	S46440	bifunctional UMP s
1284	6	0.8	455	2	B90619	NADH dehydrogenase	1357	6	0.8	477	1	A34369	t-plasminogen acti
1285	6	0.8	455	2	S50725	hypothetical prote	1358	6	0.8	477	2	JS0597	t-plasminogen acti
1286	6	0.8	456	1	KRHU5	hypothetical prote	1359	6	0.8	477	2	JS0598	hypothetical prote
1287	6	0.8	456	2	T40386	hypothetical prote	1360	6	0.8	477	2	T46304	aldehyde dehydroge
1288	6	0.8	456	2	H85022	hypothetical prote	1361	6	0.8	478	2	E90495	translation elonga
1289	6	0.8	456	2	T05612	hypothetical prote	1362	6	0.8	478	2	S36183	translation elonga
1290	6	0.8	456	2	S47924	MGAL protein - yea	1363	6	0.8	478	2	JQ2240	TYA protein - yea
1291	6	0.8	457	2	AC1056	murein peptide lig	1364	6	0.8	478	2	S52602	hypothetical prote
1292	6	0.8	457	2	B86121	probable ligase YJ	1365	6	0.8	478	2	T25899	related to aldehyd
1293	6	0.8	457	2	B91280	probable ligase [i	1366	6	0.8	479	2	TS1919	lipopolysaccharide
1294	6	0.8	457	2	S56459	UDP-N-acetylmuram	1367	6	0.8	479	2	D72354	serine/threonine p
1295	6	0.8	457	2	AH0898	PTS system, galact	1368	6	0.8	479	2	S48705	protein kinase hom
1296	6	0.8	457	2	B83643	potassium uptake p	1369	6	0.8	480	2	T04849	lipopolysaccharide
1297	6	0.8	457	2	B82268	conserved hypothet	1370	6	0.8	482	2	B35843	probable non-proce
1298	6	0.8	458	1	RWHUT4	T-cell surface gly	1371	6	0.8	482	2	E97012	altronate oxidorec
1299	6	0.8	458	2	B90621	NADH dehydrogenase	1372	6	0.8	483	2	A85723	tagaturonate reduc
1300	6	0.8	458	2	B90625	NADH dehydrogenase	1373	6	0.8	483	2	D64906	altronate oxidorec
1301	6	0.8	458	2	B90615	NADH dehydrogenase	1374	6	0.8	483	2	H90894	gag-myc polyprotei
1302	6	0.8	458	2	B90617	NADH dehydrogenase	1375	6	0.8	484	1	TMVVFET	hypothetical prote
1303	6	0.8	458	2	T11176	NADH2 dehydrogenas	1376	6	0.8	484	2	D89781	hypothetical prote
1304	6	0.8	458	2	T11528	NADH2 dehydrogenas	1377	6	0.8	484	2	T33492	transcription fact
1305	6	0.8	458	2	B99613	NADH dehydrogenase	1378	6	0.8	485	1	TVCHET	rhamnulokinase (EC
1306	6	0.8	458	2	B90627	NADH dehydrogenase	1379	6	0.8	485	2	AD0041	glutamyl-tRNA(Gln)
1307	6	0.8	458	2	B90623	NADH dehydrogenase	1380	6	0.8	485	2	B69795	probable phor prot
1308	6	0.8	458	2	B97324	sugar/Na+ (H+) simp	1381	6	0.8	485	2	A70706	probable cytochrom
1309	6	0.8	459	2	S10196	NADH2 dehydrogenas	1382	6	0.8	486	2	T32431	glutamyl-tRNA (Gln
1310	6	0.8	459	2	T11411	NADH2 dehydrogenas	1383	6	0.8	487	2	E98326	coenzyme F420-quin
1311	6	0.8	459	2	T11189	NADH2 dehydrogenas	1384	6	0.8	487	2	E98326	hypothetical prote
1312	6	0.8	459	2	T11256	NADH2 dehydrogenas	1385	6	0.8	488	1	TVFVES	transcription fact
1313	6	0.8	459	2	T11084	NADH2 dehydrogenas	1386	6	0.8	488	2	F95875	hypothetical prote
1314	6	0.8	459	2	AE0679	probable membrane	1387	6	0.8	488	2	F95875	shaw protein - Cal
1315	6	0.8	459	2	G90080	probable thiophene	1388	6	0.8	489	2	JC4787	nicotinate phospho
1316	6	0.8	459	2	G81187	Na+/H+ antiporter	1389	6	0.8	490	2	D70008	hypothetical prote
1317	6	0.8	459	2	F81914	probable transmemb	1390	6	0.8	490	2	G70108	UDP-N-acetylmuram
1318	6	0.8	459	2	T24742	hypothetical prote	1391	6	0.8	491	2	AI0068	amino acid transpo
1319	6	0.8	459	2	D86256	hypothetical prote	1392	6	0.8	491	2	D97311	hypothetical prote
1320	6	0.8	460	2	T24248	hypothetical prote	1393	6	0.8	491	2	AG1838	hypothetical prote
1321	6	0.8	461	2	A43782	keratin, type II -	1394	6	0.8	492	2	S71112	catalase (EC 1.11.
1322	6	0.8	461	2	C86935	probable carboxype	1395	6	0.8	492	2	S41288	genome polypeptid
1323	6	0.8	461	2	D81418	probable transmemb	1396	6	0.8	492	2	C86316	protein T10022.7 l
1324	6	0.8	461	2	T00621	hypothetical prote	1397	6	0.8	493	2	TS1453	serine/threonine s
1325	6	0.8	462	2	T28699	hypothetical prote	1398	6	0.8	493	2	A85441	cytochrome P450-11
1326	6	0.8	463	2	S72992	probable phosphory	1399	6	0.8	495	2	S60589	acetylcholine rece
1327	6	0.8	463	2	T39621	peptidyl prolyl ci	1400	6	0.8	495	2	G82371	FixG-related prote
1328	6	0.8	464	2	AG2774	glutathione-disulf	1401	6	0.8	496	2	T11376	cytochrome-c oxida
1329	6	0.8	464	2	E97554	glutathione-disulf	1402	6	0.8	496	2	H70668	probable polyketid
1330	6	0.8	464	2	AF0761	probable CoA-depen	1403	6	0.8	496	2	G87546	acid-CoA ligase, p
1331	6	0.8	464	2	C83328	hypothetical prote	1404	6	0.8	496	2	T17908	proline/lysine-ric
1332	6	0.8	465	2	S03325	transforming prote	1405	6	0.8	497	2	B81728	serine proteinase,
1333	6	0.8	465	2	T40697	conserved tata bind	1406	6	0.8	497	2	S27785	acetyl-CoA acetyl
1334	6	0.8	466	2	C64690	conserved hypothet	1407	6	0.8	498	1	S52570	phosphoprotein pho
1335	6	0.8	467	2	E64974	sensory kinase Bae	1408	6	0.8	498	2	B95893	potassium channel
1336	6	0.8	467	2	AE12956	hypothetical prote	1409	6	0.8	498	2	A41359	nitrogenase (EC 1.
1337	6	0.8	469	2	AE1220	ethanolamine utili	1410	6	0.8	499	1	B29042	phosphoprotein pho
1338	6	0.8	469	2	AE1573	ethanolamine utili	1411	6	0.8	499	1	A55346	nicotinic acetylch
1339	6	0.8	470	2	B90481	glycosyltransferas	1412	6	0.8	499	2	A24572	glutelin 2 precurs
1340	6	0.8	470	2	D85111	hypothetical prote	1413	6	0.8	499	2	B34332	glutelin type I pr
1341	6	0.8	470	2	T31049	hypothetical prote	1414	6	0.8	499	2	S06350	glutelin precursor
1342	6	0.8	470	2	T49272	hypothetical prote	1415	6	0.8	499	2	A27033	hypothetical prote
1343	6	0.8	471	2	S35019	noIX protein - Rhi	1416	6	0.8	499	2	H87460	



QY 88 FENCKSCRN 96  
|||||  
Db 23 FENCKSCRN 31

## RESULT 3

T29125  
ketoacyl reductase homolog - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29125  
R/Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A/Reference number: Z17215  
A/Accession: T29125  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-276 <PAR>  
A/Cross-references: UNIPROT:O86553; EMBL:AL031350; PIDN:CAA20507.1  
C/Genetics:  
A/Note: SC1F2.16c  
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homolog

Query Match 1.28; Score 9; DB 2; Length 276;  
Best Local Similarity 100.0%; Pred. No. 0.53; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 AVSFPGRAS 678  
|||||  
Db 225 AVSFPGRAS 233

## RESULT 4

BMHUI  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human  
N/Alternate names: bone morphogenic protein 1 (BMP1)  
C/Species: Homo sapiens (man)  
C/Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999  
C/Accession: A37278; E58788  
R/Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1998  
A/Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A37278; MUID:89072730; PMID:3201241  
A/Accession: A37278  
A/Molecule type: mRNA  
A/Residues: 1-730 <WOZ>  
A/Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500  
C/Genetics:

A/Gene: GDB:BMP1  
A/Cross-references: GDB:125203; OMIM:112264  
A/Map position: 8p21-8p21  
C/Function:  
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
C/Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; B  
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g  
F/1-22/Domain: signal sequence #status predicted <SIG>  
F/130-321/Domain: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>  
F/322-431/Domain: astacin homology <AST>  
F/322-431/Domain: C1r/C1s repeat homology <C1R1>  
F/322-431/Domain: C1r/C1s repeat homology <C1R2>  
F/551-587/Domain: EGF homology <EGF>  
F/591-700/Domain: C1r/C1s repeat homology <C1R3>  
F/91,142,332,363,599/Binding site: carboxydrate (Asn) (covalent) #status predicted  
F/163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66  
F/213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted  
F/214/Active site: Glu #status predicted  
F/565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.28; Score 9; DB 1; Length 730;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
|||||  
Db 377 YDYVEVRDG 385

## RESULT 5

A58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human  
N/Alternate names: bone morphogenic protein splice form BMP-1/HIS  
C/Species: Homo sapiens (man)  
C/Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999  
C/Accession: A37278; A58788  
R/Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He;  
Science 242, 1528-1534, 1998  
A/Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A37278; MUID:89072730; PMID:3201241  
A/Accession: A37278  
A/Molecule type: mRNA  
A/Residues: 1-702, 'EKRPALQPPGRPHQLKFRVQKRNRTPO' <WOZ>  
A/Cross-references: GB:M22488; NID:G179499; PIDN:AAA51833.1; PID:G179500  
R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.  
J. Biol. Chem. 269, 32572-32578, 1994  
A/Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enco  
A/Reference number: A58788; MUID:95096114; PMID:7798260  
A/Accession: A58788  
A/Molecule type: mRNA  
A/Residues: 703-823 <TAK>  
A/Cross-references: GB:U35278; NID:G619423; PIDN:AAC41703.1; PID:G619424  
C/Genetics:  
A/Gene: GDB:BMP1; BMP-1  
A/Cross-references: GDB:125203; OMIM:112264  
A/Map position: 8p21-8p21  
C/Function:

A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen typ  
C/Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology;  
F/1-22/Domain: signal sequence #status predicted <SIG>  
F/23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>  
F/130-321/Domain: astacin homology <AST>  
F/322-431/Domain: C1r/C1s repeat homology <C1R1>  
F/322-431/Domain: C1r/C1s repeat homology <C1R2>  
F/551-587/Domain: EGF homology <EGF>  
F/591-700/Domain: C1r/C1s repeat homology <C1R3>  
F/738-752/Region: histidine-rich  
F/91,142,332,363,599/Binding site: carboxydrate (Asn) (covalent) #status predicted  
F/163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-6  
F/213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted  
F/214/Active site: Glu #status predicted  
F/565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.28; Score 9; DB 1; Length 823;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
|||||  
Db 377 YDYVEVRDG 385

## RESULT 6

B58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human  
N/Alternate names: bone morphogenic protein 1, tolloid-like splice form  
C/Species: Homo sapiens (man)  
C/Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 09-Jul-2004  
C/Accession: A37278; B58788  
R/Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He;  
Science 242, 1528-1534, 1998  
A/Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A37278; MUID:89072730; PMID:3201241  
A/Accession: A37278  
A/Molecule type: mRNA  
A/Residues: 1-702, 'EKRPALQPPGRPHQLKFRVQKRNRTPO' <WOZ>



A;Cross-references: UNIPROT:P13497; GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500  
 R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.  
 J. Biol. Chem. 269, 32572-32578, 1994  
 A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encoded  
 A;Reference number: A58788; MUID:95096114; PMID:7798260  
 A;Accession: B58788  
 A;Molecule type: mRNA  
 A;Residues: 703-986 <TK>  
 A;Cross-references: GB:L35279; NID:g619860; PIDN:AAC41710.1; PID:g619861  
 C;Genetics:  
 A;Gene: GDB:BMPL1; BMP-1  
 A;Map position: 8p21-8p21  
 C;Function:  
 A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; B  
 C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl  
 F;1-22/Domain: signal sequence #status predicted <SIG>  
 F;23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted  
 F;130-321/Domain: astacin homology <AST>  
 F;322-431/Domain: C1r/C1s repeat homology <C1R1>  
 F;435-544/Domain: C1r/C1s repeat homology <C1R2>  
 F;551-587/Domain: EGF homology <EG1>  
 F;591-700/Domain: C1r/C1s repeat homology <C1R3>  
 F;707-742/Domain: EGF homology <EG2>  
 F;747-856/Domain: C1r/C1s repeat homology <C1R4>  
 F;860-973/Domain: C1r/C1s repeat homology <C1R5>  
 F;91-142,332,359/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66  
 F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F;214/Active site: Glu #status predicted  
 F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 Query Match 1.2%; Score 9; DB 1; Length 986;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 179 YDYVEVRDG 187  
 |||||  
 DB 377 YDYVEVRDG 385  
 RESULT 7  
 I49540  
 C;Superfamily: procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I49540  
 R;Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.  
 Dev. Biol. 163, 175-183, 1994  
 A;Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel  
 A;Reference number: I49540; MUID:94229342; PMID:8174772  
 A;Accession: I49540  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-991 <RES>  
 A;Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607  
 C;Genetics:  
 A;Gene: Bmp-1  
 C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; B  
 C;Keywords: hydrolase; metalloproteinase; zinc  
 F;135-326/Domain: astacin homology <AST>  
 F;556-592/Domain: EGF homology <EG1>  
 F;596-705/Domain: C1r/C1s repeat homology <C1R>  
 F;712-747/Domain: EGF homology <EG2>  
 F;218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F;219/Active site: Glu #status predicted  
 Query Match 1.2%; Score 9; DB 2; Length 991;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 179 YDYVEVRDG 187

DB 382 YDYVEVRDG 390  
 |||||  
 RESULT 8  
 S58984  
 development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 19-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: S58984  
 R;Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.  
 Genetics 141, 271-281, 1995  
 A;Title: The tolkin gene is a tolloid/BMP-1 homologue that is essential for Drosophila  
 A;Reference number: S58984; MUID:96042912; PMID:8536976  
 A;Accession: S58984  
 A;Molecule type: mRNA  
 A;Residues: 1-1464 <PIN>  
 A;Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:g1002985; PIDN:AAC47015.1; PID:g10  
 A;Note: the authors did not translate the codon for residue 722  
 C;Genetics:  
 A;Gene: tolkin  
 A;Cross-references: FlyBase:FBgn0004885  
 C;Keywords: hydrolase; metalloproteinase; zinc  
 F;529-722/Domain: astacin homology <AST>  
 F;958-993/Domain: EGF homology <EGF>  
 F;118-1153/Domain: EGF homology <EGF1>  
 F;614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F;615/Active site: Glu #status predicted  
 Query Match 1.2%; Score 9; DB 2; Length 1464;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 179 YDYVEVRDG 187  
 |||||  
 DB 897 YDYVEVRDG 905  
 RESULT 9  
 T31070  
 notch homolog - sea urchin (Lytechinus variegatus)  
 C;Species: Lytechinus variegatus (variegated urchin)  
 C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
 C;Accession: T31070  
 R;Sherwood, D.R.; McClay, D.R.  
 Development 124, 3363-3374, 1997  
 A;Title: Identification and localization of a sea urchin Notch homologue: insights into  
 A;Reference number: Z20966; MUID:97454256; PMID:9310331  
 A;Accession: T31070  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-2531 <SHE>  
 A;Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1  
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
 Query Match 1.2%; Score 9; DB 2; Length 2531;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 260 CACLAGYTG 268  
 |||||  
 DB 537 CACLAGYTG 545  
 RESULT 10  
 S00996  
 Ig kappa chain precursor V region (A10) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 23-Jul-1999  
 C;Accession: S00996  
 R;Straubinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.  
 Biol. Chem. Hoppe-Seyler 369, 601-607, 1988  
 A;Title: Two unusual human immunoglobulin V-kappa genes.

A;Reference number: S00996; MUID:89134397; PMID:2852016  
A;Accession: S00996  
A;Molecule type: DNA  
A;Residues: 1-114 <STR>  
A;Cross-references: EMBL:M27750; NID:g185914; PIDN:AAA58912.1; PID:g553479  
A;Note: this sequence was determined from the germline gene  
C;Genetics: 16/1  
A;introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotrimer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-114/Product: Ig kappa chain V region #status predicted <MAT>  
F;42-107/Disulfide bonds: #status predicted

Query Match 1.1%; Score 8; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSSLH 215  
DB 46 QSIGSSSLH 53  
|||||

RESULT 11  
G70323  
conserved hypothetical protein aq\_260 - Aquifex aeolicus  
C;Species: Aquifex aeolicus  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C;Accession: G70323  
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
V.  
Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: G70323  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-158 <AQF>  
A;Cross-references: UNIPROT:O66619; GB:AE000681; NID:g2982963; PIDN:AAC06588.1; PID:g298298  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: aq\_260  
C;Superfamily: nus operon 15K protein

Query Match 1.1%; Score 8; DB 2; Length 158;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GKREVVGY 64  
DB 114 GKREVVGY 121  
|||||

RESULT 12  
D42696  
thrombin (EC 3.4.21.5) B chain - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
C;Accession: D42696  
R;Banfield, D.K.; MacGillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence  
A;Reference number: A42696; MUID:92212913; PMID:1557383  
A;Accession: D42696  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-235 <BAN>  
A;Cross-references: UNIPROT:Q91001; GB:M81391  
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
C;Keywords: hydrolase; serine proteinase  
F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650  
DB 157 VTDNMFCA 164  
|||||

RESULT 13  
H42696  
thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)  
C;Species: Acipenser transmontanus (white sturgeon)  
C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
C;Accession: H42696  
R;Banfield, D.K.; MacGillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence  
A;Reference number: A42696; MUID:92212913; PMID:1557383  
A;Accession: H42696  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-235 <BAN>  
A;Cross-references: UNIPROT:Q90244; GB:M81399  
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
C;Keywords: hydrolase; serine proteinase  
F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650  
DB 157 VTDNMFCA 164  
|||||

RESULT 14  
C42696  
thrombin (EC 3.4.21.5) B chain - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
C;Accession: C42696  
R;Banfield, D.K.; MacGillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence  
A;Reference number: A42696; MUID:92212913; PMID:1557383  
A;Accession: C42696  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-236 <BAN>  
A;Cross-references: UNIPROT:Q28731; GB:M81396  
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
C;Keywords: hydrolase; serine proteinase  
F;1-227/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDNMFCA 650  
DB 158 VTDNMFCA 165  
|||||

RESULT 15  
AB0338  
probable membrane protein dedD [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AB0338  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001  
A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AB0338  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-240 <KUR>  
A;Cross-references: UNIPROT:Q8ZD23; GB:AL590842; PIDN:CAC93009.1; PID:gl5980748; GSPDB:G  
C;Genetics:  
A;Gene: dedD  
C;Superfamily: dedD protein

Query Match 1.1%; Score 8; DB 2; Length 240;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 SKQKLQSA 387  
|||||||  
Db 212 SKQKLQSA 219

Search completed: May 8, 2005, 16:11:41  
Job time : 28 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 8, 2005, 16:08:34 ; Search time 50 Seconds  
(without alignments)  
7373.940 Million cell updates/sec

Title: US-10-063-692-38  
Perfect score: 720  
Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Uniprot\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	720	100.0	720	2	Q6UXH9
2	563	78.2	720	2	Q6N062
3	446	61.9	737	2	Q96JW2
4	386	53.6	417	2	Q71RE9
5	178	24.7	181	2	Q9Y432
6	61	8.5	720	2	Q8BU25
7	41	5.7	720	2	Q8K2B8
8	24	3.3	722	2	Q6DIV5
9	9	1.2	222	2	Q91WZ0
10	9	1.2	232	1	Y836 AQUAE
11	9	1.2	276	2	Q86553
12	9	1.2	593	2	Q6PUN5
13	9	1.2	639	1	BMPH STRPU
14	9	1.2	691	1	O57658
15	9	1.2	775	2	Q6P550
16	9	1.2	860	2	Q7QAH1
17	9	1.2	923	1	NRP1 BRARE
18	9	1.2	923	2	Q69DB8
19	9	1.2	986	1	BMP1 HUMAN
20	9	1.2	991	1	BMP1 MOUSE
21	9	1.2	991	2	Q6NZM2
22	9	1.2	1015	2	Q9Y6L7
23	9	1.2	1078	2	Q9UQ00
24	9	1.2	1464	2	Q23595
25	9	1.2	1464	2	Q24132
26	9	1.2	1464	2	Q9VC47
27	9	1.2	2531	2	O16004
28	9	1.1	81	2	Q79204
29	8	1.1	133	2	Q6LTX4
30	8	1.1	136	2	Q8CEX5
31	8	1.1	152	2	Q924X1

32	8	1.1	158	1	Y260 AQUAE
33	8	1.1	234	2	Q90244
34	8	1.1	235	2	Q28731
35	8	1.1	240	2	Q668X3
36	8	1.1	240	2	Q82D23
37	8	1.1	242	2	Q8DOT9
38	8	1.1	360	1	MTSB_LACLC
39	8	1.1	367	2	Q9XUN6
40	8	1.1	385	2	Q90WS2
41	8	1.1	395	1	VIBC VIBCH
42	8	1.1	407	1	FA7_BOVIN
43	8	1.1	411	2	Q67UZ3
44	8	1.1	413	2	Q7X370
45	8	1.1	486	1	YDBH_SCHPO
46	8	1.1	556	2	Q7UX12
47	8	1.1	569	2	Q62KZ6
48	8	1.1	569	2	Q63TF6
49	8	1.1	607	2	Q91001
50	8	1.1	608	2	Q9PTW7
51	8	1.1	611	2	Q94HU9
52	8	1.1	611	2	Q7XG00
53	8	1.1	719	2	Q9PVY2
54	8	1.1	737	2	Q8VTB7
55	8	1.1	740	1	CATB_STRRE
56	8	1.1	752	2	O42374
57	8	1.1	764	2	Q8XTM0
58	8	1.1	963	2	O44393
59	8	1.1	1019	1	LFC_CARRO
60	8	1.1	1019	2	Q8T5S1
61	8	1.1	1019	2	Q8T5S1
62	8	1.1	1070	2	Q91972
63	8	1.1	1083	2	Q26423
64	8	1.1	1238	2	Q9N614
65	8	1.1	1238	2	Q9VCD8
66	8	1.1	1316	2	Q96JU7
67	7	1.0	36	2	Q7UL51
68	7	1.0	37	2	Q8F0D9
69	7	1.0	47	2	Q75GQ9
70	7	1.0	50	2	Q6Z6D5
71	7	1.0	54	2	Q8NQ87
72	7	1.0	55	2	Q768X9
73	7	1.0	59	2	Q931M9
74	7	1.0	59	2	Q99SV1
75	7	1.0	59	2	Q7A0F7
76	7	1.0	59	2	Q6G7Z5
77	7	1.0	59	2	Q6GFB7
78	7	1.0	61	2	Q8GRP5
79	7	1.0	61	2	Q8GRP6
80	7	1.0	61	2	Q8GZF3
81	7	1.0	61	2	Q8GZF4
82	7	1.0	61	2	Q8GZF5
83	7	1.0	61	2	Q8GZF7
84	7	1.0	61	2	Q8GZF8
85	7	1.0	61	2	Q8GZF9
86	7	1.0	62	2	Q7PIZ1
87	7	1.0	67	2	Q9EMT6
88	7	1.0	71	2	Q855B3
89	7	1.0	75	2	Q9C8F3
90	7	1.0	81	2	Q7R3P2
91	7	1.0	81	2	Q9EMT8
92	7	1.0	81	2	Q79209
93	7	1.0	81	2	Q90D16
94	7	1.0	82	2	Q7X3H3
95	7	1.0	86	2	Q9M3B7
96	7	1.0	91	2	Q87074
97	7	1.0	106	2	Q62QF8
98	7	1.0	108	2	Q966A7
99	7	1.0	109	2	Q91967
100	7	1.0	112	2	P91967
101	7	1.0	114	2	Q9YCI9
102	7	1.0	120	2	Q8T6A0
103	7	1.0	123	2	Q6W1F1
104	7	1.0	124	2	Q7WC39

O66619	aquifex aeo
Q28711	oryctolagus
Q668X3	versinia ps
Q82D23	versinia pe
Q8d0t9	versinia pe
P34878	lactococcus
Q9XUN6	caenorhabdi
Q90WS2	elaphe sp.
O07898	vibrio chol
P22457	bos taurus
Q67uz3	oryza sativ
Q7x370	uncultured
Q10367	schistosacch
Q7ux12	rhodopiell
Q62kz6	burkholderi
Q63tf6	burkholderi
Q91001	gallus gall
Q9ptw7	struthio ca
Q94hu9	oryza sativ
Q7xg00	oryza sativ
Q9pvY2	triakis scy
Q8ybt7	anabaena sp
Q87854	streptomyce
O42374	brachydania
Q8xtm0	ralstonia s
Q44393	pisaster oc
Q26422	carcinoscoc
Q28175	tachypleus
Q8t9a1	tachypleus
P91972	apiysia cal
Q26423	carcinoscoc
Q9nc14	drosophila
Q9vcD8	drosophila
Q96ju7	homo sapien
Q7ul51	rhodopiell
Q8f0d9	leptospira
Q75GQ9	oryza sativ
Q6Z6D5	oryza sativ
Q8NQ87	corynebacte
Q768X9	uncultured
Q931M9	staphylococ
Q99SV1	staphylococ
Q7A0F7	staphylococ
Q6G7Z5	staphylococ
Q6GFB7	staphylococ
Q8GRP5	arabidopsis
Q8GRP6	arabidopsis
Q8GZF3	arabidopsis
Q8GZF4	arabidopsis
Q8GZF5	arabidopsis
Q8GZF7	arabidopsis
Q8GZF8	arabidopsis
Q8GZF9	arabidopsis
Q7piZ1	anopheles g
Q9emT6	amsacta moo
Q855B3	mycobacteri
Q9C8F3	arabidopsis
Q7R3P2	giardia lam
Q9emT8	amsacta moo
Q79209	human immun
Q90D16	human immun
Q7X3H3	thiocapsa r
Q9M3B7	arabidopsis
Q87074	suid herpes
Q62QF8	bacillus li
Q966A7	caenorhabdi
P91967	trichinella
Q9YCI9	aeropyrum p
Q8T6A0	aplysia cal
Q6W1F1	rhizobium s
Q7WC39	bordetella

105	7	1.0	124	2	Q81G20	Q81g20 bacillus ce	178	7	1.0	211	2	Q8ZEH2	Q8zeh2 yersinia pe
106	7	1.0	124	2	Q8G3X3	Q8g3x3 bifidobacte	179	7	1.0	211	2	Q6D4T7	Q6ddt7 erwina car
107	7	1.0	126	2	Q6NQG5	Q6ngq5 arabidopsis	180	7	1.0	212	1	OMPW_ECOLI	P21364 escherichia
108	7	1.0	129	2	Q87FS3	Q87fs3 vibrio para	181	7	1.0	212	1	OMPW_SALTI	Q8zre2 salmonella
109	7	1.0	132	2	Q8WG97	Q8wg97 apatania zo	182	7	1.0	212	1	OMPW_SALTY	Q8zp50 salmonella
110	7	1.0	132	2	Q9L158	Q9l158 streptomyce	183	7	1.0	212	2	Q7Q8A2	Q7q8a2 anopheles g
111	7	1.0	136	2	Q6SV41	Q6sv41 metarhizium	184	7	1.0	212	2	Q8XCB6	Q8xcb6 escherichia
112	7	1.0	141	2	Q6A6B6	Q6a6e6 propionibac	185	7	1.0	213	2	Q9CF55	Q9cf55 lactococcus
113	7	1.0	143	2	Q9S9X5	Q9s9x5 arabidopsis	186	7	1.0	214	2	Q87K02	Q87k02 vibrio para
114	7	1.0	144	2	Q8WG98	Q8wg98 moropsysche	187	7	1.0	215	2	Q74TX0	Q74tx0 yersinia pe
115	7	1.0	146	2	Q6RGN1	Q6rgn1 sus scrofa	188	7	1.0	215	2	Q8D0J8	Q8d0j8 yersinia pe
116	7	1.0	146	2	Q75Q50	Q75q50 hartigiola	189	7	1.0	215	2	Q9RKP8	Q9rkp8 streptomyce
117	7	1.0	146	2	Q75QF3	Q75qf3 rhopalomyia	190	7	1.0	221	2	Q9S824	Q9s824 drosophila
118	7	1.0	146	2	Q75QF4	Q75qf4 rhopalomyia	191	7	1.0	222	2	Q9VWV7	Q9vvw7 drosophila
119	7	1.0	146	2	Q75QF5	Q75qf5 rhopalomyia	192	7	1.0	222	2	Q871A9	Q871a9 neurospora
120	7	1.0	146	2	Q75QF6	Q75qf6 rhopalomyia	193	7	1.0	222	2	Q6ESR8	Q6esr8 oryza sativ
121	7	1.0	146	2	Q75QF7	Q75qf7 rhopalomyia	194	7	1.0	222	2	Q8KQW4	Q8kqm4 saccharopol
122	7	1.0	146	2	Q75QF8	Q75qf8 rhopalomyia	195	7	1.0	223	2	Q7Z724	Q7z7z4 inocybe sie
123	7	1.0	146	2	Q75QF9	Q75qf9 rhopalomyia	196	7	1.0	225	2	Q8M0X1	Q8m0x1 gynodiastyl
124	7	1.0	146	2	Q75QG0	Q75qg0 rhopalomyia	197	7	1.0	225	2	Q8W5L0	Q8w5l0 oryza sativ
125	7	1.0	146	2	Q75QG1	Q75qg1 rhopalomyia	198	7	1.0	225	2	Q7XH60	Q7xh60 oryza sativ
126	7	1.0	146	2	Q75QG2	Q75qg2 rhopalomyia	199	7	1.0	226	2	Q632M1	Q632m1 bacillus ce
127	7	1.0	146	2	Q75QG3	Q75qg3 rhopalomyia	200	7	1.0	226	2	Q816L1	Q816l1 bacillus ce
128	7	1.0	146	2	Q75QG4	Q75qg4 rhopalomyia	201	7	1.0	226	2	Q81KC5	Q81kc5 bacillus an
129	7	1.0	146	2	Q75QG5	Q75qg5 rhopalomyia	202	7	1.0	226	2	Q6HC61	Q6hc61 bacillus th
130	7	1.0	146	2	Q69T63	Q69t63 oryza sativ	203	7	1.0	227	2	Q29875	Q29875 archaeoglob
131	7	1.0	147	2	Q67MY5	Q67my5 symbiobacte	204	7	1.0	227	2	Q7Z8D8	Q7z8d8 inocybe ada
132	7	1.0	154	2	Q50211	Q50211 mycobacteri	205	7	1.0	227	2	Q88Q18	Q88q18 pseudomonas
133	7	1.0	156	2	Q6PFF6	Q6pf6 oryza sativ	206	7	1.0	228	2	Q7Z825	Q7z825 inocybe che
134	7	1.0	156	2	Q8PFF6	Q8pf6 xanthomonas	207	7	1.0	228	2	Q889S0	Q889s0 pseudomonas
135	7	1.0	157	2	Q95W21	Q95w21 anthonomus	208	7	1.0	231	2	Q7NBJ8	Q7nbj8 mycoplasma
136	7	1.0	158	2	Q9A4V8	Q9av48 oryza sativ	209	7	1.0	231	2	Q9Z795	Q9z795 chlamydia p
137	7	1.0	158	2	Q654W6	Q654w6 oryza sativ	210	7	1.0	232	2	Q9HWW1	Q9hww1 pseudomonas
138	7	1.0	163	2	Q75L20	Q75l20 oryza sativ	211	7	1.0	233	2	Q7Z824	Q7z824 inocybe che
139	7	1.0	164	2	Q960K6	Q96qk6 homo sapien	212	7	1.0	235	2	Q8LD25	Q8ld25 arabidopsis
140	7	1.0	167	1	YPA2_ASCIM	P22375 ascobolus i	213	7	1.0	235	2	Q8VY63	Q8vy63 arabidopsis
141	7	1.0	168	2	Q8DJF0	Q8djf0 synechococc	214	7	1.0	235	2	Q6VTS3	Q6vts3 oryza sativ
142	7	1.0	168	2	Q28BU3	Q28bj3 chlamydia p	215	7	1.0	236	2	Q91004	Q91004 gecko gecko
143	7	1.0	169	2	Q87NK8	Q87nk8 vibrio para	216	7	1.0	237	2	Q9HOG1	Q9hg1 halobacteri
144	7	1.0	170	2	Q84RT8	Q84rt8 chamaemelum	217	7	1.0	237	2	Q7ZWL3	Q7zw13 xenopus lae
145	7	1.0	170	2	Q84SG4	Q84sg4 chamaemelum	218	7	1.0	238	2	Q8CW43	Q8cw43 escherichia
146	7	1.0	171	2	Q9ROP0	Q9rop0 vibrio chol	219	7	1.0	238	2	Q7Z721	Q7z721 inocybe ste
147	7	1.0	171	2	Q9K279	Q9k279 chlamydia p	220	7	1.0	239	2	Q9KQD6	Q9kgd6 vibrio chol
148	7	1.0	172	2	Q9CLF6	Q9cly6 pasteurella	221	7	1.0	239	2	Q91218	Q91218 oncorhynch
149	7	1.0	172	2	Q9DFD1	Q9dfd1 oncorhynch	222	7	1.0	240	2	Q89IB3	Q89ib3 bradyrhizob
150	7	1.0	175	2	Q7NK23	Q7nk23 gloeobacter	223	7	1.0	241	2	Q8FRK8	Q8frk8 corynebacte
151	7	1.0	176	2	Q9PUC7	Q9puc7 gallus gall	224	7	1.0	242	2	Q7Z9K7	Q7z9k7 desulfotvibr
152	7	1.0	178	2	Q9LMH2	Q9lmh2 arabidopsis	225	7	1.0	243	2	Q7M413	Q7m413 megabombus
153	7	1.0	181	2	Q87NZ6	Q87nz6 vibrio para	226	7	1.0	244	2	Q7X990	Q7x990 oryza sativ
154	7	1.0	185	2	Q9KMW2	Q9kw2 salmonella	227	7	1.0	244	2	Q6DIS2	Q6dis2 xenopus tro
155	7	1.0	186	2	Q6BL42	Q6bl42 debaryomyce	228	7	1.0	247	2	Q8FCQ3	Q8fcq3 escherichia
156	7	1.0	187	2	Q84S30	Q84sj0 matricaria	229	7	1.0	247	2	Q8FCQ3	Q8fcq3 escherichia
157	7	1.0	187	2	Q6MTT3	Q6mtt3 mycoplasma	230	7	1.0	247	2	Q8X6U7	Q8x6u7 escherichia
158	7	1.0	189	2	Q84S31	Q84sj1 matricaria	231	7	1.0	248	2	Q83P08	Q83pu8 shigella fl
159	7	1.0	190	1	YR15_GLOVI	Q7nh22 gloeobacter	232	7	1.0	248	2	Q83P08	Q83pu8 shigella fl
160	7	1.0	190	2	Q6BSX0	Q6bsx0 debaryomyce	233	7	1.0	249	2	Q81Q08	Q81q08 mus musculu
161	7	1.0	191	2	MAF_BACAN	Q81ld6 bacillus an	234	7	1.0	249	2	Q6IE63	Q6ie63 rattus norv
162	7	1.0	191	2	Q633Y9	Q633y9 bacillus ce	235	7	1.0	250	2	Q81Q08	Q81q08 mus musculu
163	7	1.0	191	2	Q9RSA2	Q9rsa2 deinococcus	236	7	1.0	254	2	Q8ZFK6	Q8zfk6 yersinia pe
164	7	1.0	191	2	Q6HD71	Q6hd71 bacillus th	237	7	1.0	254	2	Q8ZFK6	Q8zfk6 yersinia pe
165	7	1.0	193	1	Y377_MYCGE	P47617 mycoplasma	238	7	1.0	255	1	Q6N3M7	Q6n3m7 rhodopseudo
166	7	1.0	195	2	Q6AMF5	Q6amf5 desulfocalé	239	7	1.0	255	2	V29K_PERV	Q6n3m7 rhodopseudo
167	7	1.0	196	1	CRBD_CHICK	P49152 gallus gall	240	7	1.0	255	2	Q9Y7A9	P14850 pea early b
168	7	1.0	198	2	Q8XR75	Q8xr75 ralstonia s	241	7	1.0	259	2	Q84700	Q84700 pea early b
169	7	1.0	201	1	ABP1_MAIZE	P13689 zea mays (m	242	7	1.0	259	2	Q69EZ7	Q69ez7 homo sapien
170	7	1.0	202	2	Q6ZSF8	Q6zsf8 homo sapien	243	7	1.0	260	1	Q8UDL2	Q8udl2 agrobacteri
171	7	1.0	203	2	Q72ZK1	Q72zk1 bacillus ce	244	7	1.0	263	1	COLI_RANRI	P22923 r corticotr
172	7	1.0	204	2	Q8JIS7	Q8jis7 xenopus lae	245	7	1.0	263	1	COLI_RANCA	P11885 r corticotr
173	7	1.0	208	2	Q9Z315	Q9z315 bradyrhizob	246	7	1.0	265	2	O6LJ76	O6lj76 photobacter
174	7	1.0	209	1	NODS_BRAJA	P26026 bradyrhizob	247	7	1.0	265	2	O07812	O07812 mycobacteri
175	7	1.0	210	2	Q75C57	Q75c57 ashbya goss	248	7	1.0	265	2	Q68AV7	Q68av7 uncultured
176	7	1.0	211	2	Q6ESR9	Q6esr9 oryza sativ	249	7	1.0	265	2	O07181	O07181 mycobacteri
177	7	1.0	211	2	Q66AK7	Q66ak7 yersinia ps	250	7	1.0	266	2	Q81916	Q81916 biomia trop

251	7	1.0	266	2	06JYB6	Q6jye6 elasmosteth	324	7	1.0	355	2	047485	047485 carabus cra
252	7	1.0	266	2	Q73QA7	Q73qa7 treponema d	325	7	1.0	355	2	047486	047486 carabus sic
253	7	1.0	266	2	Q9QU80	Q9qu80 tt virus. o	326	7	1.0	355	2	047487	047487 carabus tat
254	7	1.0	268	2	Q9XY56	Q9xy56 ctencephal	327	7	1.0	355	2	078724	078724 carabus bla
255	7	1.0	268	2	Q6N9D3	Q6n9d3 rhodopseudo	328	7	1.0	355	2	079585	079585 carabus tit
256	7	1.0	271	2	Q9NPW7	Q9npw7 homo sapien	329	7	1.0	355	2	079586	079586 carabus sui
257	7	1.0	272	2	Q51013	Q51013 neisseria g	330	7	1.0	355	2	099052	099052 carabus por
258	7	1.0	273	2	Q83DW2	Q83dw2 coxiella bu	331	7	1.0	355	2	099053	099053 carabus por
259	7	1.0	278	2	Q84C08	Q84c08 pseudomonas	332	7	1.0	355	2	099054	099054 carabus por
260	7	1.0	280	2	Q87X78	Q87x78 pseudomonas	333	7	1.0	355	2	099054	099054 carabus por
261	7	1.0	281	2	Q8U4H8	Q8u4h8 pyrococcus	334	7	1.0	355	2	092098	092098 carabus mar
262	7	1.0	281	2	Q6JYN8	Q6jyn8 lestonia ha	335	7	1.0	355	2	092100	092100 carabus wag
263	7	1.0	282	2	Q8JXE9	Q8jxe9 roselinia	336	7	1.0	355	2	092101	092101 carabus lep
264	7	1.0	284	2	Q96089	Q96089 haemaphysal	337	7	1.0	355	2	092102	092102 carabus lud
265	7	1.0	286	2	Q9H7G9	Q9h7g9 homo sapien	338	7	1.0	355	2	092103	092103 carabus bor
266	7	1.0	291	1	PCAR_PSRPU	Q52154 pseudomonas	339	7	1.0	355	2	092103	092103 carabus bor
267	7	1.0	291	2	Q9R9T0	Q9r9t0 pseudomonas	340	7	1.0	355	2	092103	092103 carabus bor
268	7	1.0	291	2	Q8N441	Q8n441 pseudomonas	341	7	1.0	355	2	092103	092103 carabus bor
269	7	1.0	292	2	Q54441	Q54441 bacillus ps	342	7	1.0	355	2	092103	092103 carabus bor
270	7	1.0	294	1	PEPM_MYTED	P56839 mytilus edu	343	7	1.0	355	2	092103	092103 carabus bor
271	7	1.0	295	2	Q69E28	Q69e28 homo sapien	344	7	1.0	355	2	092103	092103 carabus bor
272	7	1.0	295	2	Q6D6J3	Q6d6j3 erwinia car	345	7	1.0	355	2	092103	092103 carabus bor
273	7	1.0	299	2	Q8T8D9	Q8t8d9 trypanosoma	346	7	1.0	355	2	092103	092103 carabus bor
274	7	1.0	299	2	Q7PMA7	Q7pma7 anopheles g	347	7	1.0	355	2	092103	092103 carabus bor
275	7	1.0	300	2	Q8IN70	Q8in70 drosophila	348	7	1.0	355	2	092103	092103 carabus bor
276	7	1.0	301	2	Q7ZSX7	Q7zxs7 fugu rubrip	349	7	1.0	355	2	092103	092103 carabus bor
277	7	1.0	303	1	LPXC_XANAC	Q8ppa3 xanthomonas	350	7	1.0	355	2	092103	092103 carabus bor
278	7	1.0	303	2	Q74ZD4	Q74zd4 ashbya goss	351	7	1.0	355	2	092103	092103 carabus bor
279	7	1.0	303	2	Q6VQ99	Q6vq99 tetraodon n	352	7	1.0	355	2	092103	092103 carabus bor
280	7	1.0	304	2	Q8XXF6	Q8xxf6 ralstonia s	353	7	1.0	355	2	092103	092103 carabus bor
281	7	1.0	305	1	LPXC_RALSO	Q8xh16 ralstonia s	354	7	1.0	355	2	092103	092103 carabus bor
282	7	1.0	306	2	Q8L5B0	Q8l5b0 oryza sativ	355	7	1.0	355	2	092103	092103 carabus bor
283	7	1.0	307	2	Q7Q528	Q7q528 anopheles g	356	7	1.0	355	2	092103	092103 carabus bor
284	7	1.0	307	2	Q9KV89	Q9kv89 vibrio chol	357	7	1.0	355	2	092103	092103 carabus bor
285	7	1.0	308	1	T2RC_MOUSE	P59532 mus musculu	358	7	1.0	355	2	092103	092103 carabus bor
286	7	1.0	308	2	Q7MT04	Q7mt04 mus musculu	359	7	1.0	355	2	092103	092103 carabus bor
287	7	1.0	312	2	Q12125	Q12125 saccharomyc	360	7	1.0	355	2	092103	092103 carabus bor
288	7	1.0	314	2	Q6F0P3	Q6fup3 candida gla	361	7	1.0	355	2	092103	092103 carabus bor
289	7	1.0	315	1	Y001_CAUCR	Q9acs9 caulobacter	362	7	1.0	355	2	092103	092103 carabus bor
290	7	1.0	315	2	Q55220	Q55220 streptomyce	363	7	1.0	355	2	092103	092103 carabus bor
291	7	1.0	317	2	Q9KWA7	Q9kwa7 agrobacteri	364	7	1.0	355	2	092103	092103 carabus bor
292	7	1.0	318	2	Q6CP66	Q6cp66 kluyveromyc	365	7	1.0	355	2	092103	092103 carabus bor
293	7	1.0	321	2	Q671F3	Q671f3 symbiobacte	366	7	1.0	355	2	092103	092103 carabus bor
294	7	1.0	324	2	Q90Z55	Q90z55 scophthalmu	367	7	1.0	355	2	092103	092103 carabus bor
295	7	1.0	329	2	Q8U2M3	Q8u2m3 pyrococcus	368	7	1.0	355	2	092103	092103 carabus bor
296	7	1.0	329	2	Q89MG1	Q89mg1 bradyrhizob	369	7	1.0	355	2	092103	092103 carabus bor
297	7	1.0	330	2	Q30523	Q30523 vibrio shil	370	7	1.0	355	2	092103	092103 carabus bor
298	7	1.0	332	2	Q8NXI9	Q8nxi9 staphylococ	371	7	1.0	355	2	092103	092103 carabus bor
299	7	1.0	333	2	Q9K7W7	Q9k7w7 bacillus ha	372	7	1.0	355	2	092103	092103 carabus bor
300	7	1.0	336	2	Q69510	Q69510 mycobacteri	373	7	1.0	355	2	092103	092103 carabus bor
301	7	1.0	336	2	Q8PR42	Q8pr42 xanthomonas	374	7	1.0	355	2	092103	092103 carabus bor
302	7	1.0	336	2	Q6MS16	Q6ms16 mycoplasma	375	7	1.0	355	2	092103	092103 carabus bor
303	7	1.0	336	2	Q7WL07	Q7wl07 bordetella	376	7	1.0	355	2	092103	092103 carabus bor
304	7	1.0	337	2	Q9YDH3	Q9ydh3 aeropyrum p	377	7	1.0	355	2	092103	092103 carabus bor
305	7	1.0	338	2	Q8PE85	Q8pe85 xanthomonas	378	7	1.0	355	2	092103	092103 carabus bor
306	7	1.0	342	2	Q7XE33	Q7xe33 oryza sativ	379	7	1.0	355	2	092103	092103 carabus bor
307	7	1.0	343	2	Q7VV13	Q7vv13 bordetella	380	7	1.0	355	2	092103	092103 carabus bor
308	7	1.0	343	2	Q8D7G2	Q8d7g2 vibrio vuln	381	7	1.0	355	2	092103	092103 carabus bor
309	7	1.0	344	2	Q84QA9	Q84qa9 oryza sativ	382	7	1.0	355	2	092103	092103 carabus bor
310	7	1.0	344	2	Q92M18	Q92m18 rhizobium m	383	7	1.0	355	2	092103	092103 carabus bor
311	7	1.0	345	2	Q7W7L8	Q7w7l8 bordetella	384	7	1.0	355	2	092103	092103 carabus bor
312	7	1.0	346	2	Q6UY16	Q6jy16 eupolemus s	385	7	1.0	355	2	092103	092103 carabus bor
313	7	1.0	347	2	Q6EZC2	Q6ezc2 escherichia	386	7	1.0	355	2	092103	092103 carabus bor
314	7	1.0	347	2	Q7P022	Q7p022 chromobacte	387	7	1.0	355	2	092103	092103 carabus bor
315	7	1.0	348	1	RTCA_PYRAE	Q8zet4 pyrobaculum	388	7	1.0	355	2	092103	092103 carabus bor
316	7	1.0	349	2	Q9YBV1	Q9ybv1 aeropyrum p	389	7	1.0	355	2	092103	092103 carabus bor
317	7	1.0	349	2	Q6ND77	Q6ndf7 rhodopseudo	390	7	1.0	355	2	092103	092103 carabus bor
318	7	1.0	350	2	Q18122	Q18122 caenorhabdi	391	7	1.0	355	2	092103	092103 carabus bor
319	7	1.0	351	1	MSS2_YEAST	P40990 saccharomyc	392	7	1.0	355	2	092103	092103 carabus bor
320	7	1.0	352	2	Q8C9H0	Q8c9h0 mus musculu	393	7	1.0	355	2	092103	092103 carabus bor
321	7	1.0	354	2	Q99Q08	Q99q08 bradyrhizob	394	7	1.0	355	2	092103	092103 carabus bor
322	7	1.0	354	2	Q99Q08	Q99q08 bradyrhizob	395	7	1.0	355	2	092103	092103 carabus bor
323	7	1.0	355	2	047484	047484 carabus vir	396	7	1.0	355	2	092103	092103 carabus bor



397	7	1.0	355	2	Q85GT9	Q85gt9 carabus tor	470	7	1.0	355	2	Q9MR78	Q9mr78 carabus por
398	7	1.0	355	2	Q85GU0	Q85gu0 carabus tor	471	7	1.0	355	2	Q9MR79	Q9mr79 carabus por
399	7	1.0	355	2	Q85GU1	Q85gu1 carabus tor	472	7	1.0	355	2	Q9MR80	Q9mr80 carabus por
400	7	1.0	355	2	Q85GU2	Q85gu2 carabus cha	473	7	1.0	355	2	Q9MR81	Q9mr81 carabus por
401	7	1.0	355	2	Q85GU3	Q85gu3 carabus tor	474	7	1.0	355	2	Q9T227	Q9t227 carabus bla
402	7	1.0	355	2	Q85GU4	Q85gu4 carabus pra	475	7	1.0	355	2	Q9T391	Q9t391 carabus bla
403	7	1.0	355	2	Q8HAX6	Q8hax6 carabus tit	476	7	1.0	355	2	Q9T392	Q9t392 carabus bla
404	7	1.0	355	2	Q8HDX2	Q8hdx2 carabus abc	477	7	1.0	355	2	Q9T393	Q9t393 carabus bla
405	7	1.0	355	2	Q8HDX3	Q8hdx3 carabus mas	478	7	1.0	355	2	Q9T3V1	Q9t3v1 carabus bla
406	7	1.0	355	2	Q8HDX4	Q8hdx4 carabus mas	479	7	1.0	355	2	Q9T3V2	Q9t3v2 carabus bla
407	7	1.0	355	2	Q8HDX5	Q8hdx5 carabus inf	480	7	1.0	355	2	Q9T3V3	Q9t3v3 carabus bla
408	7	1.0	355	2	Q8HDX6	Q8hdx6 carabus inf	481	7	1.0	355	2	Q9T3V4	Q9t3v4 carabus bla
409	7	1.0	355	2	Q8HDY8	Q8hdy8 carabus min	482	7	1.0	355	2	Q9T3V5	Q9t3v5 carabus bla
410	7	1.0	355	2	Q8HE25	Q8he25 carabus tic	483	7	1.0	355	2	Q9T3Z7	Q9t3z7 carabus bla
411	7	1.0	355	2	Q9B9L8	Q9b9l8 carabus hum	484	7	1.0	355	2	Q9T4D6	Q9t4d6 carabus del
412	7	1.0	355	2	Q9B9L9	Q9b9l9 carabus hum	485	7	1.0	355	2	Q9T4K2	Q9t4k2 carabus bla
413	7	1.0	355	2	Q9B9M0	Q9b9m0 carabus hum	486	7	1.0	355	2	Q9T4R4	Q9t4r4 carabus bla
414	7	1.0	355	2	Q9B9M6	Q9b9m6 carabus ruf	487	7	1.0	355	2	Q9T4T8	Q9t4t8 carabus sem
415	7	1.0	355	2	Q9B9R6	Q9b9r6 carabus ruf	488	7	1.0	355	2	Q9T4V4	Q9t4v4 carabus bla
416	7	1.0	355	2	Q9B9R7	Q9b9r7 carabus bai	489	7	1.0	355	2	Q9TDX8	Q9tdx8 carabus cla
417	7	1.0	355	2	Q9B9R8	Q9b9r8 carabus str	490	7	1.0	355	2	Q9TDX9	Q9tdx9 carabus mao
418	7	1.0	355	2	Q9B9R9	Q9b9r9 carabus lat	491	7	1.0	355	2	Q9TDY0	Q9tdy0 carabus cle
419	7	1.0	355	2	Q9B9S0	Q9b9s0 carabus aen	492	7	1.0	355	2	Q9TDY1	Q9tdy1 carabus iri
420	7	1.0	355	2	Q9B9S1	Q9b9s1 carabus aen	493	7	1.0	355	2	Q9TDY2	Q9tdy2 carabus arr
421	7	1.0	355	2	Q9B9S2	Q9b9s2 carabus sac	494	7	1.0	355	2	Q9TDY3	Q9tdy3 carabus lao
422	7	1.0	355	2	Q9B9S3	Q9b9s3 carabus lin	495	7	1.0	355	2	Q9TDY4	Q9tdy4 carabus lao
423	7	1.0	355	2	Q9B9S4	Q9b9s4 carabus kad	496	7	1.0	355	2	Q9TDY5	Q9tdy5 carabus cya
424	7	1.0	355	2	Q9B9S5	Q9b9s5 carabus str	497	7	1.0	355	2	Q9TDY6	Q9tdy6 carabus tou
425	7	1.0	355	2	Q9B9S6	Q9b9s6 carabus str	498	7	1.0	355	2	Q9TDY7	Q9tdy7 carabus tux
426	7	1.0	355	2	Q9B9K4	Q9b9k4 carabus con	499	7	1.0	355	2	Q9TDY8	Q9tdy8 carabus ton
427	7	1.0	355	2	Q9B9K5	Q9b9k5 carabus con	500	7	1.0	355	2	Q9TDY9	Q9tdy9 carabus ton
428	7	1.0	355	2	Q9B9K6	Q9b9k6 carabus gly	501	7	1.0	355	2	Q9TDY0	Q9tdy0 carabus ton
429	7	1.0	355	2	Q9GBK7	Q9gbk7 carabus gly	502	7	1.0	355	2	Q9TE01	Q9te01 carabus tru
430	7	1.0	355	2	Q9GBK8	Q9gbk8 carabus sma	503	7	1.0	355	2	Q9TE02	Q9te02 carabus can
431	7	1.0	355	2	Q9GBK9	Q9gbk9 carabus ale	504	7	1.0	355	2	Q9TE03	Q9te03 carabus can
432	7	1.0	355	2	Q9GBL0	Q9gbl0 carabus ale	505	7	1.0	355	2	Q9TE04	Q9te04 carabus can
433	7	1.0	355	2	Q9GBL1	Q9gbl1 carabus hae	506	7	1.0	355	2	Q9TE05	Q9te05 carabus can
434	7	1.0	355	2	Q9GBL2	Q9gbl2 carabus hae	507	7	1.0	355	2	Q9TE08	Q9te08 carabus sei
435	7	1.0	355	2	Q9GBL3	Q9gbl3 carabus pot	508	7	1.0	355	2	Q9TE09	Q9te09 carabus sei
436	7	1.0	355	2	Q9GBL4	Q9gbl4 carabus pot	509	7	1.0	355	2	Q9TE10	Q9te10 carabus sei
437	7	1.0	355	2	Q9GBL5	Q9gbl5 carabus ari	510	7	1.0	355	2	Q9TE11	Q9te11 carabus sei
438	7	1.0	355	2	Q9GBL6	Q9gbl6 carabus ari	511	7	1.0	355	2	Q9TE12	Q9te12 carabus sei
439	7	1.0	355	2	Q9GBL7	Q9gbl7 carabus exi	512	7	1.0	355	2	Q9TE13	Q9te13 carabus sei
440	7	1.0	355	2	Q9GBL8	Q9gbl8 carabus cra	513	7	1.0	355	2	Q9TE14	Q9te14 carabus sei
441	7	1.0	355	2	Q9GBL9	Q9gbl9 carabus cra	514	7	1.0	355	2	Q9TE15	Q9te15 carabus kor
442	7	1.0	355	2	Q9GBM0	Q9gbm0 carabus uen	515	7	1.0	355	2	Q9TE22	Q9te22 carabus bla
443	7	1.0	355	2	Q9GBM1	Q9gbm1 carabus vir	516	7	1.0	355	2	Q9TE23	Q9te23 carabus bla
444	7	1.0	355	2	Q9GBM2	Q9gbm2 carabus bra	517	7	1.0	355	2	Q9TE24	Q9te24 carabus bla
445	7	1.0	355	2	Q9GBM3	Q9gbm3 carabus ign	518	7	1.0	355	2	Q9TE25	Q9te25 carabus bla
446	7	1.0	355	2	Q9GBM4	Q9gbm4 carabus mir	519	7	1.0	355	2	Q9TE26	Q9te26 carabus bla
447	7	1.0	355	2	Q9GBM5	Q9gbm5 carabus oga	520	7	1.0	355	2	Q9TE27	Q9te27 carabus bla
448	7	1.0	355	2	Q9GBM6	Q9gbm6 carabus oga	521	7	1.0	355	2	Q9TE83	Q9te83 carabus bla
449	7	1.0	355	2	Q9GBM7	Q9gbm7 carabus oga	522	7	1.0	355	2	Q9TE84	Q9te84 carabus bla
450	7	1.0	355	2	Q9GBM8	Q9gbm8 carabus hum	523	7	1.0	355	2	Q9TE85	Q9te85 carabus bla
451	7	1.0	355	2	Q9GBM9	Q9gbm9 carabus vir	524	7	1.0	355	2	Q9TE86	Q9te86 carabus bla
452	7	1.0	355	2	Q9GBN0	Q9gbn0 carabus sma	525	7	1.0	355	2	Q9TE87	Q9te87 carabus bla
453	7	1.0	355	2	Q9GBN1	Q9gbn1 carabus sma	526	7	1.0	355	2	Q9TE88	Q9te88 carabus bla
454	7	1.0	355	2	Q9GBN2	Q9gbn2 carabus nan	527	7	1.0	355	2	Q9TE89	Q9te89 carabus bla
455	7	1.0	355	2	Q9GBN3	Q9gbn3 carabus con	528	7	1.0	355	2	Q9TE90	Q9te90 carabus bla
456	7	1.0	355	2	Q9GBN4	Q9gbn4 carabus con	529	7	1.0	355	2	Q9TE91	Q9te91 carabus bla
457	7	1.0	355	2	Q9MDD3	Q9mdD3 carabus por	530	7	1.0	355	2	Q9TE92	Q9te92 carabus bla
458	7	1.0	355	2	Q9MDR4	Q9mdR4 carabus sch	531	7	1.0	355	2	Q9TE93	Q9te93 carabus bla
459	7	1.0	355	2	Q9MDR5	Q9mdR5 carabus por	532	7	1.0	355	2	Q9TE94	Q9te94 carabus bla
460	7	1.0	355	2	Q9MDT2	Q9mdT2 carabus por	533	7	1.0	355	2	Q9TE95	Q9te95 carabus bla
461	7	1.0	355	2	Q9ME14	Q9me14 carabus por	534	7	1.0	355	2	Q9TE96	Q9te96 carabus bla
462	7	1.0	355	2	Q9MI23	Q9mi23 carabus geh	535	7	1.0	355	2	Q9TE97	Q9te97 carabus bla
463	7	1.0	355	2	Q9MI24	Q9mi24 carabus geh	536	7	1.0	355	2	Q9TE98	Q9te98 carabus bla
464	7	1.0	355	2	Q9MI25	Q9mi25 carabus lop	537	7	1.0	355	2	Q9TE99	Q9te99 carabus bla
465	7	1.0	355	2	Q9MI26	Q9mi26 carabus lee	538	7	1.0	355	2	Q9TEA0	Q9tea0 carabus bla
466	7	1.0	355	2	Q9MI27	Q9mi27 carabus sma	539	7	1.0	355	2	Q9TEA1	Q9tea1 carabus bla
467	7	1.0	355	2	Q9MIJ0	Q9miJ0 carabus van	540	7	1.0	355	2	Q9TEA2	Q9tea2 carabus bla
468	7	1.0	355	2	Q9MJ04	Q9mj04 carabus van	541	7	1.0	355	2	Q9TEA3	Q9tea3 carabus bla
469	7	1.0	355	2	Q9MJ05	Q9mj05 carabus van	542	7	1.0	355	2	Q9TEA4	Q9tea4 carabus bla
	7	1.0	355	2	Q9MJ06	Q9mj06 carabus van							Q9tea5 carabus bla
	7	1.0	355	2	Q9MKJ0	Q9mkJ0 carabus van							
	7	1.0	355	2	Q9MR76	Q9mr76 carabus por							
	7	1.0	355	2	Q9MR77	Q9mr77 carabus por							

543	7	1.0	355	2	Q9TEA6	Q9tea6 carabus bla	616	7	1.0	446	2	Q6FCC9	Q6fcc9 acinetobact
544	7	1.0	355	2	Q9TEA7	Q9tea7 carabus bla	617	7	1.0	447	2	Q8TA85	Q8ta85 homo sapien
545	7	1.0	355	2	Q9TEA8	Q9tea8 carabus bla	618	7	1.0	449	2	Q8BI18	Q8bi18 mus musculu
546	7	1.0	355	2	Q9TEA9	Q9tea9 carabus bla	619	7	1.0	453	2	Q6CVL9	Q6cvl9 kluyveromyc
547	7	1.0	355	2	Q9TEB0	Q9teb0 carabus bla	620	7	1.0	453	2	Q6VAT4	Q6vat4 umbraculum
548	7	1.0	355	2	Q9TEB1	Q9teb1 carabus bla	621	7	1.0	453	2	Q8P704	Q8p704 xanthomonas
549	7	1.0	355	2	Q9TEB2	Q9teb2 carabus bla	622	7	1.0	453	2	Q8P1B8	Q8p1b8 xanthomonas
550	7	1.0	355	2	Q928B6	Q928b6 bradyrhizob	623	7	1.0	455	2	Q6LFB2	Q6lfb2 photobacter
551	7	1.0	357	2	Q6ZSC3	Q6zsc3 homo sapien	624	7	1.0	459	2	Q96349	Q96349 brassica na
552	7	1.0	358	2	Q882Y3	Q882y3 pseudomonas	625	7	1.0	459	2	Q67L10	Q67l10 symbiobacte
553	7	1.0	359	2	Q6JYI3	Q6jy13 pseudomonas	626	7	1.0	461	2	Q7D565	Q7d565 mycobacteri
554	7	1.0	359	2	Q6JYI3	Q6jy13 amphacens sp	627	7	1.0	461	2	Q06380	Q06380 mycobacteri
555	7	1.0	359	2	Q6JYI5	Q6jy15 stauralia c	628	7	1.0	461	2	Q744A5	Q744a5 mycobacteri
556	7	1.0	359	2	Q65XU7	Q65xu7 oryza sativ	629	7	1.0	462	2	Q7TW31	Q7tw31 mycobacteri
557	7	1.0	360	1	ARO8_BUCAP	Q8k939 buchnera ap	630	7	1.0	462	2	Q75EJ7	Q75ej7 aahbya goos
558	7	1.0	363	2	Q8WP22	Q8wp22 macaca fasc	631	7	1.0	462	2	Q6PAG2	Q6pag2 xenopus lae
559	7	1.0	364	2	Q7MEH3	Q7meh3 vibrio vuln	632	7	1.0	463	1	FMNL_HUMAN	Q95466 homo sapien
560	7	1.0	367	2	Q8N7P6	Q8n7f6 homo sapien	633	7	1.0	463	2	Q8N671	Q8n671 homo sapien
561	7	1.0	367	2	Q8W27	Q8w27 homo sapien	634	7	1.0	465	2	Q84XL8	Q84xl8 xerophyta h
562	7	1.0	368	2	Q32860	Q32860 mycobacteri	635	7	1.0	465	2	Q8GM44	Q8gm44 arabidopsis
563	7	1.0	372	2	Q9H2B5	Q9hzb5 pseudomonas	636	7	1.0	468	2	Q6K2N9	Q6k2n9 oryza sativ
564	7	1.0	373	2	Q7O4D8	Q7o4d8 thermoprote	637	7	1.0	469	2	Q8LEG9	Q8leg9 arabidopsis
565	7	1.0	373	2	Q803F1	Q803f1 brachydanio	638	7	1.0	469	2	Q81NL2	Q81nl2 bacillus an
566	7	1.0	374	1	TGT_ANASP	Q8yvt9 anabaena sp	639	7	1.0	471	2	Q6DQ98	Q6dq98 nicotiana t
567	7	1.0	375	2	Q9JX36	Q9jx36 neisseria m	640	7	1.0	472	2	Q09657	Q09657 caenorhabdi
568	7	1.0	375	2	Q9K1G5	Q9k1g5 neisseria m	641	7	1.0	475	1	GID_BRAJA	Q89121 bradyrhizob
569	7	1.0	376	2	Q7VX11	Q7vx11 bordetella	642	7	1.0	476	2	Q6HMS5	Q6hms5 bacillus an
570	7	1.0	377	2	Q7NY19	Q7ny19 chromobacte	643	7	1.0	476	2	Q735G8	Q735g8 bacillus ce
571	7	1.0	378	2	Q8XQ55	Q8xq55 ralstonia s	644	7	1.0	476	2	Q81BL6	Q81bl6 bacillus ce
572	7	1.0	382	2	Q88BC3	Q88bc3 pseudomonas	645	7	1.0	476	2	Q6HGR8	Q6hgr8 bacillus th
573	7	1.0	382	2	Q90WT4	Q90wt4 crocodylus	646	7	1.0	478	2	Q6FPY7	Q6fp7 candida gla
574	7	1.0	383	2	Q65Q28	Q65q28 manheimia	647	7	1.0	479	2	Q99RL5	Q99rl5 staphylococ
575	7	1.0	383	2	Q7W5V6	Q7w5v6 bordetella	648	7	1.0	479	2	Q7A3S4	Q7a3s4 staphylococ
576	7	1.0	383	2	Q7W6K8	Q7w6k8 bordetella	649	7	1.0	483	2	Q89BC3	Q89bc3 bradyrhizob
577	7	1.0	387	2	Q8GJW2	Q8gjm2 synecococc	650	7	1.0	484	2	Q7PHP7	Q7php7 anopheles g
578	7	1.0	387	2	P73853	P73853 synecocyst	651	7	1.0	487	2	Q8ET76	Q8et76 oceanobacil
579	7	1.0	387	2	Q8Z0N9	Q8z0n9 anabaena sp	652	7	1.0	489	1	MEP3_YEAST	P53390 saccharomyc
580	7	1.0	387	2	Q7U6M7	Q7u6m7 synecococc	653	7	1.0	489	2	Q6B2F5	Q6b2f5 saccharomyc
581	7	1.0	387	2	Q7V6M7	Q7v6m7 prochloroco	654	7	1.0	489	2	Q91QQ1	Q91qq1 soybean dwa
582	7	1.0	387	2	Q8DGX2	Q8dgx2 synecococc	655	7	1.0	490	2	Q74I35	Q74i35 lactobacill
583	7	1.0	388	2	Q44330	Q44330 manduca sex	656	7	1.0	490	2	Q7VH13	Q7vh13 helicobacte
584	7	1.0	389	1	PYRC_SULTO	Q970x5 sulfobolus	657	7	1.0	491	1	MURC_PHOLL	Q7n148 photorhabdu
585	7	1.0	391	2	Q91V12	Q91v12 mus musculu	658	7	1.0	492	1	MEPI_YEAST	P40260 saccharomyc
586	7	1.0	392	2	Q63W65	Q63w65 burkholderi	659	7	1.0	492	2	Q45659	Q45659 caenorhabdi
587	7	1.0	394	2	P91817	P91817 tachypleus	660	7	1.0	492	2	Q88215	Q88215 lactobacill
588	7	1.0	396	2	Q7XTQ4	Q7xtq4 oryza sativ	661	7	1.0	493	1	CAMA_CHICK	P05099 gallus gall
589	7	1.0	397	2	Q94J66	Q94j66 oryza sativ	662	7	1.0	493	2	Q972W0	Q972w0 sulfobolus
590	7	1.0	397	2	Q8RJW1	Q8rjw1 xanthomonas	663	7	1.0	493	2	Q90XP7	Q90xp7 brachydanio
591	7	1.0	398	2	Q91374	Q91374 pseudomonas	664	7	1.0	494	1	CD5_MOUSE	P13379 mus musculu
592	7	1.0	399	2	Q7RY56	Q7ry56 neurospora	665	7	1.0	494	2	Q8VDV0	Q8vdv0 mus musculu
593	7	1.0	407	2	Q627S5	Q627s5 oryza sativ	666	7	1.0	494	2	Q91X69	Q91x69 mus musculu
594	7	1.0	408	2	Q9VMA6	Q9vma6 drosophila	667	7	1.0	494	2	Q8BMS0	Q8bms0 mus musculu
595	7	1.0	408	2	Q8XWX2	Q8xwx2 ralstonia s	668	7	1.0	494	2	Q9ER20	Q9er20 mus musculu
596	7	1.0	410	2	Q6E824	Q6e824 umbonia cra	669	7	1.0	497	2	Q54706	Q54706 streptococc
597	7	1.0	410	2	Q6E826	Q6e826 umbonia cra	670	7	1.0	497	2	Q54749	Q54749 streptococc
598	7	1.0	410	2	Q6E838	Q6e838 platycotis	671	7	1.0	497	2	Q51503	Q51503 borrelia bu
599	7	1.0	410	2	Q6E840	Q6e840 platycotis	672	7	1.0	497	2	Q9A1S4	Q9a1s4 streptococc
600	7	1.0	413	2	Q29192	Q29192 archaeoglob	673	7	1.0	497	2	Q73VS8	Q73vs8 mycobacteri
601	7	1.0	413	2	Q6LYH5	Q6lyh5 methanococc	674	7	1.0	498	2	Q6CLP0	Q6clp0 yarrowia li
602	7	1.0	414	2	Q6UDM0	Q6udm0 psittacid h	675	7	1.0	501	2	Q9NDD6	Q9ndd6 riftia pach
603	7	1.0	416	2	Q88RT5	Q88rt5 pseudomonas	676	7	1.0	504	1	GPMI_RHOPA	Q6ncx7 rhodopseudo
604	7	1.0	420	1	Q63A_DROME	Q9vzw8 drosophila	677	7	1.0	505	1	GPMI_MYCPU	Q98qa7 mycoplasma
605	7	1.0	421	2	Q73KB7	Q73kb7 treponema d	678	7	1.0	505	1	MATK_SPIOL	Q9m3n0 spinacia ol
606	7	1.0	426	2	Q6BX74	Q6bx74 debaryomyc	679	7	1.0	505	2	Q95EA3	Q95ea3 gymnocalyci
607	7	1.0	429	2	Q7SYF9	Q7syf9 acipenser b	680	7	1.0	507	1	MATK_BROHE	Q95ea5 brownlingia
608	7	1.0	432	2	Q73AL5	Q73al5 bacillus ce	681	7	1.0	507	2	Q94NC4	Q94nc4 stetsonia c
609	7	1.0	436	2	Q67NQ5	Q67nq5 symbiobacte	682	7	1.0	507	2	Q94P31	Q94p31 haagocoreu
610	7	1.0	437	2	Q51640	Q51640 burkholderi	683	7	1.0	507	2	Q94P94	Q94p94 eriosyce na
611	7	1.0	437	2	Q7UDY7	Q7udy7 rhodopirell	684	7	1.0	507	2	Q94PY9	Q94py9 acanthocaly
612	7	1.0	439	2	Q9LV67	Q9lv67 arabidopsis	685	7	1.0	507	2	Q95E87	Q95e87 neowderma
613	7	1.0	441	2	Q62LB1	Q62lb1 burkholderi	686	7	1.0	507	2	Q95E88	Q95e88 eriosyce au
614	7	1.0	442	2	Q604X1	Q604x1 fugu rubrip	687	7	1.0	507	2	Q95E89	Q95e89 eriosyce is
615	7	1.0	445	2	Q67RK6	Q67rk6 symbiobacte	688	7	1.0	507	2	Q95E90	Q95e90 eriosyce au

589	7	1.0	507	2	Q95E93	Q95E93	parodia maa	762	7	1.0	544	2	Q8TFN9	Q8TFN9	emericella
590	7	1.0	507	2	Q95E96	Q95E96	matucana in	763	7	1.0	545	2	Q67LM0	Q67LM0	symbiobacte
591	7	1.0	507	2	Q95E97	Q95E97	rauhocereus	764	7	1.0	549	2	Q9DW53	Q9DW53	rat cytomeg
592	7	1.0	507	2	Q95EA0	Q95EA0	trichocereu	765	7	1.0	553	2	Q97S10	Q97S10	streptococc
593	7	1.0	507	2	Q95EA1	Q95EA1	uebelmannia	766	7	1.0	553	2	Q9DQR3	Q9DQR3	streptococc
594	7	1.0	507	2	Q95EA2	Q95EA2	coleocephal	767	7	1.0	556	1	NUZM_PODAN	NUZM_PODAN	p15578 podospo
595	7	1.0	507	2	Q95EA4	Q95EA4	browningia	768	7	1.0	556	2	Q6DEK7	Q6DEK7	brachydanio
596	7	1.0	507	2	Q95EC4	Q95EC4	copiapoia la	769	7	1.0	560	2	Q49141	Q49141	arabidopsis
597	7	1.0	507	2	Q95EC5	Q95EC5	copiapoia br	770	7	1.0	560	2	Q50057	Q50057	arabidopsis
598	7	1.0	507	2	Q95EC6	Q95EC6	copiapoia so	771	7	1.0	561	2	Q9KYS9	Q9KYS9	streptomyc
599	7	1.0	507	2	Q95ED8	Q95ED8	pereskiopsi	772	7	1.0	561	2	Q9RXL1	Q9RXL1	delinococcus
700	7	1.0	507	2	Q7HFB7	Q7HFB7	parodia mag	773	7	1.0	563	2	Q74JC6	Q74JC6	lactobacill
701	7	1.0	507	2	Q7HFB8	Q7HFB8	oreocereus	774	7	1.0	568	2	Q88W64	Q88W64	lactobacill
702	7	1.0	507	2	Q7HFB9	Q7HFB9	samaipitice	775	7	1.0	576	2	Q6YID6	Q6YID6	penaeus mon
703	7	1.0	507	2	Q7HFC0	Q7HFC0	micranthoce	776	7	1.0	579	2	Q65XT5	Q65XT5	oryza sativ
704	7	1.0	507	2	Q7HFC1	Q7HFC1	cereus alac	777	7	1.0	580	2	Q9ZQP6	Q9ZQP6	arabidopsis
705	7	1.0	508	2	Q95EB2	Q95EB2	pfeiffera m	778	7	1.0	581	1	YD15_SCHPO	YD15_SCHPO	schizosacch
706	7	1.0	508	2	Q93SM9	Q93SM9	staphylococ	779	7	1.0	581	2	Q9LKH1	Q9LKH1	mesembryant
707	7	1.0	508	2	Q6GB44	Q6GB44	staphylococ	780	7	1.0	581	2	Q8D7C1	Q8D7C1	vibrio vuln
708	7	1.0	509	2	Q95EB3	Q95EB3	leptismum c	781	7	1.0	582	2	Q23492	Q23492	arabidopsis
709	7	1.0	509	2	Q95EB5	Q95EB5	rhinopalais f	782	7	1.0	584	2	Q9SQZ0	Q9SQZ0	arabidopsis
710	7	1.0	509	2	Q95EB6	Q95EB6	hattoria sal	783	7	1.0	584	2	Q67RH6	Q67RH6	symbiobacte
711	7	1.0	509	2	Q95EB8	Q95EB8	parodia ott	784	7	1.0	585	2	Q17491	Q17491	caenorhabdi
712	7	1.0	509	2	Q95E91	Q95E91	parodia mic	785	7	1.0	585	2	Q8SZY4	Q8SZY4	drosophila
713	7	1.0	509	2	Q95E92	Q95E92	disocactus	786	7	1.0	600	2	Q93GX8	Q93GX8	streptomyc
714	7	1.0	509	2	Q95E96	Q95E96	selenicereu	787	7	1.0	600	2	Q6AT22	Q6AT22	xenopus lae
715	7	1.0	509	2	Q95EA7	Q95EA7	hylocereus	788	7	1.0	602	2	Q65DM0	Q65DM0	bacillus li
716	7	1.0	509	2	Q95EA8	Q95EA8	pachycereus	789	7	1.0	607	2	Q6DFJ5	Q6DFJ5	xenopus lae
717	7	1.0	509	2	Q95EA9	Q95EA9	echinocereu	790	7	1.0	608	2	Q9GNB0	Q9GNB0	sus scrofa
718	7	1.0	509	2	Q95EB1	Q95EB1	pfeiffera m	791	7	1.0	611	2	Q7MEC8	Q7MEC8	vibrio vuln
719	7	1.0	509	2	Q95EB4	Q95EB4	pfeiffera i	792	7	1.0	612	2	Q804W7	Q804W7	fugu musculu
720	7	1.0	509	2	Q95EB5	Q95EB5	corryocactu	793	7	1.0	614	1	SPAS_MOUSE	SPAS_MOUSE	mus musculu
721	7	1.0	509	2	Q95EB6	Q95EB6	eulychnia i	794	7	1.0	615	2	Q6GNK4	Q6GNK4	homopus lae
722	7	1.0	509	2	Q95EB7	Q95EB7	austrocactu	795	7	1.0	616	1	SPAS_HUMAN	SPAS_HUMAN	homo sapien
723	7	1.0	509	2	Q95EB8	Q95EB8	neoraimondi	796	7	1.0	617	1	THRB_RAT	THRB_RAT	rattus norv
724	7	1.0	509	2	Q95EB9	Q95EB9	castellanos	797	7	1.0	617	2	Q97UG5	Q97UG5	sulfolobus
725	7	1.0	509	2	Q95EC0	Q95EC0	leptocereus	798	7	1.0	618	1	CTR3_MOUSE	CTR3_MOUSE	mus musculu
726	7	1.0	509	2	Q95EC1	Q95EC1	armatocereu	799	7	1.0	618	1	THRB_MOUSE	THRB_MOUSE	mus musculu
727	7	1.0	509	2	Q95EC2	Q95EC2	acanthocereu	800	7	1.0	620	2	Q38940	Q38940	arabidopsis
728	7	1.0	509	2	Q95EC3	Q95EC3	calymmanthi	801	7	1.0	622	1	THRB_HUMAN	THRB_HUMAN	homo sapien
729	7	1.0	509	2	Q95EC7	Q95EC7	aztekium xi	802	7	1.0	622	2	Q727P3	Q727P3	homo sapien
730	7	1.0	509	2	Q95EC8	Q95EC8	astrophytum	803	7	1.0	624	2	Q94CF4	Q94CF4	arabidopsis
731	7	1.0	509	2	Q95ED0	Q95ED0	echinocactu	804	7	1.0	625	1	THIC_BOVIN	THIC_BOVIN	bos taurus
732	7	1.0	509	2	Q95ED1	Q95ED1	frailea pha	805	7	1.0	629	1	THIC_PSESM	THIC_PSESM	pseudomonas
733	7	1.0	509	2	Q95ED2	Q95ED2	frailea gra	806	7	1.0	631	2	Q90Z56	Q90Z56	scophthalmu
734	7	1.0	509	2	Q95ED3	Q95ED3	blossfeldia	807	7	1.0	633	2	Q9NKD7	Q9NKD7	drosophila
735	7	1.0	509	2	Q95ED4	Q95ED4	opuntia qui	808	7	1.0	651	2	Q7NGA4	Q7NGA4	gloeobacter
736	7	1.0	509	2	Q95ED5	Q95ED5	austrocactu	809	7	1.0	651	2	Q65466	Q65466	arabidopsis
737	7	1.0	509	2	Q95ED9	Q95ED9	pereskia st	810	7	1.0	658	2	Q8U2H8	Q8U2H8	pyrococcus
738	7	1.0	509	2	Q95EE0	Q95EE0	pereskia gu	811	7	1.0	674	2	Q9A4E2	Q9A4E2	arabidopsis
739	7	1.0	509	2	Q95EE2	Q95EE2	grahamia br	812	7	1.0	678	2	Q9A4E2	Q9A4E2	caulobacter
740	7	1.0	509	2	Q95EE3	Q95EE3	neurospora	813	7	1.0	680	2	Q8GX18	Q8GX18	arabidopsis
741	7	1.0	509	2	Q95EE4	Q95EE4	symbiobacte	814	7	1.0	682	2	Q6DKG5	Q6DKG5	homo sapien
742	7	1.0	510	1	MATK_GRABR	MATK_GRABR	methanosarc	815	7	1.0	682	2	Q8EWF4	Q8EWF4	mycoplasma
743	7	1.0	510	2	Q7SEH0	Q7SEH0	methanosarc	816	7	1.0	684	2	Q8EUC0	Q8EUC0	arabidopsis
744	7	1.0	517	2	Q67SH0	Q67SH0	metanosaic	817	7	1.0	700	2	Q8EUC0	Q8EUC0	arabidopsis
745	7	1.0	521	1	GM12_METAC	GM12_METAC	metanosaic	818	7	1.0	703	2	Q8R917	Q8R917	thermoanaer
746	7	1.0	521	1	GPMT_METMA	GPMT_METMA	brachydanio	819	7	1.0	705	2	Q7R5J9	Q7R5J9	giardia lam
747	7	1.0	524	2	Q7SXH8	Q7SXH8	debaromyce	820	7	1.0	707	1	EMPI_XENLA	EMPI_XENLA	xenopus lae
748	7	1.0	525	2	Q6BJ17	Q6BJ17	homo sapien	821	7	1.0	708	2	Q87239	Q87239	lactococcus
749	7	1.0	526	2	Q96AV5	Q96AV5	xanthomonas	822	7	1.0	713	2	Q62A96	Q62A96	burkholderi
750	7	1.0	527	2	Q8P606	Q8P606	caenorhabdi	823	7	1.0	720	2	Q63NR2	Q63NR2	burkholderi
751	7	1.0	529	2	Q17403	Q17403	caenorhabdi	824	7	1.0	732	2	Q65Q18	Q65Q18	mannheimia
752	7	1.0	529	2	Q7ND04	Q7ND04	homo sapien	825	7	1.0	735	2	Q57381	Q57381	xenopus lae
753	7	1.0	530	2	Q94900	Q94900	homo sapien	826	7	1.0	735	2	Q66K13	Q66K13	xenopus lae
754	7	1.0	532	2	Q9YDE4	Q9YDE4	aeropyrum p	827	7	1.0	746	2	Q6M7J3	Q6M7J3	corynebacte
755	7	1.0	533	2	Q9BI47	Q9BI47	caenorhabdi	828	7	1.0	746	2	Q97R74	Q97R74	streptococc
756	7	1.0	535	2	Q9JP77	Q9JP77	thermonos	829	7	1.0	749	2	Q9YGE8	Q9YGE8	oncorhynch
757	7	1.0	535	2	Q6MR14	Q6MR14	bdellovibri	830	7	1.0	754	2	Q49144	Q49144	arabidopsis
758	7	1.0	541	2	Q7P546	Q7P546	fusobacteri	831	7	1.0	754	2	Q7G196	Q7G196	arabidopsis
759	7	1.0	541	2	Q8RFL3	Q8RFL3	fusobacteri	832	7	1.0	765	2	Q8XY74	Q8XY74	arabidopsis
760	7	1.0	541	2	Q7WPA4	Q7WPA4	borderetella	833	7	1.0	778	2	Q6CP63	Q6CP63	kiuyveromyc
761	7	1.0	542	1	MODU_DROME	MODU_DROME	drosophila	834	7	1.0	783	1	YX11_PSEAE	YX11_PSEAE	pseudomonas

835	7	1.0	783	2	Q7R5Y0	Q7r5y0 giardia lam	908	7	1.0	1450	2	Q6BCK1	Q6bck1 tetrahymena
836	7	1.0	783	2	Q86DL3	Q86dl3 giardia lam	909	7	1.0	1506	2	Q6NS59	Q6ns59 mus musculus
837	7	1.0	783	2	Q6DW76	Q6dw76 glycine max	910	7	1.0	1522	1	DNA2 YEAST	D38859 saccharomyc
838	7	1.0	783	2	Q9E1Z6	Q9e1z6 ceratophthec	911	7	1.0	1527	2	Q6FII8	Q6fi18 candida gla
839	7	1.0	786	2	Q6DW74	Q6dw74 lotus japon	912	7	1.0	1544	2	Q86ZB3	Q86zb3 botrytis ci
840	7	1.0	787	2	Q6VIE8	Q6vie8 drosophila	913	7	1.0	1569	2	Q9FHD0	Q9fhd0 arabidopsis
841	7	1.0	790	1	CADI_HUMAN	Q13634 homo sapien	914	7	1.0	1608	2	Q95V45	Q95vas drosophila
842	7	1.0	790	2	Q8NSZ2	Q8nsz2 homo sapien	915	7	1.0	1631	2	Q8DZ37	Q8dz37 streptococc
843	7	1.0	791	2	Q49137	Q49137 arabidopsis	916	7	1.0	1640	2	Q86Z91	Q86z91 gibberella
844	7	1.0	791	2	O49139	O49139 arabidopsis	917	7	1.0	1660	2	Q94729	Q94729 oryza sativ
845	7	1.0	791	2	O50073	O50073 arabidopsis	918	7	1.0	1660	2	Q7XFK3	Q7xfk3 oryza sativ
846	7	1.0	793	2	Q7QUH8	Q7quh8 giardia lam	919	7	1.0	1660	2	Q8LP68	Q8lp68 chlamydomon
847	7	1.0	799	2	Q7SAU1	Q7sau1 ashbya goss	920	7	1.0	1666	2	Q7RV31	Q7rv31 neurospora
848	7	1.0	799	2	Q8NSU9	Q8nsu9 corynebacte	921	7	1.0	1755	2	Q7RV31	Q7rv31 neurospora
849	7	1.0	803	2	Q6FV15	Q6fv15 candida gla	922	7	1.0	1768	2	Q9N8K7	Q9n8k7 trypanosoma
850	7	1.0	805	2	Q95RK7	Q95rk7 drosophila	923	7	1.0	1822	1	SC72 SCHPO	Q9p7k5 trypanosoma
851	7	1.0	805	2	Q636U8	Q636u8 bacillus ce	924	7	1.0	1826	2	Q7RXK8	Q7rxk8 neurospora
852	7	1.0	805	2	Q733A2	Q733a2 bacillus ce	925	7	1.0	1831	2	Q86T77	Q86t77 homo sapien
853	7	1.0	805	2	Q81WV6	Q81wv6 bacillus an	926	7	1.0	1863	2	Q8IVX2	Q8ivx2 homo sapien
854	7	1.0	805	2	Q6HF81	Q6hf81 bacillus th	927	7	1.0	1865	2	Q7Z401	Q7z401 homo sapien
855	7	1.0	806	2	Q81A60	Q81a60 bacillus ce	928	7	1.0	1877	2	Q9XXW1	Q9xxw1 plasmodium
856	7	1.0	808	2	Q9S7D1	Q9s7d1 arabidopsis	929	7	1.0	1879	2	Q7PDP1	Q7pdp1 plasmodium
857	7	1.0	826	2	Q8PUF4	Q8puf4 methanosarc	930	7	1.0	1903	2	Q9UON7	Q9uon7 plasmodium
858	7	1.0	826	2	Q8TQX6	Q8tx6 methanosarc	931	7	1.0	1952	2	Q95SN5	Q95sn5 drosophila
859	7	1.0	826	2	Q9TU41	Q9tu41 arabidopsis	932	7	1.0	1961	2	Q6W889	Q6w889 rattus norv
860	7	1.0	841	1	TRK1 SCHPO	P47946 schizosacch	933	7	1.0	1966	2	Q81QA6	Q81qa6 drosophila
861	7	1.0	842	2	Q9LS88	Q9ls88 arabidopsis	934	7	1.0	1966	2	Q9NHX6	Q9nhx6 drosophila
862	7	1.0	859	1	ALR1 YEAST	Q8269 saccharomyc	935	7	1.0	1968	2	Q8XOC5	Q8xoc5 neurospora
863	7	1.0	864	2	Q68VK4	Q68vk4 arabidopsis	936	7	1.0	1985	2	Q8T9N4	Q8t9n4 drosophila
864	7	1.0	867	2	Q21186	Q21186 caenorhabdi	937	7	1.0	1985	2	Q7KUA8	Q7kua8 drosophila
865	7	1.0	869	2	Q8IG55	Q8ig55 caenorhabdi	938	7	1.0	1988	2	Q9VSK5	Q9vsk5 drosophila
866	7	1.0	873	2	Q9S0Z4	Q9s0z4 escherichia	939	7	1.0	2381	2	Q86BH2	Q86bh2 drosophila
867	7	1.0	917	2	Q9V4B8	Q9v4b8 drosophila	940	7	1.0	2393	2	Q8I461	Q8i461 plasmodium
868	7	1.0	921	2	Q9VJ29	Q9vj29 drosophila	941	7	1.0	2549	2	Q7PPU7	Q7ppu7 anopheles g
869	7	1.0	921	2	Q9BDU0	Q9bdu0 dendrohyrax	942	7	1.0	2605	2	Q5O858	Q5o858 myxococcus
870	7	1.0	922	2	Q6BTJ4	Q6btj4 debaryomyce	943	7	1.0	2906	2	Q9WUH9	Q9wuh9 rattus norv
871	7	1.0	950	2	Q8RXZ0	Q8rxz0 oryza sativ	944	7	1.0	2907	1	FBN2_MOUSE	Q61555 mus musculu
872	7	1.0	955	2	Q726R1	Q726r1 desulfovibrio	945	7	1.0	2911	1	FBN2_HUMAN	Q35556 homo sapien
873	7	1.0	961	2	Q8SVH3	Q8svh3 encephalito	946	7	1.0	3306	2	Q9FT44	Q9ft44 arabidopsis
874	7	1.0	970	2	Q7XF23	Q7xf23 oryza sativ	947	7	1.0	3446	2	Q8GAC8	Q8gac8 dictyosteli
875	7	1.0	970	2	Q9AYF2	Q9ayf2 oryza sativ	948	7	1.0	3523	2	Q7QCP4	Q7qcp4 anopheles g
876	7	1.0	977	2	Q91925	Q91925 xenopus lae	949	7	1.0	3564	1	CSM1_MOUSE	Q92313 mus musculu
877	7	1.0	980	2	Q22088	Q22088 caenorhabdi	950	7	1.0	3666	2	Q6UDX0	Q6udx0 plasmodium
878	7	1.0	982	2	Q6CWM6	Q6cwm6 kluyveromyc	951	7	1.0	3972	2	Q9S0R8	Q9s0r8 streptomyce
879	7	1.0	991	2	Q8TDH1	Q8tdh1 homo sapien	952	7	1.0	3996	2	Q7KTP2	Q7ktp2 drosophila
880	7	1.0	995	1	YPD1 CAEEL	P48053 caenorhabdi	953	7	1.0	4547	2	Q9W343	Q9w343 drosophila
881	7	1.0	1007	2	Q8JT28	Q8jt28 xenopus lae	954	7	1.0	4569	2	Q7PS35	Q7ps35 anopheles g
882	7	1.0	1013	2	Q6MP67	Q6mf67 parachlamydo	955	7	1.0	4899	2	Q9VR91	Q9vr91 drosophila
883	7	1.0	1022	1	TLD_BRARE	O57460 brachydanio	956	7	1.0	23015	2	Q8IQ18	Q8iq18 drosophila
884	7	1.0	1031	2	Q8G5K2	Q8g5k2 bifidobacte	957	6	0.8	27	1	ANF_ANGJA	P18144 anguilla ja
885	7	1.0	1046	2	Q6C1R8	Q6c1r8 yarrowia li	958	6	0.8	33	2	Q8FZE0	Q8fze0 bruceella su
886	7	1.0	1047	2	Q9PKW9	Q9fkW9 arabidopsis	959	6	0.8	33	2	Q8B9R2	Q8b9r2 emiliania h
887	7	1.0	1048	2	Q9NA71	Q9na71 caenorhabdi	960	6	0.8	33	2	Q8B9R3	Q8b9r3 emiliania h
888	7	1.0	1074	2	Q831Z5	Q831z5 enterococcu	961	6	0.8	33	2	Q8B9R4	Q8b9r4 emiliania h
889	7	1.0	1079	2	Q6MLZ8	Q6mlz8 bdellovibri	962	6	0.8	33	2	Q8B9R5	Q8b9r5 emiliania h
890	7	1.0	1081	2	Q8BZL9	Q8bz19 mus musculu	963	6	0.8	33	2	Q8B9R6	Q8b9r6 emiliania h
891	7	1.0	1100	2	Q86UH1	Q86uh1 homo sapien	964	6	0.8	33	2	Q8B9R7	Q8b9r7 emiliania h
892	7	1.0	1111	2	Q855Z2	Q855z2 mycobacteri	965	6	0.8	33	2	Q8B9R8	Q8b9r8 emiliania h
893	7	1.0	1120	2	Q8RPS7	Q8rps7 corynebacte	966	6	0.8	35	2	Q8B9R9	Q8b9r9 emiliania h
894	7	1.0	1135	2	Q7Q137	Q7q137 anopheles g	967	6	0.8	35	2	Q9KSL5	Q9ksl5 vibrio chol
895	7	1.0	1136	2	Q81UD8	Q81jd8 plasmodium	968	6	0.8	36	2	Q96W36	Q96w36 ophiostoma
896	7	1.0	1158	2	Q7Q253	Q7q253 anopheles g	969	6	0.8	36	2	Q72CQ3	Q72cq3 desulfovibr
897	7	1.0	1201	2	Q71RU0	Q71ru0 nitrobaacter	970	6	0.8	37	2	Q7DRP2	Q7drp2 human immun
898	7	1.0	1233	2	Q6CAC2	Q6cac2 yarrowia li	971	6	0.8	38	2	Q7VM96	Q7vm96 haemophilus
899	7	1.0	1234	2	Q7SF30	Q7sf30 neurospora	972	6	0.8	39	2	Q23160	Q23160 sus scrofa
900	7	1.0	1240	1	DLT_DROME	Q8t626 drosophila	973	6	0.8	39	2	Q61E99	Q61e99 macaca mula
901	7	1.0	1240	2	Q65468	Q65468 arabidopsis	974	6	0.8	40	2	Q9R4D0	Q9rad0 thermus aqu
902	7	1.0	1243	2	O35954	O35954 mus musculu	975	6	0.8	40	2	Q73510	Q73510 bacillus ce
903	7	1.0	1300	2	Q8XOV5	Q8xov5 neurospora	976	6	0.8	40	2	Q9KLT1	Q9klt1 vibrio chol
904	7	1.0	1327	2	Q6C4J5	Q6c4j5 yarrowia li	977	6	0.8	40	2	Q8UM87	Q8um87 human immun
905	7	1.0	1340	2	Q9GTY4	Q9gyt4 anopheles g	978	6	0.8	40	2	Q8USM4	Q8uem4 human immun
906	7	1.0	1346	2	Q9ZG12	Q9zg12 streptomyce	979	6	0.8	41	2	Q90SM4	Q90sm4 human immun
907	7	1.0	1355	2	Q7Q7S9	Q7q7s9 anopheles g	980	6	0.8	41	2	Q90SM5	Q90sm5 human immun



1127	6	0.8	71	2	Q77JL5	Q77j15 bacterioph	1200	6	0.8	81	2	Ol0811	O10811 human immun
1128	6	0.8	71	2	Q77JMS	Q77jms bacterioph	1201	6	0.8	81	2	Q91893	Q91893 human immun
1129	6	0.8	71	2	Q9XJ51	Q9xj51 lactococcus	1202	6	0.8	81	2	Q04271	Q04271 human immun
1130	6	0.8	71	2	Q75I61	Q75i61 oryza sativ	1203	6	0.8	81	2	Q90MJ9	Q90mj9 human immun
1131	6	0.8	71	2	Q6FCL0	Q6fcl0 acinetobact	1204	6	0.8	81	2	Q90VH8	Q90vh8 human immun
1132	6	0.8	71	2	Q6ZEL3	Q6zel3 synechocyst	1205	6	0.8	81	2	Q6JN14	Q6jni4 human immun
1133	6	0.8	71	2	Q7MYC6	Q7myc6 photorhabdu	1206	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1134	6	0.8	71	2	Q83NLI	Q83nl9 tropheryma	1207	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1135	6	0.8	71	2	Q9CB16	Q9cb16 lactococcus	1208	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1136	6	0.8	71	2	Q79955	Q79955 human immun	1209	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1137	6	0.8	71	2	Q79957	Q79957 human immun	1210	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1138	6	0.8	71	2	Q79959	Q79959 human immun	1211	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1139	6	0.8	71	2	Q79965	Q79965 human immun	1212	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1140	6	0.8	71	2	Q79967	Q79967 human immun	1213	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1141	6	0.8	71	2	Q79969	Q79969 human immun	1214	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1142	6	0.8	71	2	Q79970	Q79970 human immun	1215	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1143	6	0.8	71	2	Q79971	Q79971 human immun	1216	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1144	6	0.8	71	2	Q79974	Q79974 human immun	1217	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1145	6	0.8	71	2	Q79976	Q79976 human immun	1218	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1146	6	0.8	71	2	Q79979	Q79979 human immun	1219	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1147	6	0.8	71	2	Q79982	Q79982 human immun	1220	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1148	6	0.8	71	2	Q9PIH3	Q9pih3 homo sapien	1221	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1149	6	0.8	72	2	Q26687	Q26687 trypanosoma	1222	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1150	6	0.8	72	2	Q49229	Q49229 mycoplasma	1223	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1151	6	0.8	72	2	Q64F11	Q64f11 bacteroides	1224	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1152	6	0.8	72	2	Q8K7S9	Q8k7s9 streptococc	1225	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1153	6	0.8	72	2	Q7NLJ8	Q7nlj8 gloeobacter	1226	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1154	6	0.8	72	2	Q83214	Q83214 enterococcu	1227	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1155	6	0.8	72	2	Q87XL9	Q87xl9 pseudomonas	1228	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1156	6	0.8	72	2	P90297	P90297 human immun	1229	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1157	6	0.8	72	2	Q78461	Q78461 human immun	1230	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1158	6	0.8	72	2	Q79534	Q79534 human immun	1231	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1159	6	0.8	72	2	Q79551	Q79551 human immun	1232	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1160	6	0.8	72	2	Q79561	Q79561 human immun	1233	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1161	6	0.8	73	2	Q8RXW8	Q8rxw8 arabidopsis	1234	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1162	6	0.8	73	2	Q69U82	Q69u82 oryza sativ	1235	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1163	6	0.8	73	2	Q97HT9	Q97ht9 clostridium	1236	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1164	6	0.8	73	2	Q8F557	Q8f557 leptospira	1237	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1165	6	0.8	73	2	Q9HY80	Q9hy80 pseudomonas	1238	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1166	6	0.8	74	2	Q8TKU9	Q8tku9 methanosa	1239	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1167	6	0.8	74	2	Q8FWB5	Q8fwb5 brucella su	1240	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1168	6	0.8	74	2	P88432	P88432 human immun	1241	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1169	6	0.8	75	1	YOR4_SMYEA	Q00848 strawberry	1242	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1170	6	0.8	75	2	Q8PYR9	Q8pyr9 methanosa	1243	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1171	6	0.8	75	2	Q9P169	Q9p169 homo sapien	1244	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1172	6	0.8	75	2	Q7PGQ2	Q7pgq2 anophelies g	1245	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1173	6	0.8	75	2	Q69TW9	Q69tw9 oryza sativ	1246	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1174	6	0.8	75	2	Q8U5R3	Q8u5r3 agrobacteri	1247	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1175	6	0.8	75	2	Q835D8	Q835d8 enterococcu	1248	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1176	6	0.8	75	2	Q87C72	Q87c72 xylella fas	1249	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1177	6	0.8	75	2	Q9PB10	Q9pb10 xylella fas	1250	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1178	6	0.8	75	2	Q41279	Q41279 strawberry	1251	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1179	6	0.8	76	2	Q84XF0	Q84xf0 oryza sativ	1252	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1180	6	0.8	76	2	Q09529	Q09529 human immun	1253	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1181	6	0.8	77	1	YXCB_CVAPA	P48332 cyanophora	1254	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1182	6	0.8	77	2	Q6ZD12	Q6zdl2 oryza sativ	1255	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1183	6	0.8	77	2	Q9LDK3	Q9ldk3 oryza sativ	1256	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1184	6	0.8	77	2	Q8YU14	Q8yu14 anabaena sp	1257	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1185	6	0.8	78	1	YVFB_VACCC	P20560 vaccinia vi	1258	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1186	6	0.8	78	2	Q96HW0	Q96hw0 homo sapien	1259	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1187	6	0.8	78	2	Q6YL42	Q6yl42 homo sapien	1260	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1188	6	0.8	78	2	Q7THW1	Q7thw1 cowpox viru	1261	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1189	6	0.8	79	1	Y476_ARCFU	Q29774 archaeoglob	1262	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1190	6	0.8	79	2	Q8C3F5	Q8c3f5 mus musculu	1263	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1191	6	0.8	80	1	NUEM_CERCA	Q34052 ceratitidis c	1264	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1192	6	0.8	80	2	Q8U4J1	Q8u4j1 pyrococcus	1265	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1193	6	0.8	80	2	Q8KJW5	Q8kjw5 proteus vul	1266	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1194	6	0.8	80	2	Q7U3T4	Q7u3t4 synechococc	1267	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1195	6	0.8	80	2	Q7UUVG1	Q7uvg1 rhodopirell	1268	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1196	6	0.8	80	2	Q8DQ12	Q8dql2 streptococc	1269	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1197	6	0.8	80	2	Q99IV0	Q99iv0 uncultured	1270	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1198	6	0.8	80	2	Q7ZPI4	Q7zpi4 human immun	1271	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun
1199	6	0.8	81	2	Q7ULV1	Q7ulv1 rhodopirell	1272	6	0.8	81	2	Q6JNLI	Q6jnl1 human immun

1273	6	0.8	90	2	Q9IQN8	Q9icn8 human immun	1346	6	0.8	102	2	Q87GJ3	Q87gJ3 vibrio para
1274	6	0.8	91	2	Q8Z6F7	Q8z6f7 salmonella	1347	6	0.8	102	2	Q89H29	Q89h29 bradyrhizob
1275	6	0.8	91	2	Q8ZPV4	Q8zpv4 salmonella	1348	6	0.8	102	2	Q9K8L0	Q9k8l0 bacillus ha
1276	6	0.8	91	2	Q9JVM4	Q9jvm4 neisseria m	1349	6	0.8	103	2	Q97ZJ7	Q97zj7 sulfobolus
1277	6	0.8	91	2	Q70004	Q70004 human immun	1350	6	0.8	103	2	Q95M89	Q95m89 equus cabal
1278	6	0.8	91	2	Q70009	Q70009 human immun	1351	6	0.8	103	2	Q74GQ6	Q74gq6 geobacter s
1279	6	0.8	91	2	Q72787	Q72787 human immun	1352	6	0.8	103	2	Q7UGU8	Q7ug8 rhodopirell
1280	6	0.8	92	1	YLXF_BACSU	P32730 bacillus eu	1353	6	0.8	103	2	Q877Q6	Q877q6 vibrio para
1281	6	0.8	92	2	Q8HQJ5	Q8hqj5 ornithodor	1354	6	0.8	103	2	Q6D9M5	Q6dm5 erwinia car
1282	6	0.8	92	2	Q93KE9	Q93ke9 chlamydia p	1355	6	0.8	103	2	Q8D5D6	Q8ds6 mus musculu
1283	6	0.8	92	2	Q65JIO	Q65jio bacillus li	1356	6	0.8	104	2	Q8SQY2	Q8sqy2 encephalito
1284	6	0.8	92	2	Q8VIZ9	Q8viz9 emiliania h	1357	6	0.8	104	2	Q8SX12	Q8sx12 drosophila
1285	6	0.8	92	2	Q85FIO	Q85fi0 adiantum ca	1358	6	0.8	104	2	Q6IK98	Q6ik98 drosophila
1286	6	0.8	93	2	Q8LMZ6	Q8lmz6 oryza sativ	1359	6	0.8	104	2	Q7R8C5	Q7r8c5 plasmodium
1287	6	0.8	93	2	Q42278	Q42278 arabidopsis	1360	6	0.8	104	2	Q38556	Q38556 bacterioph
1288	6	0.8	93	2	Q629K2	Q629k2 haemophilus	1361	6	0.8	104	2	Q6V8N3	Q6v8n3 malus domes
1289	6	0.8	93	2	Q41565	Q41565 human immun	1362	6	0.8	104	2	Q45117	Q45117 bacteroides
1290	6	0.8	94	2	Q6IL90	Q6il90 drosophila	1363	6	0.8	104	2	Q73I39	Q73i39 wolbachia p
1291	6	0.8	94	2	Q7QW1	Q7qwn1 giardia lam	1364	6	0.8	104	2	Q7P0H7	Q7p0h7 chromobacte
1292	6	0.8	94	2	Q9BDR2	Q9bdr2 bos taurus	1365	6	0.8	104	2	Q8B594	Q8b594 mus musculu
1293	6	0.8	94	2	Q94MT3	Q94mt3 bacterioph	1366	6	0.8	105	2	Q27553	Q27553 methanobact
1294	6	0.8	94	2	Q49475	Q49475 mycoplasma	1367	6	0.8	105	2	Q97C63	Q97c63 thermoplasm
1295	6	0.8	94	2	Q9ZBM8	Q9zbm8 mycobacteri	1368	6	0.8	105	2	Q23899	Q23899 dictyostell
1296	6	0.8	94	2	Q8VIZ6	Q8viz6 emiliania h	1369	6	0.8	105	2	Q8S005	Q8s005 oryza sativ
1297	6	0.8	94	2	Q8VIZ8	Q8viz8 emiliania h	1370	6	0.8	105	2	Q6ZLD9	Q6zld9 oryza sativ
1298	6	0.8	94	2	Q8VZ02	Q8vz02 emiliania h	1371	6	0.8	105	2	Q7LHN1	Q7lhn1 arabidopsis
1299	6	0.8	94	2	Q8VZ03	Q8vz03 emiliania h	1372	6	0.8	105	2	Q7N4V8	Q7n4v8 photorhabdu
1300	6	0.8	94	2	Q8VZ04	Q8vz04 emiliania h	1373	6	0.8	105	2	Q7NT32	Q7nt32 chromobacte
1301	6	0.8	94	2	Q41599	Q41599 human immun	1374	6	0.8	106	1	Q8BP51	Q8bp51 mus musculu
1302	6	0.8	94	2	Q70001	Q70001 human immun	1375	6	0.8	106	1	RNPA_SULSO	Q97WJ1 sulfobolus
1303	6	0.8	95	2	Q9I4U5	Q9i4u5 pseudomonas	1376	6	0.8	106	2	Q74KE5	Q74ke5 lactobacill
1304	6	0.8	95	2	Q80X28	Q80x28 mus musculu	1377	6	0.8	107	1	RL21_CHLTR	Q84425 chlamydia t
1305	6	0.8	95	2	Q6IEC0	Q6iec0 ictalurus p	1378	6	0.8	107	2	Q6IGL6	Q6igl6 drosophila
1306	6	0.8	95	2	Q7PFK0	Q7pfk0 anopheles g	1379	6	0.8	107	2	Q8E7H9	Q8e7h9 streptococc
1307	6	0.8	96	2	Q7QSG2	Q7qsg2 giardia lam	1380	6	0.8	107	2	Q9CBP1	Q9cbp1 mycobacteri
1308	6	0.8	96	2	Q9MPY9	Q9mpy9 anopheles c	1381	6	0.8	107	2	Q6AKQ7	Q6akq7 desulfotale
1309	6	0.8	96	2	Q9C7L8	Q9c7l8 arabidopsis	1382	6	0.8	107	2	Q8BW14	Q8bw14 mus musculu
1310	6	0.8	96	2	Q7NWJ1	Q7nwj1 chromobacte	1383	6	0.8	108	1	PT05_STVPL	P28197 styela plic
1311	6	0.8	96	2	Q7UGN6	Q7ugn6 rhodopirell	1384	6	0.8	108	2	Q6UAT7	Q6uat7 bacterioph
1312	6	0.8	97	2	Q7RIM5	Q7rim5 giardia lam	1385	6	0.8	108	2	Q82328	Q82328 arabidopsis
1313	6	0.8	97	2	Q7YVG4	Q7yvg4 trypanosoma	1386	6	0.8	108	2	Q6K4F7	Q6k4f7 oryza sativ
1314	6	0.8	97	2	Q884H1	Q884h1 pseudomonas	1387	6	0.8	108	2	Q7NMX6	Q7nmx6 gloeobacter
1315	6	0.8	98	2	Q8Q0E3	Q8q0e3 methanosarc	1388	6	0.8	108	2	O10826	O10826 human immun
1316	6	0.8	98	2	Q6RZ23	Q6rzz3 endoxyla sp	1389	6	0.8	108	2	Q9QN58	Q9qn58 human immun
1317	6	0.8	98	2	Q25731	Q25731 plasmodium	1390	6	0.8	108	2	Q9QN68	Q9qn68 human immun
1318	6	0.8	98	2	Q9NPH0	Q9nfh0 plasmodium	1391	6	0.8	109	1	TCMT_STRGA	P39890 streptomyc
1319	6	0.8	98	2	Q6SEG0	Q6seg0 lactobacill	1392	6	0.8	109	2	Q9M272	Q9m272 arabidopsis
1320	6	0.8	98	2	Q52096	Q52096 pseudomonas	1393	6	0.8	109	2	Q92LF5	Q92lf5 rhizobium m
1321	6	0.8	98	2	Q69509	Q69509 mycobacteri	1394	6	0.8	110	1	M280_ARATH	P93292 arabidopsis
1322	6	0.8	98	2	Q7TUT9	Q7tut9 prochloroco	1395	6	0.8	110	2	Q46207	Q46207 clostridium
1323	6	0.8	98	2	Q9KMT4	Q9kmt4 vibrio chol	1396	6	0.8	110	2	Q92SA8	Q92sa8 rhizobium m
1324	6	0.8	98	2	Q65PM7	Q65pm7 lactobacill	1397	6	0.8	110	2	Q9FSI4	Q9fsi4 bradyrhizob
1325	6	0.8	98	2	Q6D5N1	Q6d5n1 erwinia car	1398	6	0.8	110	2	Q8CDY6	Q8cdy6 mus musculu
1326	6	0.8	99	1	YQJ2_CABEL	P34625 caenorhabdi	1399	6	0.8	110	2	Q69141	Q69141 human herpe
1327	6	0.8	99	2	Q9L564	Q9l564 arabidopsis	1400	6	0.8	111	2	Q8TQ56	Q8tq56 methanosarc
1328	6	0.8	99	2	Q82VD8	Q82vd8 nitrosomona	1401	6	0.8	111	2	Q6IHE6	Q6ihe6 drosophila
1329	6	0.8	99	2	Q89H95	Q89h95 bradyrhizob	1402	6	0.8	111	2	Q6DN49	Q6dn49 streptomyc
1330	6	0.8	99	2	Q924W3	Q924w3 rattus norv	1403	6	0.8	111	2	Q72SM5	Q72sm5 desulfovibr
1331	6	0.8	99	2	P88433	P88433 human immun	1404	6	0.8	111	2	Q8FLL7	Q8fll7 corynebacte
1332	6	0.8	100	2	Q64DE3	Q64de3 uncultured	1405	6	0.8	111	2	Q9J8B8	Q9j8b8 spodoptera
1333	6	0.8	100	2	Q50101	Q50101 pyrococcus	1406	6	0.8	112	1	PT17_STVPL	P28209 styela plic
1334	6	0.8	100	2	Q6YVY4	Q6yvy4 oryza sativ	1407	6	0.8	112	2	Q9GLK5	Q9glk5 felis silve
1335	6	0.8	100	2	Q7MS23	Q7ms23 wolinnella s	1408	6	0.8	112	2	P72474	P72474 streptococc
1336	6	0.8	101	2	Q979B6	Q979b6 thermoplasm	1409	6	0.8	112	2	Q62J69	Q62j69 burkholderi
1337	6	0.8	101	2	Q9JPF2	Q9jpf2 neisseria m	1410	6	0.8	112	2	Q63SW1	Q63sw1 sulfolobus
1338	6	0.8	101	2	Q91Z64	Q91z64 sigmodon hi	1411	6	0.8	112	2	Q684B5	Q684b5 burkholderi
1339	6	0.8	101	2	Q8BTY4	Q8bty4 mus musculu	1412	6	0.8	112	2	Q8PSU2	Q8psu2 xenopus lae
1340	6	0.8	101	2	Q8K3D7	Q8k3d7 mus musculu	1413	6	0.8	113	2	Q8L5K1	Q8l5k1 petunia hyb
1341	6	0.8	102	2	Q14278	Q14278 homo sapien	1414	6	0.8	113	2	Q84V28	Q84v28 crypthecodi
1342	6	0.8	102	2	Q7R3J1	Q7r3j1 giardia lam	1415	6	0.8	113	2	Q49970	Q49970 mycobacteri
1343	6	0.8	102	2	Q67TQ7	Q67tq7 oryza sativ	1416	6	0.8	113	2	Q925X2	Q925x2 frankia sp.
1344	6	0.8	102	2	Q925K2	Q925k2 mycobacteri	1417	6	0.8	113	2	Q64GA6	Q64ga6 cylindrospe
1345	6	0.8	102	2	Q65RC9	Q65rg9 mannheimia	1418	6	0.8	113	2	Q87DR0	Q87dr0 xylella fas



1419	6	0.8	113	2	Q8FJ25	Q8fj25 escherichia
1420	6	0.8	114	2	Q8GUR2	Q8gur2 axonopus co
1421	6	0.8	114	2	Q6MMV6	Q6mmv6 dbellovibri
1422	6	0.8	114	2	Q89D11	Q89d11 bradyrhizob
1423	6	0.8	114	2	Q8Q6K9	Q8q6k9 human immun
1424	6	0.8	115	1	CTE9 MOUSE	Q8cr37 mus musculus
1425	6	0.8	115	2	Q9YD49	Q9yd49 aeropyrum p
1426	6	0.8	115	2	Q9BTD1	Q9btd1 homo sapien
1427	6	0.8	115	2	Q8LTJ8	Q8ltj8 lactococcus
1428	6	0.8	115	2	Q38132	Q38132 bacterioph
1429	6	0.8	115	2	Q8D410	Q8d410 vibrio vuln
1430	6	0.8	115	2	Q6PB12	Q6pb12 brachydanio
1431	6	0.8	115	2	Q67257	Q67257 human immun
1432	6	0.8	116	1	RL22_GLOVI	Q9nef7 gloebacter
1433	6	0.8	116	2	Q9HLD4	Q9hld4 thermoplas
1434	6	0.8	116	2	Q6B883	Q6b883 ixodes paci
1435	6	0.8	116	2	Q6B8C4	Q6b8c4 ixodes paci
1436	6	0.8	116	2	Q6B8E6	Q6b8e6 ixodes paci
1437	6	0.8	116	2	Q8H8A2	Q8ha82 salmonella
1438	6	0.8	116	2	Q9XIA6	Q9xia6 arabidopsis
1439	6	0.8	116	2	Q67R66	Q67r66 symbiobacte
1440	6	0.8	116	2	Q7MFI1	Q7mfi1 vibrio vuln
1441	6	0.8	116	2	P87922	P87922 human immun
1442	6	0.8	116	2	Q902G8	Q902g8 human immun
1443	6	0.8	116	2	Q6Q453	Q6q453 human immun
1444	6	0.8	117	1	RL22_STAAM	Q99s26 staphylococ
1445	6	0.8	117	1	RL22_STAAN	Q7a460 staphylococ
1446	6	0.8	117	1	RL22_STAAM	Q7a079 staphylococ
1447	6	0.8	117	1	RL22_STAEP	Q8cr95 staphylococ
1448	6	0.8	117	2	Q9YA74	Q9ya74 aeropyrum p
1449	6	0.8	117	2	Q7S013	Q7s013 neurospora
1450	6	0.8	117	2	Q7Q0N3	Q7q0n3 anopheles g
1451	6	0.8	117	2	Q7QK15	Q7qk15 anopheles g
1452	6	0.8	117	2	Q7RPA0	Q7rpa0 plasmodium
1453	6	0.8	117	2	Q6G776	Q6g776 staphylococ
1454	6	0.8	117	2	Q6G8I8	Q6gei8 staphylococ
1455	6	0.8	118	2	Q44226	Q44226 drosophila
1456	6	0.8	118	2	Q61GT2	Q6igt2 drosophila
1457	6	0.8	118	2	Q7QIG7	Q7qig7 anopheles g
1458	6	0.8	118	2	Q69UD4	Q69ud4 oryza sativ
1459	6	0.8	118	2	Q6ZAF7	Q6zaf7 oryza sativ
1460	6	0.8	118	2	Q7BTW1	Q7btw1 yersinia pe
1461	6	0.8	118	2	Q84040	Q84040 chlamydia t
1462	6	0.8	118	2	Q72MY2	Q72my2 leptospira
1463	6	0.8	118	2	Q8F8Q9	Q8f8q9 leptospira
1464	6	0.8	119	2	Q9MG24	Q9mg24 callithrix
1465	6	0.8	119	2	Q9MG25	Q9mg25 callithrix
1466	6	0.8	119	2	Q46457	Q46457 chlamydia t
1467	6	0.8	119	2	Q53469	Q53469 mycobacteri
1468	6	0.8	119	2	Q7T250	Q7t250 mycobacteri
1469	6	0.8	119	2	Q35755	Q35755 rattus norv
1470	6	0.8	120	2	Q05715	Q05715 saccharomyc
1471	6	0.8	120	2	Q74LT1	Q74lt1 lactobacill
1472	6	0.8	120	2	Q8C3D7	Q8c3d7 mus musculu
1473	6	0.8	120	2	Q6DN28	Q6dn28 xenopus tro
1474	6	0.8	121	2	Q6BN47	Q6bn47 debaryomyce
1475	6	0.8	121	2	Q7YXC5	Q7yxc5 caenorhabdi
1476	6	0.8	121	2	Q867A3	Q867a3 cryctolagus
1477	6	0.8	121	2	Q7V633	Q7v633 prochloroco
1478	6	0.8	121	2	Q91450	Q91450 salvelinus
1479	6	0.8	121	2	Q79786	Q79786 human immun
1480	6	0.8	122	1	RL14_MYCGE	P47407 mycoplasma
1481	6	0.8	122	1	RL14_MYCPN	P50308 mycoplasma
1482	6	0.8	122	2	Q9MP21	Q9mp21 anopheles f
1483	6	0.8	122	2	Q9TGJ5	Q9tgj5 taenia hyda
1484	6	0.8	122	2	P96093	P96093 thioabacillu
1485	6	0.8	123	1	NEF_HV1B1	P03404 human immun
1486	6	0.8	123	1	NEF_HV1H2	P04601 human immun
1487	6	0.8	123	2	O58242	O58242 pyrococcus
1488	6	0.8	123	2	P95954	P95954 sulfolobus
1489	6	0.8	123	2	Q9TGK1	Q9tgk1 taenia soli
1490	6	0.8	123	2	Q47794	Q47794 enterococcu
1491	6	0.8	123	2	Q63DY7	Q63dy7 bacillus ce

## ALIGNMENTS

## RESULT 1

Q6UXH9	PRELIMINARY;	PRT;	720 AA.
AC Q6UXH9			
DT 05-JUL-2004	(TREMBLrel. 27, Created)		
DT 05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DE ELGC699			
GN ORFNames=UNO699;			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI_TaxID=9606;			
RP [1]			
RN SEQUENCE FROM N.A.			
RX MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA Vandien R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,			
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA Godowski P.,			
RT "The secreted protein discovery initiative (SPDI), a large-scale			
RT effort to identify novel human secreted and transmembrane proteins: a			
RT bioinformatics assessment."			
RL Genome Res. 13:2265-2270(2003).			
CC -I- SIMILARITY: Belongs to peptidase family S1.			
CC -I- SIMILARITY: Contains 1 EGF-like domain.			
DR EMBL; AY358346; AAQ88712.1; -			
DR HSSP; P00734; 1BB0			
DR GO; GO:0005509; F:calcium ion binding; IEA.			
DR GO; GO:0004263; F:chymotrypsin activity; IEA.			
DR GO; GO:0008233; F:peptidase activity; IEA.			
DR GO; GO:0004295; F:trypsin activity; IEA.			
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR InterPro; IPR000859; CUB			
DR InterPro; IPR000742; EGF_2.			
DR InterPro; IPR001881; EGF_Ca.			
DR InterPro; IPR006209; EGF-like.			
DR InterPro; IPR006210; IEGF.			
DR InterPro; IPR001254; Peptidase S1.			
DR InterPro; IPR001314; Peptidase_S1A.			
DR InterPro; IPR009003; Pept_Ser_Cys.			
DR InterPro; IPR000436; Sushi_SCR_CCP.			
DR Pfam; PF00431; CUB; 1.			
DR Pfam; PF00008; EGF; 1.			
DR Pfam; PF00084; Sushi; 1.			
DR PRINTS; PR00722; CHYMOTRYPSIN.			
DR SMART; SM0032; CCP; 2.			
DR SMART; SM00042; CUB; 1.			
DR SMART; SM00181; EGF; 2.			
DR SMART; SM00179; EGF_Ca; 1.			
DR SMART; SM00020; Tryp_SPC; 1.			
DR PROSITE; PS01180; CUB; 1.			
DR PROSITE; PS00022; EGF_1; 1.			
DR PROSITE; PS01186; EGF_2; 1.			

DR PROSITE; PS50026; EGF 3; 1.  
DR PROSITE; PS50923; SUSHI; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ' SEQUENCE 720 AA; 80196 MW; DC898BC7241289D3 CRC64;  
  
Query Match 100.0%; Score 720; DB 2; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MELGCTWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60  
Db 1 MELGCTWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60  
  
QY 61 VVGYYTTPCCRNENECDSCLIHPGCTIFENCKSCRNCGSGTLLDDFFVVGKGYCAECRAGW 120  
Db 61 VVGYYTTPCCRNENECDSCLIHPGCTIFENCKSCRNCGSGTLLDDFFVVGKGYCAECRAGW 120  
  
QY 121 YGDCMRCGCVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
Db 121 YGDCMRCGCVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
  
QY 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSLIHLVLFHSDGSKNFDGFHAIYEEITACS 240  
Db 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSLIHLVLFHSDGSKNFDGFHAIYEEITACS 240  
  
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDGPGVNGYQKITGGPGLI 300  
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDGPGVNGYQKITGGPGLI 300  
  
QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360  
Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360  
  
QY 361 PMOVQSRRETLHLQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR 420  
Db 361 PMOVQSRRETLHLQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR 420  
  
QY 421 RLGSRRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL 480  
Db 421 RLGSRRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL 480  
  
QY 481 HKGAWFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVLGKPYRDDDRDEKTIQS 540  
Db 481 HKGAWFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVLGKPYRDDDRDEKTIQS 540  
  
QY 541 LQISAILHNPYDPIILDADIALIKLDDKARISTRVQPICLAASRDISTSFQESHITVAG 600  
Db 541 LQISAILHNPYDPIILDADIALIKLDDKARISTRVQPICLAASRDISTSFQESHITVAG 600  
  
QY 601 WNVLADVRSPGKNDTLRSGVSVVDSLLCEEQHEHDHGIPIVSVTDNMFCASWEPAPSIDI 660  
Db 601 WNVLADVRSPGKNDTLRSGVSVVDSLLCEEQHEHDHGIPIVSVTDNMFCASWEPAPSIDI 660  
  
QY 661 CTAETGGAIAVSPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720  
Db 661 CTAETGGAIAVSPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 2

Q6N062 PRELIMINARY; PRT; 720 AA.  
ID Q6N062  
AC Q6N062;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686N24154.  
GN Name=DKFZp686N24154;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Colon endothel;  
RG The German cDNA Consortium;  
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.  
CC -!- SIMILARITY: Contains 1 EGF-like domain.  
DR EMBL; BX640676; CAE45808.1; -.  
DR HSSP; P00734; IBB0.  
DR GO; GO:000509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0004233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:000508; F:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS50923; SUSHI; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;  
KW Serine protease.  
SQ SEQUENCE 720 AA; 80196 MW; E98A9F9948EE777D CRC64;  
  
Query Match 78.2%; Score 563; DB 2; Length 720;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 1 MELGCTWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60  
  
QY 61 VVGYYTTPCCRNENECDSCLIHPGCTIFENCKSCRNCGSGTLLDDFFVVGKGYCAECRAGW 120  
Db 61 VVGYYTTPCCRNENECDSCLIHPGCTIFENCKSCRNCGSGTLLDDFFVVGKGYCAECRAGW 120  
  
QY 121 YGDCMRCGCVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
Db 121 YGDCMRCGCVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
  
QY 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSLIHLVLFHSDGSKNFDGFHAIYEEITACS 240  
Db 181 YVEVRDGDNRDGOIIRKVCNERNPAPIQSIGSSLIHLVLFHSDGSKNFDGFHAIYEEITACS 240  
  
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDGPGVNGYQKITGGPGLI 300  
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDGPGVNGYQKITGGPGLI 300  
  
QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360  
Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360  
  
QY 361 PMOVQSRRETLHLQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR 420  
Db 361 PMOVQSRRETLHLQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR 420

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Db 361 PMQVSRTPPLHQLYSAAFSKQKLSQAPTKKPALPFGDLPMGYOHLHTLQYECISPPYR 420
Qy 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTTSGVHDGSL 480
Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTTSGVHDGSL 480
Qy 481 HKGAWFLVCSGALNERTVVAACHVTLGLKVTMIKTADLVKLVGKPYRDDREKTIQS 540
Db 481 HKGAWFLVCSGALNERTVVAACHVTLGLKVTMIKTADLVKLVGKPYRDDREKTIQS 540
Qy 541 LQISAILHPNYDPILLADIAILKLDKARISTRVOPICLAASRDLSSTFQESHITVAG 600
Db 541 LRISAILHPNYDPILLADIAILKLDKARISTRVOPICLAASRDLSSTFQESHITVAG 600
Qy 601 WNVLADVRSPGKNDLTRSGVSVVSDLLCEEQHEHGIPVSVTDNNMFCASWEPTAPSDI 660
Db 601 WNVLADVRSPGKNDLTRSGVSVVSDLLCEEQHEHGIPVSVTDNNMFCASWEPTAPSDI 660
Qy 661 CTAE 664
Db 661 CTAE 664

RESULT 3
Q96JW2 PRELIMINARY; PRT; 737 AA.
ID Q96JW2
AC Q96JW2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14935.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi Y., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosiiri T., Kaku Y., Kodaiki H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Inose N.,
RA Mugaehino K., Yuuki H., Oshina A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono Y., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hakiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45 (2004).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; AK027841; BAB55404.1; -

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DR HSP; P00736; IGPZ.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCF; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS50923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;

Query Match 61.9%; Score 446; DB 2; Length 737;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 LEERNCSDDPGVNGYQKITGGPLNGRHAKTGTVVSPFCNNSYVLSGNEKRTCCQNGE 334
Db 292 LEERNCSDDPGVNGYQKITGGPLNGRHAKTGTVVSPFCNNSYVLSGNEKRTCCQNGE 351
Qy 335 WSGKQPIKACREPISDLVRRVRLPMQVSRTPPLHQLYSAAFSKQKLSQAPTKKPAL 394
Db 352 WSGKQPIKACREPISDLVRRVRLPMQVSRTPPLHQLYSAAFSKQKLSQAPTKKPAL 411
Qy 395 PFGDLPMGYOHLHTLQYECISPPYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITA 454
Db 412 PFGDLPMGYOHLHTLQYECISPPYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITA 471
Qy 455 PKTQGLRWPQAAIYRTTSGVHDGSLHKGAWFLVCSGALNERTVVAACHVTLGLKVTM 514
Db 472 PKTQGLRWPQAAIYRTTSGVHDGSLHKGAWFLVCSGALNERTVVAACHVTLGLKVTM 531
Qy 515 IKTADLVKLVGKPYRDDREKTIQSILQISAILHPNYDPILLADIAILKLDKARIST 574
Db 532 IKTADLVKLVGKPYRDDREKTIQSILQISAILHPNYDPILLADIAILKLDKARIST 591
Qy 575 RVQIPICLAASRDLSSTFQESHITVAGNNVLADVRSPGKNDLTRSGVSVVSDLLCEEQ 634
Db 592 RVQIPICLAASRDLSSTFQESHITVAGNNVLADVRSPGKNDLTRSGVSVVSDLLCEEQ 651
Qy 635 EDHGIPVSVTDNNMFCASWEPTAPSDICTARTGIAAVSPFGRASPEPRHMLGLVSVSYD 694
Db 652 EDHGIPVSVTDNNMFCASWEPTAPSDICTARTGIAAVSPFGRASPEPRHMLGLVSVSYD 711
Qy 695 KTCSHRLSTAFKVLPPKOWIERNMK 720
Db 712 KTCSHRLSTAFKVLPPKOWIERNMK 737

RESULT 4
Q71RE9 PRELIMINARY; PRT; 417 AA.
ID Q71RE9
AC Q71RE9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FP938.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF370388; AAQ15224.1; -.
DR HSSP; P00734; IBB0.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR PRINTS; PR00722; CHYMOTRYPSIN_GCP.
DR SMART; SM00020; TRYSPC; 1.
DR PROSITE; PS00923; SUSHI; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 53.68; Score 386; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 WSGKQPIKACREPKISDLVRRVLPQVQSRRTPLHLQYSAFSAFKQLQSAPTKKPAL 394
DB 32 WSGKQPIKACREPKISDLVRRVLPQVQSRRTPLHLQYSAFSAFKQLQSAPTKKPAL 91
QY 395 PFGDLPNGYQHLHTQLQYECISPPYRLGSSRTCLRTGWSGRAPSCIPICGKIENITA 454
DB 92 PFGDLPNGYQHLHTQLQYECISPPYRLGSSRTCLRTGWSGRAPSCIPICGKIENITA 151
QY 455 PKTQGLRWPNQAAIYRRTSGVHDSLHKGAWELVCSGALVNERVTVAACHVTDLGKVTM 514
DB 152 PKTQGLRWPNQAAIYRRTSGVHDSLHKGAWELVCSGALVNERVTVAACHVTDLGKVTM 211
QY 515 IKTADLKVVLGKGYRDDREKTIQSIQISAILHPNYDPIILLDADIAILKLLDKARIST 574
DB 212 IKTADLKVVLGKGYRDDREKTIQSIQISAILHPNYDPIILLDADIAILKLLDKARIST 271
QY 575 RVQPICLAAARDLSTSPQESHITVAGNNVLADVRSPGFKNDTLRSQVSVVSDSLLCBQ 634
DB 272 RVQPICLAAARDLSTSPQESHITVAGNNVLADVRSPGFKNDTLRSQVSVVSDSLLCBQ 331
QY 635 EDHGIPVSVTDNMFCAWETAPSDICTAETGGIAAVSFPCRASPEPRHLMGLVSWSYD 694
DB 332 EDHGIPVSVTDNMFCAWETAPSDICTAETGGIAAVSFPCRASPEPRHLMGLVSWSYD 391
QY 695 KTCSHRLSTAFKVLPPFKDWIERNMK 720
DB 392 KTCSHRLSTAFKVLPPFKDWIERNMK 417

RESULT 5
QY432 QY432 PRELIMINARY; PRT; 181 AA.
AC QY432;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp586H2123 (Fragment).
GN Name=DKFZp586H2123;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ansoorge W., Witkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050214; CAB43317.1; -.
DR PIR; T08805; T08805.
DR HSSP; P00736; IMD7.
DR MEROPS; S01.998; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Pept Ser Cys.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; TRYSPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
FT NON_TER 1
SQ SEQUENCE 181 AA; 19962 MW; ABC793B58682D439 CRC64;

Query Match 24.7%; Score 178; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.5e-181;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 543 ISAIILHPNYDPIILLDADIAILKLLDKARISTRVQPICLAAARDLSTSPQESHITVAGN 602
DB 4 ISAIILHPNYDPIILLDADIAILKLLDKARISTRVQPICLAAARDLSTSPQESHITVAGN 63
QY 603 VLADVRSPGFKNDTLRSQVSVVSDSLLCBQHDHGIPVSVTDNMFCAWETAPSDICT 662
DB 64 VLADVRSPGFKNDTLRSQVSVVSDSLLCBQHDHGIPVSVTDNMFCAWETAPSDICT 123
QY 663 AETGGIAAVSFPCRASPEPRHLMGLVSWSYDKTCSHRLSTAFKVLPPFKDWIERNMK 720
DB 124 AETGGIAAVSFPCRASPEPRHLMGLVSWSYDKTCSHRLSTAFKVLPPFKDWIERNMK 181

RESULT 6
QY425 QY425 PRELIMINARY; PRT; 720 AA.
AC QY425;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymic cells cDNA, RIKEN full-length enriched library, clone:B430002G05 product:hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine proteases, trypsin family domain containing protein, full insert sequence.
GN Name=B430002G05Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Thymus;
RA MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=NOD; TISSUE=Thymus;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
```



DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept Ser Cys.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sushi; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00026; EGF\_3; 1.  
 DR PROSITE; PS50923; SUSHI; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW Hydrolyase; Protease; Serine protease.  
 SQ SEQUENCE 720 AA; 80377 MW; 717287F1E690FD0E CRC64;

Query Match 5.7%; Score 41; DB 2; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-34;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FLQLLISSIPREVTIVNEACPGAEWNIMRCCEYDQIEC 53  
 |||||  
 DB 13 FLQLLISSIPREVTIVNEACPGAEWNIMRCCEYDQIEC 53

RESULT 8  
 Q6DIV5 PRELIMINARY; PRT; 722 AA.  
 ID Q6DIV5  
 AC Q6DIV5  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE MGC89196 protein.  
 GN Name=MGC89196;  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8364;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole body;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavert T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole body;  
 RA Klein S., Gerhard D.S.;  
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 DR EMBL; BC075430; AAH75430.1; -.

DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sushi; 2.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00179; EGF\_Ca; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50923; SUSHI; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW EGF-like domain; Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 722 AA; 80366 MW; F173563206D1AE82 CRC64;

Query Match 3.3%; Score 24; DB 2; Length 722;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-16;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 VGYTIFFCRNEECDSCLIHPGC 85  
 |||||  
 DB 64 VGYTIFFCRNEECDSCLIHPGC 87

RESULT 9  
 Q91WZ0 PRELIMINARY; PRT; 222 AA.  
 ID Q91WZ0  
 AC Q91WZ0  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Bone morphogenetic protein 1 (Fragment).  
 GN Name=Bmp-1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=E18 whole embryo;  
 RA Kataoka H., Enomoto K.;  
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB073100; BAB69961.1; -.  
 DR HSP; Q9UCV4; INZI.  
 DR GO; GO:0008533; F:astacin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR Pfam; PF01400; Astacin; 1.  
 DR Pfam; PF00431; CUB; 2.  
 DR PROSITE; PS01180; CUB; 2.  
 FT NON\_TER 1  
 FT NON\_TER 222  
 SQ SEQUENCE 222 AA; 25426 MW; F6A9052DA98BB57A CRC64;

Query Match 1.2%; Score 9; DB 2; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 179 YDYVEVRDG 187  
 |||||

Db 80 YDYEVRDG 88

RESULT 10

Y836 AQUAE STANDARD; PRT; 232 AA.

AC 067008;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Hypothetical protein AQ\_836.

GN OrderedLocusNames=AQ\_836;

OS Aquifex aeolicus.

OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OC NCBI\_TaxID=63363;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,

RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex

RT aeolicus";

RL Nature 392:353-358 (1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC use by non-profit institutions as long as its content is in no way

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CC -----

EMBL; AE000709; AAC06970.1; --

DR EIR; E70372; E70372.

KW Complete proteome; Hypothetical protein; Transmembrane.

FT TRANSMEM 4 24 Potential.

FT TRANSMEM 42 62 Potential.

FT TRANSMEM 100 120 Potential.

FT TRANSMEM 145 165 Potential.

FT TRANSMEM 171 191 Potential.

FT SEQUENCE 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

SQ

Query Match 1.2%; Score 9; DB 1; Length 232;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96

DB 23 FENCKSCRN 31

RESULT 11

086553

ID 086553 PRELIMINARY; PRT; 276 AA.

AC 086553;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Putative dehydrogenase.

GN ORFNames=SC1P2.16c;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OC NCBI\_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,

RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147 (2002).

CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases

CC (SDR) family;

CC ENBL; AL939128; CAA20507.1; --

DR PIR; T29125; T29125.

DR HSP; P08074; 1CYD.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH\_short.

DR InterPro; IPR002347; ADH\_short\_C2.

DR Pfam; PF00106; adh\_short; 1.

DR PRINTS; PR00081; GDRDH.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH\_SHORT; 1.

KW Complete proteome; Oxidoreductase.

SQ SEQUENCE 276 AA; 29010 MW; 30F0038B70D63C7C CRC64;

Query Match 1.2%; Score 9; DB 2; Length 276;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 AVSFPGRAS 678

DB 225 AVSFPGRAS 233

RESULT 12

Q6FJNS

ID Q6FJNS PRELIMINARY; PRT; 593 AA.

AC Q6FJNS;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE TLL2 protein (Fragment).

GN Names=TLL2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.243603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Blakesley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]



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RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013871; AAH13871.1; -.
DR HSSP; P07584; 1AST.
DR GO; GO:0008533; F-actinin activity; IEA.
DR GO; GO:0008237; F-metalloproteinase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR PRINTS; PR00431; CUB; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00235; ZmMG; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Developmental protein; EGF-like domain; Embryo; Hydrolase;
FT NON TER 593 593
SQ SEQUENCE 593 AA; 66353 MW; D7483E48E8260C69 CRC64;

Query Match 1.2%; Score 9; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 406 YDYVEVRDG 414

RESULT 13
BMPH STRPU STANDARD; PRT; 639 AA.
ID P98069;
AC P98069;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Bone morphogenetic protein 1 homolog precursor (BC 3.4.24.-) (SUBMP).
DE Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Hwang S.P.L., Partin J.S., Lennarz W.J.;
RT "Characterization of a homolog of human bone morphogenetic protein 1
RT in the embryo of the sea urchin, Strongylocentrotus purpuratus.";
RL Development 120:559-568(1994).
CC -1- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in
CC -1- hatched blastula.
CC -1- DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.
CC -1- SIMILARITY: Belongs to the peptidase M12A family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L23838; AAA30081.1; -.
CC HSSP; P35555; 1EMN.
CC MEROPS; M12.005; -.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.

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DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00235; ZmMG; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Developmental protein; EGF-like domain; Embryo; Hydrolase;
KW Metalloprotease; Protease; Repeat; Signal; Zinc.
FT SIGNAL 1 23
FT PROPEP 24 109
FT CHAIN 110 639
FT DOMAIN 110 306
FT DOMAIN 307 419
FT DOMAIN 420 531
FT METAL 197 197
FT ACT_SITE 198 198
FT METAL 201 201
FT METAL 207 207
FT DISULFID 536 548
FT DISULFID 554 557
FT CARBOHYD 122 122
FT CARBOHYD 140 140
FT CARBOHYD 317 317
FT CARBOHYD 455 455
SQ SEQUENCE 639 AA; 71893 MW; 59307B265B7894AD CRC64;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 475 YDYVEVRDG 483

RESULT 14
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ID OS7658;
AC OS7658;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bone morphogenetic protein 1 (Fragment).
DE Name=BMP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20267865; PubMed=10806368; DOI=10.1016/S0378-1119(00)00114-1;
RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosier R.N.,
RA "Cloning of the chick BMP1/Tolloid cDNA and expression in skeletal
RT tissues.";
RT Gene 248:233-243(2000).

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DR EMBL; U75331; RAC02259.1; -.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.005; -.
DR GO; GO:0005333; F:astacin activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00442; CUB; 3.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00101; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00026; EGF_2; 1.
DR PROSITE; PS01186; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW EGF-like domain.
FT NON TER 1
SQ SEQUENCE 691 AA; 77843 MW; 01245982B8DC8F28 CRC64;

Query Match 1.2%; Score 9; DB 2; Length 691;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 338 YDYVEVRDG 346

RESULT 15
Q6P550 PRELIMINARY; PRT; 775 AA.
AC Q6P550;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Empl protease (Fragment).
GN Name=Bmpl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RA EMBL; BC063079; AAH63079.1; -.
DR HSSP; P00736; IAPQ.
DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001506; Peptidase_M12A.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 1.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
FT NON TER 1
SQ SEQUENCE 775 AA; 87858 MW; 1BA59AF0F86EEEE7 CRC64;

Query Match 1.2%; Score 9; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 166 YDYVEVRDG 174

Search completed: May 8, 2005, 16:13:12
Job time : 92 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 8, 2005, 16:06:14 ; Search time 21 Seconds  
(without alignments)  
2559.396 Million cell updates/sec

Title: US-10-063-692-38  
Perfect score: 720  
Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	355	49.3	570	4	US-10-067-422-9
2	16	2.2	46	4	US-10-067-422-17
3	12	1.7	12	4	US-10-067-422-16
4	9	1.2	101	3	US-09-374-135-4
5	9	1.2	110	4	US-09-341-461-28
6	9	1.2	113	4	US-09-438-046-20
7	9	1.2	730	3	US-08-872-757-2
8	9	1.2	730	4	US-09-850-048A-2
9	9	1.2	788	1	US-08-572-225-1
10	9	1.2	986	4	US-09-285-385C-19
11	9	1.2	986	4	US-09-349-016-6690
12	9	1.2	1015	4	US-09-285-385C-2
13	8	1.1	51	3	US-09-188-930-342
14	8	1.1	51	4	US-09-312-283C-342
15	8	1.1	96	4	US-09-472-087-99
16	8	1.1	152	3	US-09-188-930-187
17	8	1.1	152	4	US-09-312-283C-187
18	8	1.1	155	4	US-09-472-087-20
19	8	1.1	155	4	US-09-472-087-112
20	8	1.1	290	4	US-09-270-767-33918
21	8	1.1	290	4	US-09-270-767-49135
22	8	1.1	309	4	US-09-248-796A-26183
23	8	1.1	1019	1	US-08-396-014A-4
24	8	1.1	1019	2	US-08-596-405-4
25	8	1.1	1019	2	US-08-877-620-4
26	8	1.1	1019	4	US-09-287-368-4
27	8	1.1	1019	4	US-09-626-795-4

28	1.1	1083	1	US-08-296-014A-2	Sequence 2, Appli
29	1.1	1083	2	US-08-596-405-2	Sequence 2, Appli
30	1.1	1083	2	US-08-877-620-2	Sequence 2, Appli
31	1.1	1083	4	US-09-287-368-2	Sequence 2, Appli
32	1.1	1083	4	US-09-626-795-2	Sequence 2, Appli
33	1.1	3571	4	US-09-911-842A-2	Sequence 2, Appli
34	7	11	4	US-09-192-854-170	Sequence 170, App
35	7	42	1	US-08-293-778-11	Sequence 11, Appl
36	7	80	4	US-09-621-976-4542	Sequence 4542, Ap
37	7	83	4	US-09-543-681A-5389	Sequence 5389, Ap
38	7	99	4	US-09-270-767-62399	Sequence 62399, A
39	7	103	4	US-09-513-999C-7881	Sequence 7881, Ap
40	7	105	3	US-09-187-859-18	Sequence 18, Appl
41	7	105	4	US-09-839-542B-18	Sequence 18, Appl
42	7	105	4	US-09-535-852-18	Sequence 18, Appl
43	7	111	4	US-09-252-991A-23343	Sequence 23343, A
44	7	121	4	US-09-252-991A-22436	Sequence 22436, A
45	7	123	4	US-09-621-976-5058	Sequence 5058, Ap
46	7	142	4	US-09-489-039A-10461	Sequence 10461, A
47	7	144	3	US-08-906-769-153	Sequence 153, App
48	7	144	3	US-08-906-616-153	Sequence 153, App
49	7	144	3	US-08-639-075A-153	Sequence 153, App
50	7	144	3	US-09-004-731-81	Sequence 81, Appl
51	7	144	3	US-09-012-431-153	Sequence 153, App
52	7	144	3	US-08-749-699-81	Sequence 81, Appl
53	7	144	3	US-09-012-692-153	Sequence 153, App
54	7	144	3	US-08-906-613-153	Sequence 153, App
55	7	144	4	US-09-004-729-81	Sequence 81, Appl
56	7	164	4	US-09-248-796A-19751	Sequence 19751, A
57	7	172	4	US-09-198-452A-368	Sequence 368, App
58	7	172	4	US-09-438-185A-352	Sequence 352, App
59	7	187	4	US-09-107-532A-6736	Sequence 6736, Ap
60	7	210	4	US-09-198-452A-869	Sequence 869, App
61	7	214	4	US-09-543-681A-4600	Sequence 4600, App
62	7	220	4	US-09-248-796A-17809	Sequence 17809, A
63	7	222	4	US-09-270-767-34290	Sequence 34290, A
64	7	222	4	US-09-270-767-49507	Sequence 49507, A
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69	7	242	4	US-09-438-185A-813	Sequence 813, App
70	7	245	4	US-09-252-991A-28491	Sequence 28491, A
71	7	255	4	US-09-540-236-2829	Sequence 2829, Ap
72	7	257	4	US-09-328-352-7049	Sequence 7049, Ap
73	7	259	3	US-08-944-483-52	Sequence 52, Appl
74	7	259	4	US-10-165-442-2	Sequence 2, Appli
75	7	259	4	US-10-165-442-4	Sequence 4, Appli
76	7	265	4	US-09-050-739-16	Sequence 16, Appl
77	7	266	3	US-09-004-731-24	Sequence 24, Appl
78	7	266	3	US-08-749-699-24	Sequence 24, Appl
79	7	266	4	US-09-004-729-24	Sequence 24, Appl
80	7	268	3	US-09-032-215-42	Sequence 42, Appl
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82	7	295	4	US-10-165-442-1	Sequence 1, Appli
83	7	310	4	US-09-107-532A-4185	Sequence 4185, App
84	7	312	4	US-09-538-092-742	Sequence 742, App
85	7	314	4	US-09-636-382A-2	Sequence 2, Appli
86	7	376	2	US-08-558-269-10	Sequence 10, Appl
87	7	376	3	US-09-410-882-10	Sequence 10, Appl
88	7	399	4	US-09-252-991A-28974	Sequence 28974, A
89	7	418	4	US-09-248-796A-18870	Sequence 18870, A
90	7	422	4	US-09-489-039A-12443	Sequence 12443, A
91	7	422	4	US-09-248-796A-14435	Sequence 14435, A
92	7	437	4	US-09-489-039A-7612	Sequence 7612, Ap
93	7	448	4	US-09-328-352-5694	Sequence 5694, Ap
94	7	462	4	US-09-949-016-9566	Sequence 9566, Ap
95	7	476	4	US-09-949-016-9566	Sequence 9566, Ap
96	7	503	4	US-09-071-035-360	Sequence 360, App
97	7	503	4	US-09-252-991A-23870	Sequence 23870, A
98	7	525	4	US-09-583-110-5306	Sequence 5306, Ap
99	7	553	4	US-09-795-691-2	Sequence 2, Appli
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101	7	1.0	558	4	US-09-107-433-4472	Sequence 4472, Ap	174	6	0.8	44	3	US-09-220-528-85	Sequence 85, Appl
102	7	1.0	579	1	US-08-295-411-4	Sequence 4, Appli	175	6	0.8	44	4	US-09-270-767-39906	Sequence 39906, A
103	7	1.0	579	2	US-08-955-471-4	Sequence 4, Appli	176	6	0.8	44	4	US-09-270-767-55123	Sequence 55123, A
104	7	1.0	579	3	US-09-117-708-14	Sequence 14, Appl	177	6	0.8	44	4	US-09-270-767-58106	Sequence 58106, A
105	7	1.0	579	4	US-09-270-767-42996	Sequence 42996, A	178	6	0.8	45	3	US-08-899-437-13	Sequence 13, Appl
106	7	1.0	579	5	PCT-US92-1024-4	Sequence 4, Appli	179	6	0.8	45	3	US-09-126-121-13	Sequence 13, Appl
107	7	1.0	615	1	US-07-998-9728-3	Sequence 3, Appli	180	6	0.8	46	3	US-08-753-007A-16	Sequence 16, Appl
108	7	1.0	615	1	US-08-463-953-3	Sequence 3, Appli	181	6	0.8	46	3	US-09-398-496-16	Sequence 16, Appl
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111	7	1.0	616	1	US-09-949-016-6889	Sequence 6889, Ap	184	6	0.8	48	4	US-09-640-211A-1162	Sequence 1162, Ap
112	7	1.0	616	4	US-09-949-016-7740	Sequence 7740, Ap	185	6	0.8	50	3	US-09-004-406C-10	Sequence 10, Appl
113	7	1.0	622	3	US-08-952-967-8	Sequence 8, Appli	186	6	0.8	50	3	US-09-004-406C-11	Sequence 11, Appl
114	7	1.0	622	4	US-09-054-272-42	Sequence 42, Appl	187	6	0.8	52	1	US-08-294-189-17	Sequence 17, Appl
115	7	1.0	660	4	US-09-270-767-46777	Sequence 46777, A	188	6	0.8	56	3	US-09-055-075C-48	Sequence 48, Appl
116	7	1.0	805	4	US-09-252-991A-17822	Sequence 17822, A	189	6	0.8	56	4	US-09-319-124-48	Sequence 48, Appl
117	7	1.0	808	4	US-09-565-909-2	Sequence 2, Appli	190	6	0.8	59	4	US-09-765-815-9	Sequence 9, Appl1
118	7	1.0	811	4	US-09-248-796A-18641	Sequence 18641, A	191	6	0.8	59	4	US-09-800-729-163	Sequence 163, App
119	7	1.0	859	4	US-09-538-092-717	Sequence 17, App	192	6	0.8	62	4	US-09-107-532A-5665	Sequence 5665, Ap
120	7	1.0	886	3	US-08-872-757-4	Sequence 4, Appli	193	6	0.8	62	4	US-09-497-491-27	Sequence 27, Appl
121	7	1.0	986	4	US-09-850-048A-4	Sequence 4, Appli	194	6	0.8	64	4	US-09-482-273-117	Sequence 117, App
122	7	1.0	1074	4	US-09-071-035-358	Sequence 358, App	195	6	0.8	64	4	US-09-252-991A-17573	Sequence 17573, A
123	7	1.0	1074	4	US-09-071-035-394	Sequence 394, App	196	6	0.8	68	4	US-09-248-796A-24682	Sequence 24682, A
124	7	1.0	1096	4	US-09-134-000C-5764	Sequence 5764, Ap	197	6	0.8	69	4	US-08-302-756B-20	Sequence 20, Appl
125	7	1.0	1346	3	US-09-320-878-4	Sequence 4, Appli	198	6	0.8	70	4	US-09-732-210-883	Sequence 883, App
126	7	1.0	1346	3	US-09-105-537-37	Sequence 37, Appl	199	6	0.8	72	4	US-09-540-236-2199	Sequence 2199, Ap
127	7	1.0	1346	4	US-09-141-908-5	Sequence 5, Appli	200	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap
128	7	1.0	1346	4	US-09-657-440-4	Sequence 4, Appli	201	6	0.8	74	4	US-09-134-000C-6316	Sequence 6316, Ap
129	7	1.0	11877	3	US-08-105-537-6	Sequence 2, Appli	202	6	0.8	76	4	US-09-328-352-4331	Sequence 4331, Ap
130	6	0.8	11	2	US-08-464-961-2	Sequence 17, Appl	203	6	0.8	77	3	US-08-718-904-6	Sequence 6, Appl1
131	6	0.8	11	3	US-08-957-130-17	Sequence 2, Appli	204	6	0.8	77	4	US-09-449-249-6	Sequence 6, Appl1
132	6	0.8	11	3	US-08-369-315-2	Sequence 2, Appli	205	6	0.8	77	4	US-09-107-433-3411	Sequence 3411, Ap
133	6	0.8	11	5	PCT-US96-08233-2	Sequence 2, Appli	206	6	0.8	80	4	US-09-583-110-2844	Sequence 2844, Ap
134	6	0.8	12	1	US-09-205-258-304	Sequence 304, App	207	6	0.8	81	4	US-09-270-767-46160	Sequence 46160, A
135	6	0.8	13	1	US-08-179-481-87	Sequence 87, Appl	208	6	0.8	84	4	US-09-248-796A-23422	Sequence 23422, A
136	6	0.8	17	5	US-08-205-938A-14	Sequence 14, Appl	209	6	0.8	85	4	US-09-732-210-1467	Sequence 1467, Ap
137	6	0.8	17	5	PCT-US95-02626-14	Sequence 14, Appl	210	6	0.8	86	1	US-07-847-743B-19	Sequence 19, Appl
138	6	0.8	20	1	US-08-205-338A-13	Sequence 13, Appl	211	6	0.8	86	2	US-08-456-201-19	Sequence 17, Appl
139	6	0.8	20	5	PCT-US95-02626-13	Sequence 13, Appl	212	6	0.8	86	2	US-08-330-161-17	Sequence 19, Appl
140	6	0.8	25	3	US-09-660-587-28	Sequence 28, Appl	213	6	0.8	86	2	US-08-456-241-19	Sequence 17, Appl
141	6	0.8	25	4	US-09-261-358A-28	Sequence 28, Appl	214	6	0.8	86	2	US-08-440-401-17	Sequence 17, Appl
142	6	0.8	25	4	US-09-201-458-20	Sequence 20, Appl	215	6	0.8	86	2	US-08-419-878B-17	Sequence 17, Appl
143	6	0.8	25	4	US-09-811-007A-28	Sequence 28, Appl	216	6	0.8	86	3	US-09-134-001C-3359	Sequence 3359, Ap
144	6	0.8	31	4	US-08-437-943D-14	Sequence 14, Appl	217	6	0.8	86	3	US-09-173-480-17	Sequence 17, Appl
145	6	0.8	35	1	US-08-145-708A-15	Sequence 15, Appl	218	6	0.8	86	4	US-09-252-991A-29383	Sequence 29383, A
146	6	0.8	35	2	US-08-331-454-15	Sequence 15, Appl	219	6	0.8	86	5	PCT-US92-04295A-19	Sequence 19, Appl
147	6	0.8	37	2	US-09-066-074-14	Sequence 14, Appl	220	6	0.8	87	4	US-09-252-991A-28740	Sequence 28740, A
148	6	0.8	37	2	US-08-555-912A-14	Sequence 14, Appl	221	6	0.8	90	4	US-09-252-991A-24074	Sequence 24074, A
149	6	0.8	37	3	US-08-348-518C-24	Sequence 24, Appl	222	6	0.8	91	4	US-09-107-433-4244	Sequence 4244, Ap
150	6	0.8	37	3	US-08-476-509B-24	Sequence 24, Appl	223	6	0.8	93	4	US-09-252-991A-17535	Sequence 17535, A
151	6	0.8	37	4	US-09-252-404A-39	Sequence 39, Appl	224	6	0.8	93	4	US-09-270-767-39947	Sequence 39947, A
152	6	0.8	37	4	US-09-275-900-14	Sequence 14, Appl	225	6	0.8	93	4	US-09-270-767-55164	Sequence 55164, A
153	6	0.8	37	4	US-09-821-861-16	Sequence 16, Appl	226	6	0.8	94	3	US-08-946-329A-79	Sequence 79, Appl
154	6	0.8	38	1	US-08-145-708A-14	Sequence 14, Appl	227	6	0.8	94	3	US-08-466-368-5	Sequence 5, Appl1
155	6	0.8	38	2	US-08-331-454-14	Sequence 14, Appl	228	6	0.8	94	4	US-08-470-998-2	Sequence 2, Appl1
156	6	0.8	40	4	US-08-706-344C-19	Sequence 19, Appl	229	6	0.8	94	4	US-08-328-500-10	Sequence 10, Appl
157	6	0.8	40	4	US-08-469-260A-467	Sequence 467, App	230	6	0.8	94	4	US-09-270-767-33056	Sequence 33056, A
158	6	0.8	40	4	US-08-488-446-467	Sequence 467, App	231	6	0.8	94	4	US-09-270-767-46409	Sequence 46409, A
159	6	0.8	40	4	US-08-467-344A-467	Sequence 467, App	232	6	0.8	95	4	US-09-270-767-46409	Sequence 46409, A
160	6	0.8	40	4	US-09-270-767-40577	Sequence 40577, A	233	6	0.8	95	4	US-09-248-796A-25418	Sequence 25418, A
161	6	0.8	40	4	US-09-270-767-55793	Sequence 55793, A	234	6	0.8	96	3	US-09-230-637-44	Sequence 44, Appl
162	6	0.8	40	4	US-08-424-550B-467	Sequence 467, App	235	6	0.8	99	4	US-09-270-767-32481	Sequence 32481, A
163	6	0.8	41	1	US-08-168-091A-41	Sequence 41, Appl	236	6	0.8	99	4	US-09-270-767-47698	Sequence 47698, A
164	6	0.8	42	4	US-09-066-330-3	Sequence 3, Appli	237	6	0.8	100	4	US-09-270-767-35703	Sequence 35703, A
165	6	0.8	43	1	US-07-998-003A-73	Sequence 73, Appl	238	6	0.8	100	4	US-09-270-767-50920	Sequence 50920, A
166	6	0.8	43	1	US-08-453-274B-73	Sequence 73, Appl	239	6	0.8	100	4	US-09-471-276-832	Sequence 832, App
167	6	0.8	43	1	US-08-453-695A-73	Sequence 73, Appl	240	6	0.8	101	4	US-09-390-134B-42	Sequence 42, Appl
168	6	0.8	43	1	US-08-268-161A-73	Sequence 73, Appl	241	6	0.8	102	4	US-09-270-767-58844	Sequence 58844, A
169	6	0.8	43	2	US-08-453-702A-73	Sequence 73, Appl	242	6	0.8	103	3	US-09-199-637A-271	Sequence 271, App
170	6	0.8	43	2	US-08-751-305-4	Sequence 4, Appli	243	6	0.8	103	4	US-09-252-991A-32642	Sequence 32642, A
171	6	0.8	43	3	US-09-099-639-73	Sequence 73, Appl	244	6	0.8	103	4	US-09-543-681A-8232	Sequence 8232, Ap
172	6	0.8	43	5	PCT-US93-12588-73	Sequence 73, Appl	245	6	0.8	103	4	US-09-621-976-4109	Sequence 4109, Ap
173	6	0.8	43	5	PCT-US95-08071-73	Sequence 73, Appl	246	6	0.8	103	4	US-09-513-999C-5560	Sequence 5560, Ap

247	6	0.8	106	4	US-09-087-031E-13	Sequence 13, Appl	320	6	0.8	151	3	US-08-679-493A-74	Sequence 74, Appl
248	6	0.8	106	4	US-09-248-796A-14519	Sequence 14519, A	321	6	0.8	152	4	US-09-885-723-11	Sequence 11, Appl
249	6	0.8	107	4	US-09-732-210-230	Sequence 230, App	322	6	0.8	153	4	US-09-288-143-123	Sequence 123, App
250	6	0.8	107	4	US-09-489-039A-9954	Sequence 9954, Ap	323	6	0.8	153	4	US-09-252-991A-23634	Sequence 23634, A
251	6	0.8	107	4	US-09-710-279-1586	Sequence 1586, Ap	324	6	0.8	153	4	US-09-134-000C-5186	Sequence 5186, Ap
252	6	0.8	108	4	US-09-489-039A-9392	Sequence 9392, Ap	325	6	0.8	154	3	US-09-387-418A-8	Sequence 8, Appl
253	6	0.8	108	4	US-09-489-039A-11679	Sequence 11679, A	326	6	0.8	156	1	US-08-469-667-20	Sequence 20, Appl
254	6	0.8	109	4	US-09-134-000C-6718	Sequence 6718, Ap	327	6	0.8	156	3	US-09-224-110-20	Sequence 20, Appl
255	6	0.8	109	4	US-09-270-767-60583	Sequence 60583, A	328	6	0.8	156	4	US-09-252-991A-24413	Sequence 24413, A
256	6	0.8	110	3	US-09-376-330-24	Sequence 24, Appl	329	6	0.8	156	4	US-09-988-292A-20	Sequence 20, Appl
257	6	0.8	111	4	US-09-252-991A-17096	Sequence 17096, A	330	6	0.8	156	5	PCT-US95-07289-20	Sequence 20, Appl
258	6	0.8	111	4	US-09-294-298A-12	Sequence 12, Appl	331	6	0.8	157	2	US-08-811-949-41	Sequence 41, Appl
259	6	0.8	112	4	US-09-107-532A-7068	Sequence 7068, Ap	332	6	0.8	157	3	US-08-872-855-6	Sequence 6, Appl
260	6	0.8	112	4	US-09-270-767-34754	Sequence 34754, A	333	6	0.8	157	3	US-08-981-392-68	Sequence 68, Appl
261	6	0.8	112	4	US-09-270-767-49971	Sequence 49971, A	334	6	0.8	157	4	US-09-071-035-446	Sequence 446, App
262	6	0.8	112	4	US-09-902-540-9940	Sequence 9940, Ap	335	6	0.8	157	4	US-09-908-323-68	Sequence 68, Appl
263	6	0.8	113	4	US-09-438-046-23	Sequence 23, Appl	336	6	0.8	157	3	US-08-796-792-2	Sequence 2, Appl
264	6	0.8	115	4	US-09-270-767-47912	Sequence 47912, A	337	6	0.8	159	4	US-09-491-795-2	Sequence 2, Appl
265	6	0.8	115	4	US-09-502-540-10750	Sequence 10750, A	338	6	0.8	162	1	US-08-266-451B-29	Sequence 29, Appl
266	6	0.8	120	4	US-09-583-110-5022	Sequence 5022, Ap	339	6	0.8	162	2	US-08-748-725-29	Sequence 29, Appl
267	6	0.8	121	1	US-08-307-499-7	Sequence 7, Appl	340	6	0.8	162	4	US-09-540-236-2636	Sequence 2636, Ap
268	6	0.8	121	3	US-09-299-268-7	Sequence 7, Appl	341	6	0.8	164	4	US-09-489-039A-11750	Sequence 11750, A
269	6	0.8	121	4	US-10-101-464A-683	Sequence 683, App	342	6	0.8	167	4	US-09-270-767-41274	Sequence 41274, A
270	6	0.8	122	4	US-09-732-210-598	Sequence 598, App	343	6	0.8	167	4	US-09-270-767-56490	Sequence 56490, A
271	6	0.8	122	4	US-09-732-210-600	Sequence 600, App	344	6	0.8	170	4	US-09-252-991A-22362	Sequence 22362, A
272	6	0.8	122	4	US-10-101-464A-712	Sequence 712, App	345	6	0.8	172	4	US-09-328-352-5691	Sequence 29480, A
273	6	0.8	122	4	US-09-424-840B-14	Sequence 14, Appl	346	6	0.8	172	4	US-09-328-352-5691	Sequence 5691, Ap
274	6	0.8	122	4	US-09-107-433-3697	Sequence 3697, Ap	347	6	0.8	175	4	US-09-902-540-11425	Sequence 11425, A
275	6	0.8	123	3	US-09-124-900-10	Sequence 10, Appl	348	6	0.8	176	4	US-09-252-991A-24281	Sequence 24281, A
276	6	0.8	123	3	US-09-134-001C-3283	Sequence 3283, Ap	349	6	0.8	176	4	US-09-252-991A-24805	Sequence 24805, A
277	6	0.8	124	4	US-08-311-731A-202	Sequence 202, App	350	6	0.8	176	4	US-09-489-039A-12706	Sequence 12706, A
278	6	0.8	124	4	US-09-270-767-61747	Sequence 61747, A	351	6	0.8	177	2	US-08-770-544-20	Sequence 20, Appl
279	6	0.8	125	4	US-09-543-681A-7177	Sequence 7177, Ap	352	6	0.8	177	4	US-09-579-259-20	Sequence 20, Appl
280	6	0.8	126	4	US-09-902-540-12158	Sequence 12158, A	353	6	0.8	177	4	US-09-543-681A-5159	Sequence 5159, Ap
281	6	0.8	127	3	US-09-134-001C-2936	Sequence 2936, Ap	354	6	0.8	177	4	US-09-583-110-3692	Sequence 3692, Ap
282	6	0.8	127	3	US-09-134-001C-2337	Sequence 2337, Ap	355	6	0.8	177	4	US-09-270-767-31704	Sequence 31704, A
283	6	0.8	127	4	US-09-809-739-10	Sequence 10, Appl	356	6	0.8	178	4	US-09-270-767-46921	Sequence 46921, A
284	6	0.8	128	3	US-09-134-001C-2881	Sequence 2881, Ap	357	6	0.8	178	4	US-09-612-126-11	Sequence 11, Appl
285	6	0.8	128	4	US-09-134-000C-3953	Sequence 3953, Ap	358	6	0.8	179	3	US-09-248-796A-21646	Sequence 21646, A
286	6	0.8	128	4	US-09-513-999C-8084	Sequence 8084, Ap	359	6	0.8	179	4	US-09-543-681A-7669	Sequence 7669, Ap
287	6	0.8	129	4	US-09-513-999C-5740	Sequence 5740, Ap	360	6	0.8	180	4	US-09-270-767-37167	Sequence 37167, A
288	6	0.8	130	4	US-09-902-540-11601	Sequence 11601, A	361	6	0.8	180	4	US-09-878-281A-14	Sequence 52384, A
289	6	0.8	132	4	US-09-252-991A-29618	Sequence 29618, A	362	6	0.8	180	4	US-09-878-281A-16	Sequence 16, Appl
290	6	0.8	132	4	US-09-311-021-162	Sequence 162, App	363	6	0.8	180	4	US-09-878-281A-28	Sequence 28, Appl
291	6	0.8	133	4	US-09-252-991A-32343	Sequence 32343, A	364	6	0.8	180	4	US-09-878-281A-26	Sequence 26, Appl
292	6	0.8	133	3	US-09-134-001C-3817	Sequence 3817, Ap	365	6	0.8	180	4	US-09-878-281A-18	Sequence 18, Appl
293	6	0.8	134	4	US-09-252-991A-24835	Sequence 24835, A	366	6	0.8	180	4	US-09-878-281A-20	Sequence 20, Appl
294	6	0.8	134	4	US-09-513-999C-8169	Sequence 8169, Ap	367	6	0.8	180	4	US-09-878-281A-22	Sequence 22, Appl
295	6	0.8	136	4	US-09-252-991A-24892	Sequence 24892, A	368	6	0.8	180	4	US-09-878-281A-24	Sequence 24, Appl
296	6	0.8	138	3	US-08-630-172-1	Sequence 1, Appl	369	6	0.8	180	4	US-09-878-281A-26	Sequence 26, Appl
297	6	0.8	138	3	US-09-375-419-1	Sequence 174, App	370	6	0.8	180	4	US-09-878-281A-28	Sequence 28, Appl
298	6	0.8	139	3	US-08-444-818-174	Sequence 444, App	371	6	0.8	180	4	US-09-902-540-10368	Sequence 10368, A
299	6	0.8	139	4	US-09-270-767-44805	Sequence 44805, A	372	6	0.8	181	4	US-09-252-991A-17818	Sequence 17818, A
300	6	0.8	140	4	US-09-252-991A-31623	Sequence 31623, A	373	6	0.8	181	4	US-09-134-000C-4633	Sequence 4633, Ap
301	6	0.8	140	4	US-08-906-769-135	Sequence 13500, A	374	6	0.8	181	4	US-09-640-211A-1033	Sequence 1033, Ap
302	6	0.8	141	3	US-08-906-616-135	Sequence 135, App	375	6	0.8	183	4	US-09-621-976-4025	Sequence 4025, Ap
303	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App	376	6	0.8	183	4	US-09-976-451-2	Sequence 2, Appl
304	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App	377	6	0.8	184	3	US-08-907-800A-2	Sequence 2, Appl
305	6	0.8	141	3	US-09-012-431-135	Sequence 135, App	378	6	0.8	184	3	US-08-969-317-2	Sequence 2, Appl
306	6	0.8	141	3	US-09-012-692-135	Sequence 135, App	379	6	0.8	184	4	US-09-270-767-44233	Sequence 44233, A
307	6	0.8	141	3	US-08-906-613-135	Sequence 135, App	380	6	0.8	184	4	US-09-107-433-4306	Sequence 4306, Ap
308	6	0.8	141	4	US-09-270-767-60471	Sequence 60471, A	381	6	0.8	185	3	US-08-975-762-11	Sequence 11, Appl
309	6	0.8	143	4	US-09-538-092-237	Sequence 237, App	382	6	0.8	185	3	US-08-821-324-11	Sequence 11, Appl
310	6	0.8	144	3	US-09-199-637A-17	Sequence 17, Appl	383	6	0.8	185	3	US-09-295-028-11	Sequence 11, Appl
311	6	0.8	144	3	US-09-134-001C-4218	Sequence 4218, Ap	384	6	0.8	185	3	US-09-106-582-11	Sequence 11, Appl
312	6	0.8	145	4	US-09-252-991A-21532	Sequence 21532, A	385	6	0.8	185	4	US-09-159-463-11	Sequence 11, Appl
313	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A	386	6	0.8	185	4	US-09-693-542-11	Sequence 11, Appl
314	6	0.8	146	4	US-09-270-767-39779	Sequence 39779, A	387	6	0.8	186	3	US-09-612-126-8	Sequence 8, Appl
315	6	0.8	146	4	US-09-270-767-54996	Sequence 54996, A	388	6	0.8	187	4	US-08-635-886C-207	Sequence 207, App
316	6	0.8	146	4	US-09-248-796A-26332	Sequence 26332, A	389	6	0.8	187	4	US-08-635-886C-208	Sequence 208, App
317	6	0.8	149	2	US-08-039-364-18	Sequence 18, Appl	390	6	0.8	187	4	US-08-635-886C-209	Sequence 209, App
318	6	0.8	149	3	US-09-158-710-18	Sequence 18, Appl	391	6	0.8	187	4	US-08-974-690C-207	Sequence 207, App
319	6	0.8	150	4	US-09-252-991A-17720	Sequence 17720, A	392	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App

393	6	0.8	187	4	US-08-974-690C-209	Sequence 209, App	466	6	0.8	209	4	US-09-693-542-71	Sequence 71, Appl
394	6	0.8	187	4	US-09-248-796A-14589	Sequence 14589, A	467	6	0.8	209	4	US-09-438-185A-949	Sequence 949, App
395	6	0.8	187	4	US-09-248-796A-16267	Sequence 16267, A	468	6	0.8	210	3	US-09-162-184-33	Sequence 33, Appl
396	6	0.8	188	4	US-09-248-796A-18153	Sequence 18153, A	469	6	0.8	210	3	US-09-489-777A-33	Sequence 33, Appl
397	6	0.8	188	4	US-10-101-464A-540	Sequence 540, App	470	6	0.8	210	4	US-09-252-991A-27171	Sequence 27171, A
398	6	0.8	189	4	US-09-270-767-46721	Sequence 46721, A	471	6	0.8	211	4	US-09-252-991A-28553	Sequence 28553, A
399	6	0.8	191	2	US-08-290-665A-187	Sequence 187, App	472	6	0.8	211	4	US-09-949-016-9913	Sequence 9913, App
400	6	0.8	191	2	US-08-290-665A-189	Sequence 189, App	473	6	0.8	212	3	US-08-861-774E-22	Sequence 22, Appl
401	6	0.8	191	2	US-08-290-665A-190	Sequence 190, App	474	6	0.8	212	3	US-08-861-774E-34	Sequence 34, Appl
402	6	0.8	191	5	PCT-US95-10398-187	Sequence 187, App	475	6	0.8	212	3	US-09-538-092-500	Sequence 500, App
403	6	0.8	191	5	PCT-US95-10398-189	Sequence 189, App	476	6	0.8	213	3	US-08-861-774E-60	Sequence 60, Appl
404	6	0.8	191	5	PCT-US95-10398-190	Sequence 190, App	477	6	0.8	213	3	US-08-861-774E-64	Sequence 64, Appl
405	6	0.8	192	4	US-09-198-452A-276	Sequence 276, App	478	6	0.8	213	3	US-08-861-774E-72	Sequence 72, Appl
406	6	0.8	192	4	US-09-248-796A-22528	Sequence 22528, A	479	6	0.8	213	4	US-09-302-540-13705	Sequence 13705, A
407	6	0.8	192	4	US-09-438-185A-266	Sequence 266, App	480	6	0.8	214	3	US-08-861-774E-30	Sequence 30, Appl
408	6	0.8	193	1	US-08-248-466B-14	Sequence 14, Appl	481	6	0.8	214	3	US-08-861-774E-32	Sequence 32, Appl
409	6	0.8	193	3	US-09-041-889-5	Sequence 5, Appl	482	6	0.8	214	3	US-08-861-774E-44	Sequence 44, Appl
410	6	0.8	193	3	US-08-837-058-5	Sequence 5, Appl	483	6	0.8	214	3	US-08-861-774E-48	Sequence 48, Appl
411	6	0.8	193	4	US-09-417-264-5	Sequence 5, Appl	484	6	0.8	214	3	US-08-861-774E-54	Sequence 54, Appl
412	6	0.8	193	4	US-08-635-886C-210	Sequence 210, App	485	6	0.8	214	3	US-08-861-774E-66	Sequence 66, Appl
413	6	0.8	193	4	US-08-974-690C-210	Sequence 210, App	486	6	0.8	214	3	US-08-861-774E-76	Sequence 76, Appl
414	6	0.8	194	3	US-09-516-914-9	Sequence 9, Appl	487	6	0.8	214	3	US-08-861-774E-78	Sequence 78, Appl
415	6	0.8	194	3	US-09-489-039A-8286	Sequence 8286, Ap	488	6	0.8	214	5	PCT-US96-08950-2	Sequence 2, Appl
416	6	0.8	194	4	US-09-248-796A-16995	Sequence 16995, A	489	6	0.8	215	5	PCT-US96-09127-2	Sequence 2, Appl
417	6	0.8	196	3	US-08-981-392-35	Sequence 35, Appl	490	6	0.8	215	1	US-08-266-451B-27	Sequence 27, Appl
418	6	0.8	196	4	US-09-308-322-35	Sequence 35, Appl	491	6	0.8	215	2	US-08-748-725-27	Sequence 27, Appl
419	6	0.8	198	4	US-09-252-991A-22691	Sequence 22691, A	492	6	0.8	215	3	US-08-861-774E-40	Sequence 40, Appl
420	6	0.8	199	4	US-09-252-991A-31135	Sequence 31135, A	493	6	0.8	215	4	US-09-270-767-45086	Sequence 45086, A
421	6	0.8	200	4	US-09-101-272C-73	Sequence 73, Appl	494	6	0.8	216	3	US-08-861-774E-58	Sequence 58, Appl
422	6	0.8	200	4	US-09-252-991A-28054	Sequence 28054, A	495	6	0.8	216	3	US-08-861-774E-62	Sequence 62, Appl
423	6	0.8	200	4	US-09-489-039A-7526	Sequence 7526, Ap	496	6	0.8	218	3	US-08-861-774E-46	Sequence 46, Appl
424	6	0.8	201	3	US-08-679-493A-190	Sequence 190, App	497	6	0.8	218	3	US-08-861-774E-50	Sequence 50, Appl
425	6	0.8	202	4	US-09-252-991A-28505	Sequence 28505, A	498	6	0.8	218	4	US-09-134-000C-3898	Sequence 3898, Ap
426	6	0.8	202	4	US-09-252-991A-27017	Sequence 27017, A	499	6	0.8	218	4	US-09-828-303-23	Sequence 23, Appl
427	6	0.8	203	2	US-08-284-391B-31	Sequence 31, Appl	500	6	0.8	219	3	US-08-861-774E-70	Sequence 70, Appl
428	6	0.8	203	3	US-09-218-950-31	Sequence 31, Appl	501	6	0.8	219	4	US-09-252-991A-28228	Sequence 28228, A
429	6	0.8	203	4	US-09-543-681A-4329	Sequence 4329, Ap	502	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App
430	6	0.8	203	4	US-08-394-388A-31	Sequence 31, Appl	503	6	0.8	219	4	US-09-270-767-33084	Sequence 33084, A
431	6	0.8	203	4	US-10-101-464A-537	Sequence 537, App	504	6	0.8	219	4	US-09-270-767-48301	Sequence 48301, A
432	6	0.8	203	4	US-10-101-464A-658	Sequence 658, App	505	6	0.8	219	4	US-09-438-185A-593	Sequence 593, App
433	6	0.8	204	4	US-09-252-991A-29225	Sequence 29225, A	506	6	0.8	221	4	US-09-874-926-2	Sequence 2, Appl
434	6	0.8	204	4	US-09-543-681A-8020	Sequence 8020, Ap	507	6	0.8	222	4	US-09-252-991A-24147	Sequence 24147, A
435	6	0.8	205	3	US-09-134-001C-4766	Sequence 4766, Ap	508	6	0.8	223	4	US-09-252-991A-19065	Sequence 19065, A
436	6	0.8	205	4	US-09-252-991A-29334	Sequence 29334, A	509	6	0.8	224	4	US-09-198-452A-683	Sequence 683, App
437	6	0.8	205	4	US-09-134-000C-3913	Sequence 3913, Ap	510	6	0.8	229	3	US-08-630-915A-221	Sequence 221, App
438	6	0.8	206	3	US-08-679-493A-75	Sequence 75, Appl	511	6	0.8	229	4	US-09-879-957-221	Sequence 221, App
439	6	0.8	206	4	US-09-543-681A-4763	Sequence 4763, Ap	512	6	0.8	229	4	US-09-438-185A-648	Sequence 648, App
440	6	0.8	206	4	US-09-270-767-35977	Sequence 35977, A	513	6	0.8	230	3	US-09-516-143A-6	Sequence 6, Appl
441	6	0.8	206	4	US-09-270-767-51194	Sequence 51194, A	514	6	0.8	230	4	US-09-984-205-6	Sequence 6, Appl
442	6	0.8	207	4	US-09-198-452A-1020	Sequence 1020, Ap	515	6	0.8	231	4	US-09-543-681A-6357	Sequence 6357, Ap
443	6	0.8	208	1	US-07-935-309-2	Sequence 2, Appl	516	6	0.8	233	3	US-09-069-023-36	Sequence 36, Appl
444	6	0.8	208	1	US-08-884-682-1	Sequence 1, Appl	517	6	0.8	233	4	US-09-270-767-36462	Sequence 36462, A
445	6	0.8	208	2	US-08-039-364-2	Sequence 2, Appl	518	6	0.8	233	4	US-09-270-767-51679	Sequence 51679, A
446	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appl	519	6	0.8	234	3	US-08-861-774E-52	Sequence 52, Appl
447	6	0.8	208	2	US-09-096-082-1	Sequence 1, Appl	520	6	0.8	235	1	US-08-287-959-8	Sequence 8, Appl
448	6	0.8	208	3	US-08-718-904-5	Sequence 5, Appl	521	6	0.8	235	4	US-09-107-532A-6979	Sequence 6979, Ap
449	6	0.8	208	3	US-08-718-904-7	Sequence 7, Appl	522	6	0.8	235	4	US-09-583-110-4199	Sequence 4199, Ap
450	6	0.8	208	3	US-08-612-973-30	Sequence 30, Appl	523	6	0.8	236	4	US-09-107-433-3326	Sequence 3326, Ap
451	6	0.8	208	3	US-09-181-974-2	Sequence 2, Appl	524	6	0.8	236	4	US-09-134-000C-4896	Sequence 4896, App
452	6	0.8	208	3	US-09-158-710-2	Sequence 2, Appl	525	6	0.8	237	3	US-08-861-774E-68	Sequence 68, Appl
453	6	0.8	208	3	US-08-927-597-30	Sequence 30, Appl	526	6	0.8	238	4	US-09-252-991A-29406	Sequence 29406, A
454	6	0.8	208	3	US-09-518-950-2	Sequence 2, Appl	527	6	0.8	238	4	US-09-902-540-13083	Sequence 13083, A
455	6	0.8	208	4	US-09-449-249-5	Sequence 5, Appl	528	6	0.8	239	3	US-09-004-731-44	Sequence 44, Appl
456	6	0.8	208	4	US-09-449-249-7	Sequence 7, Appl	529	6	0.8	239	3	US-08-749-699-44	Sequence 44, Appl
457	6	0.8	208	4	US-09-252-991A-22641	Sequence 22641, A	530	6	0.8	239	3	US-08-679-493A-76	Sequence 76, Appl
458	6	0.8	208	4	US-10-138-158-18	Sequence 18, Appl	531	6	0.8	239	4	US-09-004-729-44	Sequence 44, Appl
459	6	0.8	208	4	US-09-949-016-6149	Sequence 6149, Ap	532	6	0.8	239	4	US-09-328-352-7328	Sequence 7328, Ap
460	6	0.8	209	3	US-08-975-762-71	Sequence 71, Appl	533	6	0.8	240	4	US-09-328-352-7253	Sequence 41, Appl
461	6	0.8	209	3	US-09-295-028-71	Sequence 71, Appl	534	6	0.8	242	3	US-09-004-731-41	Sequence 41, Appl
462	6	0.8	209	3	US-09-106-582-71	Sequence 71, Appl	535	6	0.8	242	3	US-09-032-215-47	Sequence 47, Appl
463	6	0.8	209	3	US-09-311-311C-20	Sequence 20, Appl	536	6	0.8	242	3	US-08-749-699-41	Sequence 41, Appl
464	6	0.8	209	4	US-09-252-991A-29571	Sequence 29571, A	537	6	0.8	242	4	US-09-004-729-41	Sequence 41, Appl
465	6	0.8	209	4	US-09-159-469-71	Sequence 71, Appl	538	6	0.8	242	4	US-09-252-991A-19021	Sequence 19021, A



539	6	0.8	242	4	US-09-107-532A-6244	Sequence 6244, Ap	612	6	0.8	281	4	US-09-270-767-43839	Sequence 43839, A
540	6	0.8	243	4	US-09-583-110-3522	Sequence 3522, Ap	613	6	0.8	282	4	US-09-252-991A-25948	Sequence 25948, A
541	6	0.8	244	4	US-09-543-681A-7356	Sequence 7356, Ap	614	6	0.8	284	4	US-08-976-063E-2	Sequence 2, Appli
542	6	0.8	245	4	US-09-461-325-463	Sequence 463, App	615	6	0.8	285	3	US-09-027-137-3	Sequence 3, Appli
543	6	0.8	246	4	US-09-252-991A-29762	Sequence 29762, A	616	6	0.8	285	3	US-09-344-441-3	Sequence 3, Appli
544	6	0.8	247	4	US-10-012-542-463	Sequence 463, App	617	6	0.8	285	4	US-09-248-796A-16474	Sequence 16474, A
545	6	0.8	248	4	US-10-115-123-463	Sequence 463, App	618	6	0.8	285	4	US-09-248-796A-20009	Sequence 20009, A
546	6	0.8	249	4	US-08-356-171E-5222	Sequence 5222, Ap	619	6	0.8	287	3	US-08-549-515-10	Sequence 10, Appl
547	6	0.8	250	4	US-08-781-986A-5222	Sequence 5222, Ap	620	6	0.8	288	4	US-09-489-039A-8919	Sequence 8919, Ap
548	6	0.8	245	4	US-09-640-211A-8333	Sequence 833, App	621	6	0.8	288	4	US-09-248-796A-16494	Sequence 16494, A
549	6	0.8	248	1	US-08-366-451B-2	Sequence 2, Appli	622	6	0.8	289	4	US-09-071-035-72	Sequence 72, Appl
550	6	0.8	248	2	US-08-748-725-2	Sequence 2, Appli	623	6	0.8	289	4	US-09-252-991A-22483	Sequence 22483, A
551	6	0.8	248	3	US-08-944-483-71	Sequence 71, Appl	624	6	0.8	292	3	US-09-027-137-1	Sequence 1, Appli
552	6	0.8	248	4	US-09-252-991A-17358	Sequence 17358, A	625	6	0.8	292	3	US-09-344-441-1	Sequence 1, Appli
553	6	0.8	249	3	US-09-010-809-21	Sequence 21, Appl	626	6	0.8	292	4	US-09-328-352-6642	Sequence 6642, Ap
554	6	0.8	250	3	US-09-010-809-3	Sequence 3, Appli	627	6	0.8	292	4	US-09-543-681A-7918	Sequence 7918, Ap
555	6	0.8	250	4	US-09-538-092-355	Sequence 355, App	628	6	0.8	295	4	US-09-134-000C-3737	Sequence 3737, Ap
556	6	0.8	251	3	US-08-630-915A-8	Sequence 8, Appli	629	6	0.8	295	6	5223394-9	Patent No. 5223394
557	6	0.8	251	4	US-09-270-767-4493	Sequence 4493, A	630	6	0.8	295	6	5223394-9	Patent No. 5223394
558	6	0.8	251	4	US-09-879-957-8	Sequence 8, Appli	631	6	0.8	296	4	US-09-252-991A-17385	Sequence 17385, A
559	6	0.8	252	3	US-08-944-483-72	Sequence 72, Appl	632	6	0.8	296	4	US-09-949-016-9495	Sequence 9495, Ap
560	6	0.8	253	2	US-09-027-337-8	Sequence 8, Appli	633	6	0.8	296	4	US-09-543-681A-7800	Sequence 7800, Ap
561	6	0.8	253	3	US-08-975-762-52	Sequence 52, Appl	634	6	0.8	298	4	US-09-252-991A-25360	Sequence 25360, A
562	6	0.8	253	3	US-08-944-483-73	Sequence 73, Appl	635	6	0.8	298	4	US-09-270-767-41339	Sequence 41339, A
563	6	0.8	253	3	US-09-295-028-52	Sequence 52, Appl	636	6	0.8	299	4	US-09-270-767-41683	Sequence 41683, A
564	6	0.8	253	3	US-09-106-582-52	Sequence 52, Appl	637	6	0.8	300	1	US-08-148-910-1	Sequence 1, Appli
565	6	0.8	253	4	US-09-644-600-8	Sequence 8, Appli	638	6	0.8	300	1	US-08-448-937A-1	Sequence 1, Appli
566	6	0.8	253	4	US-09-159-469-52	Sequence 52, Appl	639	6	0.8	300	4	US-09-252-991A-20115	Sequence 20115, A
567	6	0.8	253	4	US-09-489-039A-13739	Sequence 13739, A	640	6	0.8	301	4	US-09-252-991A-25396	Sequence 25396, A
568	6	0.8	253	4	US-09-654-600A-8	Sequence 8, Appli	641	6	0.8	301	4	US-09-134-000C-6014	Sequence 6014, Ap
569	6	0.8	253	4	US-09-693-542-52	Sequence 52, Appl	642	6	0.8	302	4	US-09-252-991A-21231	Sequence 21231, A
570	6	0.8	254	2	US-08-560-098A-49	Sequence 49, Appl	643	6	0.8	302	4	US-09-328-352-4508	Sequence 4508, Ap
571	6	0.8	254	4	US-09-270-767-46094	Sequence 46094, A	644	6	0.8	302	4	US-09-540-236-2119	Sequence 2119, Ap
572	6	0.8	254	4	US-09-248-796A-19272	Sequence 19272, A	645	6	0.8	303	4	US-09-107-532A-5585	Sequence 5585, Ap
573	6	0.8	255	3	US-09-612-126-1	Sequence 1, Appli	646	6	0.8	303	4	US-09-949-016-10112	Sequence 10112, A
574	6	0.8	256	3	US-09-230-637-29	Sequence 29, Appl	647	6	0.8	303	4	US-09-902-540-13222	Sequence 13222, A
575	6	0.8	256	4	US-09-489-039A-8774	Sequence 8774, Ap	648	6	0.8	304	4	US-09-489-039A-9424	Sequence 9424, Ap
576	6	0.8	257	2	US-08-467-265-16	Sequence 16, Appl	649	6	0.8	304	4	US-09-902-540-15483	Sequence 15483, A
577	6	0.8	257	3	US-08-467-265-16	Sequence 16, Appl	650	6	0.8	306	2	US-08-560-098A-45	Sequence 45, Appl
578	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl	651	6	0.8	306	4	US-09-252-991A-27054	Sequence 27054, A
579	6	0.8	257	3	US-09-375-907-5	Sequence 5, Appli	652	6	0.8	306	4	US-09-328-352-5398	Sequence 5398, Ap
580	6	0.8	257	4	US-09-828-447-14	Sequence 14, Appl	653	6	0.8	306	4	US-09-602-787A-572	Sequence 572, App
581	6	0.8	257	4	US-09-248-796A-24697	Sequence 24697, A	654	6	0.8	307	4	US-09-393-634-53	Sequence 53, Appl
582	6	0.8	258	3	US-09-227-357-198	Sequence 198, App	655	6	0.8	308	4	US-09-107-532A-6023	Sequence 6023, Ap
583	6	0.8	258	4	US-09-252-991A-33929	Sequence 33929, A	656	6	0.8	308	4	US-09-248-796A-18392	Sequence 18392, A
584	6	0.8	261	4	US-09-252-991A-29007	Sequence 29007, A	657	6	0.8	309	2	US-08-849-480A-6	Sequence 6, Appli
585	6	0.8	262	4	US-09-270-767-45003	Sequence 45003, A	658	6	0.8	310	3	US-08-477-460B-6	Sequence 6, Appli
586	6	0.8	263	4	US-09-270-767-32374	Sequence 32374, A	659	6	0.8	310	3	US-08-379-516-6	Sequence 6, Appli
587	6	0.8	263	4	US-09-270-767-47591	Sequence 47591, A	660	6	0.8	310	3	US-09-329-916-6	Sequence 6, Appli
588	6	0.8	264	3	US-08-484-905-120	Sequence 120, App	661	6	0.8	310	3	US-08-485-372A-6	Sequence 6, Appli
589	6	0.8	264	3	US-08-481-985B-120	Sequence 120, App	662	6	0.8	310	3	US-09-409-006A-6	Sequence 6, Appli
590	6	0.8	270	3	US-08-370-476-120	Sequence 120, App	663	6	0.8	310	4	US-08-484-681-6	Sequence 6, Appli
591	6	0.8	270	4	US-09-949-016-11038	Sequence 11038, A	664	6	0.8	310	4	US-09-766-995-6	Sequence 6, Appli
592	6	0.8	272	4	US-09-252-991A-27911	Sequence 27911, A	665	6	0.8	310	5	PCT-US93-07422-6	Sequence 6, Appli
593	6	0.8	274	4	US-09-270-767-40695	Sequence 40695, A	666	6	0.8	311	4	US-09-543-681A-5602	Sequence 5602, Ap
594	6	0.8	274	4	US-09-270-767-55911	Sequence 55911, A	667	6	0.8	311	4	US-09-489-039A-13013	Sequence 13013, A
595	6	0.8	276	3	US-08-953-326-18	Sequence 18, Appl	668	6	0.8	312	4	US-09-071-035-70	Sequence 70, Appl
596	6	0.8	276	3	US-09-553-662-18	Sequence 18, Appl	669	6	0.8	312	4	US-09-351-150A-11	Sequence 11, Appl
597	6	0.8	276	4	US-10-062-994-18	Sequence 18, Appl	670	6	0.8	312	4	US-09-599-360B-96	Sequence 96, Appl
598	6	0.8	276	4	US-09-880-503-5	Sequence 5, Appli	671	6	0.8	313	4	US-09-148-545-233	Sequence 233, App
599	6	0.8	277	4	US-09-252-991A-17567	Sequence 17567, A	672	6	0.8	313	4	US-09-248-796A-17016	Sequence 17016, A
600	6	0.8	278	4	US-09-252-991A-28712	Sequence 28712, A	673	6	0.8	315	4	US-09-270-767-42766	Sequence 42766, A
601	6	0.8	278	4	US-09-328-352-5824	Sequence 5824, Ap	674	6	0.8	315	4	US-09-270-767-43483	Sequence 43483, A
602	6	0.8	278	4	US-09-902-540-11962	Sequence 11962, A	675	6	0.8	315	4	US-09-603-208A-212	Sequence 212, App
603	6	0.8	280	4	US-09-107-532A-6088	Sequence 6088, Ap	676	6	0.8	317	4	US-09-583-110-5279	Sequence 5279, Ap
604	6	0.8	280	4	US-09-270-767-40154	Sequence 40154, A	677	6	0.8	317	4	US-09-270-767-42690	Sequence 42690, A
605	6	0.8	280	4	US-09-270-767-55370	Sequence 55370, A	678	6	0.8	318	4	US-09-252-991A-25243	Sequence 25243, A
606	6	0.8	280	4	US-10-101-464A-511	Sequence 511, App	679	6	0.8	318	6	5223394-11	Patent No. 5223394
607	6	0.8	281	3	US-09-660-587-9	Sequence 9, Appli	680	6	0.8	318	6	5223394-11	Patent No. 5223394
608	6	0.8	281	4	US-09-261-358A-9	Sequence 9, Appli	681	6	0.8	320	3	US-09-134-001C-3522	Sequence 3522, Ap
609	6	0.8	281	4	US-09-201-458-5	Sequence 5, Appli	682	6	0.8	320	3	US-09-134-001C-3823	Sequence 3823, Ap
610	6	0.8	281	4	US-09-314-701-2	Sequence 2, Appli	683	6	0.8	320	4	US-09-489-039A-10349	Sequence 10349, A
611	6	0.8	281	4	US-09-811-007A-9	Sequence 9, Appli	684	6	0.8				

685	6	0.8	320	4	US-09-489-039A-13881	Sequence 13881, A	758	359	4	US-09-583-110-3909	Sequence 3909, Ap
686	6	0.8	320	4	US-09-134-000C-5021	Sequence 5021, Ap	759	362	4	US-09-252-991A-18494	Sequence 18494, A
687	6	0.8	322	4	US-09-252-991A-29347	Sequence 29347, A	760	363	4	US-09-107-433-3869	Sequence 3869, Ap
688	6	0.8	322	4	US-09-949-016-8007	Sequence 8007, Ap	761	364	4	US-09-252-991A-19037	Sequence 19037, A
689	6	0.8	323	4	US-09-270-767-61011	Sequence 61011, A	762	364	4	US-09-438-185A-815	Sequence 815, Appl
690	6	0.8	323	4	US-09-880-503-7	Sequence 7, Appli	763	365	1	US-08-093-741-83	Sequence 83, Appl
691	6	0.8	324	4	US-09-270-767-44986	Sequence 44986, A	764	365	1	US-08-720-013-83	Sequence 3, Appl
692	6	0.8	325	4	US-08-311-731A-249	Sequence 249, App	765	365	3	US-09-231-529-3	Sequence 3, Appl
693	6	0.8	325	4	US-09-248-796A-14929	Sequence 14929, A	766	366	4	US-09-577-816-3	Sequence 2486, A
694	6	0.8	326	3	US-09-066-046-29	Sequence 29, Appl	767	366	4	US-09-252-991A-24466	Sequence 15462, A
695	6	0.8	326	3	US-09-066-047-15	Sequence 15, Appl	768	366	4	US-09-902-540-15482	Sequence 6, Appli
696	6	0.8	326	3	US-09-411-977-3	Sequence 3, Appli	769	367	3	US-08-895-707-6	Sequence 17240, A
697	6	0.8	326	4	US-09-543-681A-7709	Sequence 7709, Ap	770	367	4	US-09-252-991A-17240	Sequence 17240, A
698	6	0.8	326	4	US-10-057-951-3	Sequence 3, Appli	771	367	4	US-09-328-352-7662	Sequence 14930, A
699	6	0.8	327	4	US-09-252-991A-33067	Sequence 33067, A	772	369	4	US-09-248-796A-14930	Sequence 9972, Ap
700	6	0.8	327	4	US-09-107-433-3331	Sequence 3331, Ap	773	370	4	US-09-902-540-9972	Sequence 28586, A
701	6	0.8	328	4	US-09-248-796A-20663	Sequence 20663, A	774	372	4	US-09-973-963-4	Sequence 4, Appli
702	6	0.8	328	4	US-09-710-279-2476	Sequence 2476, Ap	775	372	4	US-09-949-016-6463	Sequence 4, Appli
703	6	0.8	330	4	US-09-710-279-2734	Sequence 2734, Ap	776	372	4	US-09-404-296B-4	Sequence 25, Appl
704	6	0.8	331	2	US-08-560-098A-46	Sequence 46, Appl	777	373	4	US-08-820-170A-25	Sequence 25, Appl
705	6	0.8	332	3	US-09-134-001C-4323	Sequence 4323, Ap	778	374	2	US-09-055-699-25	Sequence 25, Appl
706	6	0.8	333	4	US-09-328-352-7516	Sequence 7516, Ap	779	374	3	US-09-273-565-25	Sequence 25, Appl
707	6	0.8	334	3	US-09-218-363-11	Sequence 11, Appl	780	374	3	US-09-565-538-25	Sequence 25, Appl
708	6	0.8	336	1	US-07-904-073-2	Sequence 2, Appli	781	374	3	US-09-661-468-25	Sequence 25, Appl
709	6	0.8	336	1	US-07-904-071-2	Sequence 2, Appli	782	374	4	US-09-976-165-25	Sequence 25, Appl
710	6	0.8	336	1	US-08-442-043A-16	Sequence 16, Appl	783	374	4	US-09-227-853A-2	Sequence 2, Appl
711	6	0.8	336	4	US-08-441-893A-16	Sequence 16, Appl	784	374	4	US-09-540-236-2230	Sequence 2230, Ap
712	6	0.8	337	4	US-09-252-991A-26757	Sequence 26757, A	785	374	4	PCT-08955-06385-2	Sequence 2, Appl
713	6	0.8	337	4	US-09-252-991A-30261	Sequence 30261, A	786	374	5	US-08-872-979-3	Sequence 3, Appli
714	6	0.8	338	4	US-09-107-532A-5819	Sequence 5819, Ap	787	375	4	US-09-328-352-6191	Sequence 6191, Ap
715	6	0.8	340	4	US-09-543-681A-7850	Sequence 7850, Ap	788	375	4	US-09-489-039A-11560	Sequence 11560, A
716	6	0.8	340	4	US-09-816-248-15	Sequence 15, Appl	789	375	4	US-09-679-279-3	Sequence 3, Appli
717	6	0.8	341	4	US-09-543-681A-4713	Sequence 4713, Ap	790	377	4	US-09-489-039A-12546	Sequence 12546, A
718	6	0.8	341	4	US-09-248-796A-17051	Sequence 17051, A	791	377	4	US-09-553-498-10	Sequence 10, Appl
719	6	0.8	341	4	US-09-902-540-13921	Sequence 13921, A	792	378	3	US-09-618-869-10	Sequence 10, Appl
720	6	0.8	342	4	US-09-252-991A-30257	Sequence 30257, A	793	378	4	US-09-673-395A-618	Sequence 618, App
721	6	0.8	342	4	US-09-902-540-10704	Sequence 10704, A	794	378	4	US-09-252-991A-17472	Sequence 17472, A
722	6	0.8	343	4	US-09-252-991A-22307	Sequence 22307, A	795	379	4	US-09-673-395A-441	Sequence 441, App
723	6	0.8	345	3	US-09-027-900-11	Sequence 11, Appl	796	381	4	US-09-270-767-46183	Sequence 46183, A
724	6	0.8	345	4	US-09-489-039A-10740	Sequence 10740, A	797	381	4	US-08-486-037B-2	Sequence 2, Appl
725	6	0.8	346	4	US-09-252-991A-21487	Sequence 21487, A	798	383	2	US-08-558-269-6	Sequence 6, Appli
726	6	0.8	347	2	US-08-811-949-1	Sequence 1, Appli	799	383	3	US-09-410-882-6	Sequence 6, Appli
727	6	0.8	347	4	US-09-636-215-590	Sequence 590, App	800	383	3	US-09-071-224-19	Sequence 19, Appl
728	6	0.8	347	4	US-09-685-166A-590	Sequence 590, App	801	385	3	US-08-895-707-7	Sequence 7, Appli
729	6	0.8	347	4	US-09-679-426-590	Sequence 590, App	802	386	3	US-09-045-284A-2	Sequence 2, Appl
730	6	0.8	347	4	US-09-759-143-590	Sequence 590, App	803	386	3	US-09-190-911-1	Sequence 1, Appl
731	6	0.8	347	4	US-09-651-236-590	Sequence 590, App	804	386	4	US-09-786-240-11	Sequence 11, Appl
732	6	0.8	348	4	US-09-360-376-13	Sequence 13, Appl	805	386	4	US-09-489-039A-7410	Sequence 7410, Ap
733	6	0.8	349	4	US-09-489-039A-7582	Sequence 7582, Ap	806	386	4	US-09-248-796A-15757	Sequence 15757, A
734	6	0.8	351	1	US-08-324-483-2	Sequence 2, Appli	807	386	4	US-09-811-949-67	Sequence 67, Appl
735	6	0.8	351	4	US-09-902-540-12944	Sequence 12944, A	808	389	2	US-09-071-224-27	Sequence 27, Appl
736	6	0.8	354	2	US-08-811-949-61	Sequence 61, Appl	809	389	3	US-09-107-532A-6185	Sequence 6185, Ap
737	6	0.8	355	1	US-08-137-116-1	Sequence 1, Appli	810	389	4	US-09-252-991A-26543	Sequence 26543, A
738	6	0.8	355	1	US-08-217-618-1	Sequence 1, Appli	811	390	4	US-09-543-681A-7029	Sequence 7029, Ap
739	6	0.8	355	1	US-08-427-640-2	Sequence 2, Appli	812	392	1	US-09-543-681A-7029	Sequence 9, Appli
740	6	0.8	355	1	US-08-427-640-6	Sequence 6, Appli	813	392	3	US-09-027-007-9	Sequence 9, Appli
741	6	0.8	355	1	US-08-217-617A-1	Sequence 1, Appli	814	392	3	US-09-710-279-2794	Sequence 2794, Ap
742	6	0.8	355	1	US-08-217-616-1	Sequence 1, Appli	815	392	4	US-09-710-279-2874	Sequence 2874, Ap
743	6	0.8	355	2	US-08-811-949-45	Sequence 45, Appl	816	392	4	US-09-949-016-8786	Sequence 8786, Ap
744	6	0.8	355	2	US-08-811-949-47	Sequence 47, Appl	817	392	4	US-09-949-016-8787	Sequence 8787, Ap
745	6	0.8	355	2	US-08-811-949-53	Sequence 53, Appl	818	393	2	US-08-560-098A-44	Sequence 44, Appl
746	6	0.8	355	2	US-08-811-949-59	Sequence 59, Appl	819	393	3	US-08-967-024C-24	Sequence 24, Appl
747	6	0.8	355	3	US-08-794-528-1	Sequence 1, Appli	820	393	3	US-08-967-024C-25	Sequence 25, Appl
748	6	0.8	355	4	US-09-252-991A-22326	Sequence 22326, A	821	393	3	US-09-270-767-42793	Sequence 42793, A
749	6	0.8	355	4	US-09-198-452A-871	Sequence 871, App	822	393	3	US-08-466-368-2	Sequence 2, Appli
750	6	0.8	355	4	US-09-902-540-11796	Sequence 11796, A	823	394	3	US-09-144-914-4	Sequence 14502, A
751	6	0.8	355	6	5223256-1	Patent No. 5223256	824	394	4	US-08-328-500-2	Sequence 2, Appli
752	6	0.8	355	6	5223256-1	Patent No. 5223256	825	394	4	US-08-328-500-2	Patent No. 5223418
753	6	0.8	356	1	US-08-427-640-4	Sequence 4, Appli	826	394	6	5223418-2	Patent No. 5223418
754	6	0.8	356	1	US-08-427-640-8	Sequence 8, Appli	827	394	6	5223418-2	Sequence 2, Appli
755	6	0.8	356	4	US-09-252-991A-30030	Sequence 30030, A	828	395	1	US-08-485-859-2	Sequence 11, Appl
756	6	0.8	356	4	US-09-902-540-12881	Sequence 12881, A	829	395	1	US-08-706-539-11	Sequence 11, Appl
757	6	0.8	358	4	US-09-248-796A-19081	Sequence 19081, A	830	395	1	US-08-706-539-11	Sequence 11, Appl

831	6	0.8	395	1	US-08-522-166-2	Sequence 2, Appli	904	6	0.8	424	4	US-09-107-532A-5459	Sequence 5459, Ap
832	6	0.8	395	1	US-08-488-382A-2	Sequence 2, Appli	905	6	0.8	424	4	US-09-248-796A-18949	Sequence 18949, A
833	6	0.8	395	2	US-08-480-912-2	Sequence 2, Appli	906	6	0.8	424	4	US-10-027-450-45	Sequence 45, Appl
834	6	0.8	395	3	US-09-027-007-11	Sequence 11, Appl	907	6	0.8	425	3	US-09-071-224-6	Sequence 6, Appli
835	6	0.8	396	4	US-09-252-991A-18619	Sequence 18619, A	908	6	0.8	425	3	US-09-134-001C-5619	Sequence 5619, Ap
836	6	0.8	397	1	US-08-647-928-8	Sequence 8, Appli	909	6	0.8	425	4	US-09-540-236-3465	Sequence 3466, Ap
837	6	0.8	397	4	US-09-489-039A-13498	Sequence 13498, A	910	6	0.8	426	4	US-09-252-991A-25192	Sequence 25192, A
838	6	0.8	397	4	US-09-949-016-10639	Sequence 10639, A	911	6	0.8	427	4	US-09-198-452A-31	Sequence 31, Appl
839	6	0.8	397	4	US-09-949-016-10640	Sequence 10640, A	912	6	0.8	427	4	US-09-328-352-5205	Sequence 5205, Ap
840	6	0.8	398	2	US-08-284-391B-29	Sequence 29, Appl	913	6	0.8	428	1	US-08-570-157-5	Sequence 5, Appli
841	6	0.8	398	4	US-09-218-950-29	Sequence 29, Appl	914	6	0.8	428	3	US-08-029-170-31	Sequence 31, Appl
842	6	0.8	398	4	US-08-394-388A-29	Sequence 29, Appl	915	6	0.8	428	3	US-08-403-797-2	Sequence 2, Appli
843	6	0.8	399	4	US-09-489-039A-8859	Sequence 8859, Ap	916	6	0.8	428	3	US-09-076-510-5	Sequence 5, Appli
844	6	0.8	399	4	US-09-270-767-10639	Sequence 45921, A	917	6	0.8	428	4	US-09-004-349-5	Sequence 5, Appli
845	6	0.8	399	4	US-09-710-279-2576	Sequence 2576, Ap	918	6	0.8	428	4	US-09-443-745-31	Sequence 31, Appl
846	6	0.8	400	3	US-09-134-001C-31296	Sequence 4785, Ap	919	6	0.8	428	4	US-09-949-016-10965	Sequence 10965, A
847	6	0.8	400	4	US-09-252-991A-31296	Sequence 31296, A	920	6	0.8	429	4	US-09-252-991A-28788	Sequence 28788, A
848	6	0.8	400	4	US-09-248-796A-15785	Sequence 15785, A	921	6	0.8	429	4	US-09-854-133-391	Sequence 391, App
849	6	0.8	401	4	US-09-489-847-202	Sequence 202, App	922	6	0.8	430	1	US-07-942-157A-3	Sequence 3, Appli
850	6	0.8	401	4	US-09-252-991A-17090	Sequence 17090, A	923	6	0.8	430	6	5219569-2	Patent No. 5219569
851	6	0.8	401	4	US-09-902-540-10491	Sequence 10491, A	924	6	0.8	430	6	5219569-2	Patent No. 5219569
852	6	0.8	402	1	US-08-236-311-1	Sequence 1, Appli	925	6	0.8	431	3	US-09-376-689-4	Sequence 4, Appli
853	6	0.8	402	3	US-08-457-918-1	Sequence 1, Appli	926	6	0.8	431	4	US-09-101-272G-1	Sequence 1, Appli
854	6	0.8	402	4	US-10-157-408-1	Sequence 1, Appli	927	6	0.8	431	4	US-09-540-236-3536	Sequence 3536, Ap
855	6	0.8	403	4	US-09-802-213-5	Sequence 5, Appli	928	6	0.8	431	4	US-09-270-767-45503	Sequence 45503, A
856	6	0.8	403	4	US-09-880-503-6	Sequence 6, Appli	929	6	0.8	431	4	US-09-248-796A-18354	Sequence 18354, A
857	6	0.8	405	3	US-09-134-914-5	Sequence 5, Appli	930	6	0.8	431	6	518829-1	Patent No. 518829
858	6	0.8	405	4	US-09-252-991A-23838	Sequence 23838, A	931	6	0.8	431	6	518829-1	Patent No. 518829
859	6	0.8	405	4	US-09-134-000C-5465	Sequence 5465, Ap	932	6	0.8	432	2	US-08-560-098A-47	Sequence 47, Appl
860	6	0.8	408	4	US-09-252-991A-21303	Sequence 21303, A	933	6	0.8	432	3	US-08-477-460B-2	Sequence 2, Appli
861	6	0.8	408	4	US-09-198-452A-141	Sequence 141, App	934	6	0.8	432	3	US-08-379-516-2	Sequence 2, Appli
862	6	0.8	408	4	US-09-583-110-3016	Sequence 3016, Ap	935	6	0.8	432	3	US-09-329-916-2	Sequence 2, Appli
863	6	0.8	408	4	US-09-902-540-11436	Sequence 11436, A	936	6	0.8	432	3	US-08-485-372A-2	Sequence 2, Appli
864	6	0.8	409	4	US-09-710-279-2002	Sequence 2002, Ap	937	6	0.8	432	3	US-09-409-006A-2	Sequence 2, Appli
865	6	0.8	409	4	US-09-710-279-2306	Sequence 2306, Ap	938	6	0.8	432	4	US-08-484-681-2	Sequence 2, Appli
866	6	0.8	410	1	US-08-732-283A-9	Sequence 9, Appli	939	6	0.8	432	4	US-09-766-995-2	Sequence 2, Appli
867	6	0.8	410	2	US-09-105-908-9	Sequence 9, Appli	940	6	0.8	432	5	PCT-US93-07422-2	Sequence 2, Appli
868	6	0.8	410	3	US-08-630-172-17	Sequence 17, Appl	941	6	0.8	433	2	US-08-867-149-1	Sequence 1, Appli
869	6	0.8	410	3	US-09-271-713-9	Sequence 9, Appli	942	6	0.8	433	2	US-08-808-374-1	Sequence 1, Appli
870	6	0.8	410	3	US-09-375-419-17	Sequence 17, Appl	943	6	0.8	433	3	US-09-100-409A-1	Sequence 1, Appli
871	6	0.8	410	4	US-09-252-991A-25812	Sequence 25812, A	944	6	0.8	433	3	US-09-364-230-14	Sequence 14, Appl
872	6	0.8	410	4	US-09-252-991A-31937	Sequence 31937, A	945	6	0.8	433	4	US-09-792-024-78	Sequence 78, Appl
873	6	0.8	410	4	US-09-489-039A-10283	Sequence 10283, A	946	6	0.8	433	6	5171838-13	Patent No. 5171838
874	6	0.8	411	1	US-08-087-163-1	Sequence 1, Appli	947	6	0.8	433	6	5171838-13	Patent No. 5171838
875	6	0.8	411	1	US-08-286-748B-18	Sequence 18, Appl	948	6	0.8	434	3	US-08-236-311-4	Sequence 4, Appli
876	6	0.8	411	1	US-08-153-799-18	Sequence 18, Appl	949	6	0.8	434	3	US-08-457-918-4	Sequence 4, Appli
877	6	0.8	411	2	US-08-560-098A-48	Sequence 48, Appl	950	6	0.8	434	4	US-09-252-991A-23131	Sequence 23131, A
878	6	0.8	411	3	US-09-376-689-2	Sequence 2, Appli	951	6	0.8	434	4	US-09-543-681A-7154	Sequence 7154, Ap
879	6	0.8	411	3	US-09-181-816-1	Sequence 1, Appli	952	6	0.8	434	4	US-10-157-408-4	Sequence 4, Appli
880	6	0.8	411	4	US-09-403-736-2	Sequence 2, Appli	953	6	0.8	436	4	US-09-949-016-11448	Sequence 11448, A
881	6	0.8	411	4	US-09-880-503-3	Sequence 3, Appli	954	6	0.8	437	2	US-08-811-949-49	Sequence 49, Appl
882	6	0.8	412	4	US-09-902-540-13518	Sequence 13518, A	955	6	0.8	437	2	US-08-811-949-51	Sequence 51, Appl
883	6	0.8	413	4	US-09-949-016-10736	Sequence 10736, A	956	6	0.8	437	2	US-08-811-949-55	Sequence 55, Appl
884	6	0.8	413	4	US-09-949-016-10737	Sequence 10737, A	957	6	0.8	437	2	US-08-811-949-57	Sequence 57, Appl
885	6	0.8	414	4	US-09-252-991A-27828	Sequence 27828, A	958	6	0.8	437	4	US-09-710-279-2960	Sequence 2960, Ap
886	6	0.8	415	1	US-08-110-286A-6	Sequence 6, Appli	959	6	0.8	438	4	US-09-252-991A-28398	Sequence 28398, A
887	6	0.8	415	3	US-08-981-189B-10	Sequence 10, Appl	960	6	0.8	438	4	US-09-489-039A-8464	Sequence 8464, Ap
888	6	0.8	415	3	US-08-482-746-6	Sequence 6, Appli	961	6	0.8	438	4	US-09-902-540-12277	Sequence 12277, A
889	6	0.8	415	4	US-09-180-109A-9	Sequence 9, Appli	962	6	0.8	439	2	US-08-959-638-9	Sequence 9, Appli
890	6	0.8	415	4	US-09-180-109A-12	Sequence 12, Appl	963	6	0.8	439	4	US-09-543-681A-7293	Sequence 7293, Ap
891	6	0.8	415	4	US-09-580-734-6	Sequence 6, Appli	964	6	0.8	440	4	US-09-489-039A-10782	Sequence 10782, A
892	6	0.8	415	4	US-08-374-009-6	Sequence 6, Appli	965	6	0.8	441	3	US-09-457-046B-54	Sequence 54, Appl
893	6	0.8	415	4	US-09-191-724-6	Sequence 6, Appli	966	6	0.8	441	3	US-09-297-937C-11	Sequence 11, Appl
894	6	0.8	415	4	US-09-799-978-16	Sequence 16, Appl	967	6	0.8	441	4	US-09-949-016-10792	Sequence 10792, A
895	6	0.8	415	4	US-09-591-279A-42	Sequence 42, Appl	968	6	0.8	441	4	US-09-866-570B-54	Sequence 54, Appl
896	6	0.8	419	4	US-09-270-767-41700	Sequence 41700, A	969	6	0.8	443	1	US-08-570-157-6	Sequence 6, Appli
897	6	0.8	420	4	US-09-902-540-13149	Sequence 13149, A	970	6	0.8	443	3	US-09-076-510-6	Sequence 6, Appli
898	6	0.8	420	4	US-09-252-991A-17500	Sequence 17500, A	971	6	0.8	443	3	US-09-004-349-6	Sequence 6, Appli
899	6	0.8	420	4	US-09-583-110-5061	Sequence 5061, Ap	972	6	0.8	444	1	US-07-937-609-14	Sequence 14, Appl
900	6	0.8	420	4	US-09-107-433-3919	Sequence 3919, Ap	973	6	0.8	444	3	US-08-029-170-14	Sequence 14, Appl
901	6	0.8	422	4	US-09-489-847-357	Sequence 357, App	974	6	0.8	444	4	US-09-252-991A-28809	Sequence 28809, A
902	6	0.8	424	3	US-09-134-001C-5009	Sequence 5009, Ap	975	6	0.8	444	4	US-09-270-767-43807	Sequence 43807, A
903	6	0.8	424	4	US-09-173-300-45	Sequence 45, Appl	976	6	0.8	444	4	US-09-443-745-14	Sequence 14, Appl

977	6	0.8	445	4	US-09-710-279-2858	Sequence 2858, Ap	1050	492	4	US-09-248-796A-17174	Sequence 17174, A
978	6	0.8	451	4	US-09-328-352-7659	Sequence 7659, Ap	1051	493	4	US-09-543-681A-7006	Sequence 7006, Ap
979	6	0.8	451	4	US-09-328-352-7659	Sequence 3849, Ap	1052	494	4	US-09-517-773-2	Sequence 2, Appli
980	6	0.8	451	4	US-09-134-000C-3849	Sequence 4438, Ap	1053	495	4	US-08-311-773A-3	Sequence 3, Appli
981	6	0.8	454	3	US-09-134-001C-4438	Sequence 12501, A	1054	497	1	US-08-278-635B-5	Sequence 5, Appli
982	6	0.8	454	4	US-09-902-540-12501	Sequence 4, Appli	1055	497	3	US-08-464-258B-5	Sequence 5, Appli
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985	6	0.8	456	4	US-09-328-352-5446	Sequence 5446, Ap	1058	497	4	US-09-270-767-62287	Sequence 62287, A
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991	6	0.8	458	4	US-09-252-991A-30535	Sequence 30535, A	1064	501	3	US-09-902-540-16496	Sequence 1, Appli
992	6	0.8	458	4	US-09-489-039A-8987	Sequence 8987, Ap	1065	501	3	US-08-906-791-2	Sequence 7, Appli
993	6	0.8	458	4	US-09-612-402B-36	Sequence 36, Appl	1066	502	3	US-09-111-730-1	Sequence 4, Appli
994	6	0.8	458	4	US-10-092-138A-25	Sequence 25, Appl	1067	503	3	US-09-499-302A-7	Sequence 6578, Ap
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997	6	0.8	459	3	US-09-491-785-2	Sequence 20, Appl	1070	504	3	US-08-700-636-4	Sequence 4, Appli
998	6	0.8	459	3	US-09-364-230-20	Sequence 20, Appl	1071	504	3	US-08-467-574-4	Sequence 4, Appli
999	6	0.8	459	4	US-09-352-991A-29528	Sequence 29528, A	1072	504	3	US-09-217-345-4	Sequence 4, Appli
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ALIGNMENTS

RESULT 1  
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; Sequence 9, Application US/10067422  
; Patent No. 6743613  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, an  
; TITLE OF INVENTION: Antibodies  
; FILE REFERENCE: FT004P1  
; CURRENT APPLICATION NUMBER: US/10/067,422  
; CURRENT FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/685,899  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09028  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/152,933  
; PRIOR FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: 60/147,020  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: 60/131,672  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 60/130,693  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 570  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-422-9

Query Match 49.3%; Score 355; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-067-422-17
; Sequence 17, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT004PI
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
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; ORGANISM: Homo sapiens
US-10-067-422-17

Query Match 2.2%; Score 16; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 31 LEERNCSDFGPGVNGY 46

RESULT 3
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; Sequence 16, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT004PI
; CURRENT APPLICATION NUMBER: US/10/067,422
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
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; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-067-422-16

Query Match 1.7%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CACLAGYTGRC 271
DB 1 CACLAGYTGRC 12

RESULT 4
US-09-374-135-4
; Sequence 4, Application US/09374135
; Patent No. 6277972
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel E.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Safran, Douglas C.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
; TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
; FILE REFERENCE: 1703-017 US1
; CURRENT APPLICATION NUMBER: US/09/374,135
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095,982
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-4

Query Match 1.2%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 47 YDYVEVRDG 55

RESULT 5
US-09-341-461-28
; Sequence 28, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 28
; LENGTH: 110
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: amino acid sequence of Bmp-1 CUB1 domain
US-09-341-461-28

Query Match 1.2%; Score 9; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 179 YDYVEVRDG 187  
Db 56 YDYVEVRDG 64

## RESULT 6

US-09-438-046-20  
; Sequence 20, Application US/09438046  
; Patent No. 6706687  
; GENERAL INFORMATION:  
; APPLICANT: ERIKSSON, Ulf  
; APPLICANT: AASE, Karin  
; APPLICANT: LEE, Xuri  
; APPLICANT: PONTN, Annica  
; APPLICANT: UTELA, Marko  
; APPLICANT: ALITALO, Kari  
; APPLICANT: OESTMAN, Arne  
; APPLICANT: HELDIN, Carl-Henrik  
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING  
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
; FILE REFERENCE: Ulf Eriksson et al 1064-44833  
; CURRENT APPLICATION NUMBER: US/09/438,046  
; CURRENT FILING DATE: 1999-11-10  
; EARLIER APPLICATION NUMBER: 60/107,852  
; EARLIER FILING DATE: 1998-11-10  
; EARLIER APPLICATION NUMBER: 60/113,997  
; EARLIER FILING DATE: 1999-12-28  
; EARLIER APPLICATION NUMBER: 60/150,604  
; EARLIER FILING DATE: 1999-08-26  
; EARLIER APPLICATION NUMBER: 60/157,108  
; EARLIER FILING DATE: 1999-10-04  
; EARLIER APPLICATION NUMBER: 60/157,756  
; EARLIER FILING DATE: 1999-10-05  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-438-046-20

Query Match 1.2%; Score 9; DB 4; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 56 YDYVEVRDG 64

## RESULT 7

US-08-872-757-2  
; Sequence 2, Application US/08872757  
; Patent No. 6258584  
; GENERAL INFORMATION:  
; APPLICANT: Prockop, Darwin J.  
; APPLICANT: Hojima, Yoshio  
; APPLICANT: Li, Shi-Wu  
; APPLICANT: Sieron, Aleksander  
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND  
; TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/872,757  
; FILING DATE: 10-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,187  
; FILING DATE: 01-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8389-028-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 730 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-757-2

Query Match 1.2%; Score 9; DB 3; Length 730;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 377 YDYVEVRDG 385

RESULT 8  
US-09-850-048A-2  
; Sequence 2, Application US/09850048A  
; Patent No. 6562613  
; GENERAL INFORMATION:  
; APPLICANT: Prockop, Darwin J.  
; Hojima, Yoshio  
; Li, Shi-Wu  
; Sieron, Aleksander  
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND  
; TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/850,048A  
; FILING DATE: 07-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/609,187  
; FILING DATE: 1996-03-01  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8389-028-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 730 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-850-048A-2

Query Match          1.2%; Score 9; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      377 YDYVEVRDG 385

RESULT 9
US-08-572-225-1
; Sequence 1, Application US/08572225
; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/572,225
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 788 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: unknown
;   TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-572-225-1

Query Match          1.2%; Score 9; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      179 YDYVEVRDG 187
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RESULT 10
US-09-285-385C-19
; Sequence 19, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-285-385C-19

Query Match          1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      377 YDYVEVRDG 385

RESULT 11
US-09-949-016-6690
; Sequence 6690, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6690
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6690

Query Match          1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      179 YDYVEVRDG 187
Db      377 YDYVEVRDG 385

RESULT 12
US-09-285-385C-2
; Sequence 2, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
```

; APPLICANT: Scott, Ian C.  
; APPLICANT: Thomas, Christina L.  
; TITLE OF INVENTION: MAMMALIAN TOLLID-LIKE GENE AND PROTEIN  
; FILE REFERENCE: 960296.96111  
; CURRENT APPLICATION NUMBER: US/09/285.385C  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/111873  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: 60/080550  
; PRIOR FILING DATE: 1998-04-03  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1015  
; TYPE: PRT  
; ORGANISM: human  
US-09-285-385C-2

Query Match 1.2%; Score 9; DB 4; Length 1015;  
Best Local Similarity 100.0%; Pred. No. 4.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 YDVEVRDG 187  
Db 406 YDVEVRDG 414

RESULT 13  
US-09-188-930-342  
; Sequence 342, Application US/09188930A  
; Patent No. 6150502

; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; TITLE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188.930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 342  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-188-930-342

Query Match 1.1%; Score 8; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GYTGORCE 272  
Db 36 GYTGORCE 43

RESULT 14  
US-09-312-283C-342  
; Sequence 342, Application US/09312283C  
; Patent No. 6573095

; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James G.  
; APPLICANT: Kumble, Krishanand D.  
; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
; TITLE OF INVENTION: and Methods for Their Use  
; FILE REFERENCE: 11000.1011c2

; CURRENT APPLICATION NUMBER: US/09/312.283C  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 342  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-312-283C-342

Query Match 1.1%; Score 8; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GYTGORCE 272  
Db 36 GYTGORCE 43

RESULT 15  
US-09-472-087-99  
; Sequence 99, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PF1  
; CURRENT APPLICATION NUMBER: US/09/472.087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113.647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 99  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-99

Query Match 1.1%; Score 8; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 QSIGSSLH 215  
Db 27 QSIGSSLH 34

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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27	720	100.0	720	10	US-09-997-428-231
562	720	100.0	720	14	US-10-174-587-170
626	720	100.0	720	14	US-10-063-742-38
741	720	100.0	720	17	US-10-972-317-38
742	556	77.2	567	14	US-10-004-551-2
743	518	71.9	720	14	US-10-004-551-4
744	518	71.9	720	14	US-10-098-871-26
745	446	61.9	737	16	US-10-408-765A-1796
746	375	52.1	649	15	US-10-274-639-17
747	375	52.1	649	15	US-10-333-574-17
748	355	49.3	570	13	US-10-067-422-9
749	277	38.5	455	11	US-09-833-245-1401
750	276	38.3	323	11	US-09-833-243-1402
751	16	2.2	46	13	US-10-067-422-17

752	12	1.7	12	13	US-10-067-422-16	Sequence 16, Appl
753	9	1.2	101	9	US-09-887-593-4	Sequence 4, Appl
754	9	1.2	113	9	US-09-852-209A-20	Sequence 20, Appl
755	9	1.2	113	13	US-10-086-623-20	Sequence 20, Appl
756	9	1.2	113	14	US-10-260-539-20	Sequence 20, Appl
757	9	1.2	113	14	US-10-131-600-20	Sequence 20, Appl
758	9	1.2	113	15	US-10-303-997B-20	Sequence 20, Appl
759	9	1.2	113	15	US-10-439-337A-20	Sequence 20, Appl
760	9	1.2	730	9	US-09-850-048A-2	Sequence 2, Appl
761	9	1.2	823	15	US-10-016-248-98	Sequence 98, Appl
762	9	1.2	823	15	US-10-112-944-309	Sequence 309, Appl
763	9	1.2	970	15	US-10-016-248-42	Sequence 42, Appl
764	9	1.2	986	9	US-09-285-385C-19	Sequence 19, Appl
765	9	1.2	986	10	US-09-918-715-242	Sequence 242, Appl
766	9	1.2	986	15	US-10-366-345-33	Sequence 33, Appl
767	9	1.2	992	15	US-10-016-248-40	Sequence 40, Appl
768	9	1.2	1015	9	US-09-285-385C-2	Sequence 2, Appl
769	9	1.2	1015	15	US-10-016-248-97	Sequence 97, Appl
770	9	1.2	1579	16	US-10-437-963-196551	Sequence 196551, Appl
771	8	1.1	11	15	US-10-443-466A-8	Sequence 8, Appl
772	8	1.1	11	15	US-10-656-769-71	Sequence 71, Appl
773	8	1.1	51	10	US-09-866-050A-342	Sequence 342, Appl
774	8	1.1	88	9	US-09-905-243-30	Sequence 30, Appl
775	8	1.1	95	14	US-10-194-975-91	Sequence 91, Appl
776	8	1.1	95	14	US-10-194-975-92	Sequence 92, Appl
777	8	1.1	95	15	US-10-308-817-38	Sequence 38, Appl
778	8	1.1	95	15	US-10-308-817-39	Sequence 39, Appl
779	8	1.1	95	15	US-10-453-698-38	Sequence 38, Appl
780	8	1.1	95	15	US-10-453-698-39	Sequence 39, Appl
781	8	1.1	95	16	US-10-379-392-105	Sequence 105, Appl
782	8	1.1	95	16	US-10-379-392-106	Sequence 106, Appl
783	8	1.1	96	14	US-10-153-382-34	Sequence 34, Appl
784	8	1.1	108	17	US-10-805-177-67	Sequence 67, Appl
785	8	1.1	108	17	US-10-805-177-71	Sequence 71, Appl
786	8	1.1	124	9	US-09-764-877-1346	Sequence 1346, Ap
787	8	1.1	124	15	US-10-242-515-1346	Sequence 1346, Ap
788	8	1.1	126	15	US-10-362-082-2	Sequence 2, Appl
789	8	1.1	126	15	US-10-656-769-18	Sequence 18, Appl
790	8	1.1	128	15	US-10-443-466A-2	Sequence 2, Appl
791	8	1.1	128	15	US-10-443-466A-41	Sequence 41, Appl
792	8	1.1	128	15	US-10-443-466A-43	Sequence 43, Appl
793	8	1.1	128	15	US-10-443-466A-72	Sequence 72, Appl
794	8	1.1	128	15	US-10-443-466A-74	Sequence 74, Appl
795	8	1.1	128	15	US-10-443-466A-76	Sequence 76, Appl
796	8	1.1	128	15	US-10-443-466A-78	Sequence 78, Appl
797	8	1.1	151	16	US-10-437-963-107837	Sequence 107837, Appl
798	8	1.1	152	10	US-09-866-050A-187	Sequence 187, Appl
799	8	1.1	152	15	US-10-099-322-57	Sequence 57, Appl
800	8	1.1	152	15	US-10-044-564-57	Sequence 57, Appl
801	8	1.1	155	14	US-10-153-382-35	Sequence 35, Appl
802	8	1.1	157	17	US-10-644-277-36	Sequence 36, Appl
803	8	1.1	233	15	US-10-656-769-40	Sequence 40, Appl
804	8	1.1	273	14	US-10-148-671-25	Sequence 25, Appl
805	8	1.1	302	15	US-10-369-493-6656	Sequence 6656, Ap
806	8	1.1	411	16	US-10-437-963-111499	Sequence 111499, Appl
807	8	1.1	425	15	US-10-425-114-68970	Sequence 68970, A
808	8	1.1	481	15	US-10-425-114-72031	Sequence 72031, A
809	8	1.1	596	15	US-10-282-122A-50055	Sequence 50055, A
810	8	1.1	675	16	US-10-437-963-166405	Sequence 166405, Appl
811	8	1.1	807	14	US-10-132-350-42	Sequence 42, Appl
812	8	1.1	807	14	US-10-132-350-44	Sequence 44, Appl
813	8	1.1	907	16	US-10-437-963-118384	Sequence 118384, Appl
814	8	1.1	1019	14	US-10-183-992-4	Sequence 4, Appl
815	8	1.1	1019	14	US-10-183-992-8	Sequence 8, Appl
816	8	1.1	1019	16	US-10-638-125-4	Sequence 4, Appl
817	8	1.1	1068	16	US-10-437-963-195653	Sequence 195653, Appl
818	8	1.1	1083	14	US-10-183-992-6	Sequence 6, Appl
819	8	1.1	1083	16	US-10-638-125-2	Sequence 2, Appl
820	8	1.1	1316	15	US-10-028-248A-48	Sequence 48, Appl
821	8	1.1	1316	15	US-10-107-782-48	Sequence 48, Appl
822	8	1.1	3557	15	US-10-295-027-430	Sequence 430, Appl
823	8	1.1	3557	15	US-10-295-027-1297	Sequence 1297, Ap
824	8	1.1	3571	9	US-09-911-842-2	Sequence 2, Appl

825	8	1.1	3571	13	US-10-150-821-2	Sequence 2, Appli	898	7	1.0	227	15	US-10-282-122A-68048	Sequence 68048, A
826	8	1.1	3571	16	US-10-603-283-2	Sequence 2, Appli	899	7	1.0	227	16	US-10-437-963-141622	Sequence 141622, A
827	7	1.0	11	9	US-09-192-854-170	Sequence 190, App	900	7	1.0	228	15	US-10-282-122A-69437	Sequence 69437, A
828	7	1.0	11	9	US-09-968-561A-298	Sequence 298, App	901	7	1.0	230	16	US-10-437-963-178045	Sequence 178045, A
829	7	1.0	11	10	US-09-968-744A-298	Sequence 298, App	902	7	1.0	231	15	US-10-282-122A-54986	Sequence 54986, A
830	7	1.0	11	11	US-09-968-561A-298	Sequence 298, App	903	7	1.0	232	9	US-09-815-243-5151	Sequence 5151, Ap
831	7	1.0	46	15	US-10-424-599-272809	Sequence 272809, A	904	7	1.0	232	15	US-10-282-122A-43430	Sequence 43430, A
832	7	1.0	47	16	US-10-437-963-141351	Sequence 141351, A	905	7	1.0	239	15	US-10-282-122A-77383	Sequence 77383, A
833	7	1.0	54	9	US-09-738-626-5214	Sequence 5214, Ap	906	7	1.0	244	16	US-10-437-963-153684	Sequence 153684, A
834	7	1.0	57	9	US-09-864-761-45299	Sequence 45299, A	907	7	1.0	248	15	US-10-424-599-270715	Sequence 270715, A
835	7	1.0	66	15	US-10-424-599-186581	Sequence 186581, A	908	7	1.0	250	10	US-09-898-837A-45	Sequence 45, Appl
836	7	1.0	69	15	US-10-424-599-223128	Sequence 223128, A	909	7	1.0	251	10	US-09-898-837A-41	Sequence 41, Appl
837	7	1.0	71	16	US-10-437-963-195234	Sequence 195234, A	910	7	1.0	254	16	US-10-437-963-178860	Sequence 178860, A
838	7	1.0	72	16	US-10-437-963-169418	Sequence 169418, A	911	7	1.0	257	9	US-09-815-242-13845	Sequence 13845, A
839	7	1.0	73	16	US-10-437-963-170815	Sequence 170815, A	912	7	1.0	259	11	US-09-789-210-52	Sequence 52, Appl
840	7	1.0	74	11	US-09-864-408A-8324	Sequence 8324, Ap	913	7	1.0	259	15	US-10-165-442-2	Sequence 2, Appli
841	7	1.0	75	15	US-10-424-599-148860	Sequence 148860, A	914	7	1.0	259	16	US-10-165-442-4	Sequence 4, Appli
842	7	1.0	79	11	US-09-833-245-1400	Sequence 1400, Ap	915	7	1.0	259	16	US-10-699-393-2	Sequence 2, Appli
843	7	1.0	85	15	US-10-424-599-275249	Sequence 275249, A	916	7	1.0	259	16	US-10-699-393-4	Sequence 4, Appli
844	7	1.0	85	16	US-10-424-599-274378	Sequence 274378, A	917	7	1.0	259	16	US-10-872-198-5	Sequence 5, Appli
845	7	1.0	105	14	US-10-006-869-18	Sequence 59878, A	918	7	1.0	263	16	US-10-872-197A-5	Sequence 5, Appli
846	7	1.0	105	15	US-10-006-869-18	Sequence 18, Appl	919	7	1.0	263	16	US-10-822-613-30	Sequence 30, Appl
847	7	1.0	108	9	US-09-800-095A-86	Sequence 86, Appl	920	7	1.0	263	16	US-10-822-613-34	Sequence 34, Appl
848	7	1.0	108	15	US-10-424-599-253529	Sequence 253529, A	921	7	1.0	265	9	US-09-791-171-16	Sequence 16, Appl
849	7	1.0	115	15	US-10-425-114-41281	Sequence 41281, A	922	7	1.0	265	10	US-09-804-980-16	Sequence 16, Appl
850	7	1.0	115	15	US-10-425-114-41281	Sequence 41281, A	923	7	1.0	265	16	US-10-620-246-16	Sequence 16, Appl
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852	7	1.0	125	15	US-10-425-114-60253	Sequence 60253, A	925	7	1.0	271	16	US-10-408-765A-1200	Sequence 1200, Ap
853	7	1.0	130	16	US-10-424-599-147528	Sequence 147528, A	926	7	1.0	285	16	US-10-437-963-134290	Sequence 134290, A
854	7	1.0	130	16	US-10-437-963-129837	Sequence 129837, A	927	7	1.0	285	16	US-10-767-701-35097	Sequence 35097, A
855	7	1.0	134	16	US-10-437-963-151149	Sequence 151149, A	928	7	1.0	292	16	US-10-437-963-161568	Sequence 161568, A
856	7	1.0	134	15	US-10-424-599-274398	Sequence 274398, A	929	7	1.0	295	15	US-10-165-442-1	Sequence 1, Appli
857	7	1.0	136	15	US-10-424-599-274378	Sequence 274378, A	930	7	1.0	295	15	US-10-165-442-3	Sequence 3, Appli
858	7	1.0	141	16	US-10-767-701-52201	Sequence 52201, A	931	7	1.0	295	16	US-10-699-393-1	Sequence 1, Appli
859	7	1.0	142	15	US-10-424-599-274613	Sequence 274613, A	932	7	1.0	295	16	US-10-699-393-3	Sequence 3, Appli
860	7	1.0	146	15	US-10-437-963-102869	Sequence 102869, A	933	7	1.0	306	16	US-10-437-963-182869	Sequence 182869, A
861	7	1.0	149	15	US-10-424-599-274289	Sequence 274289, A	934	7	1.0	308	10	US-09-510-332-155	Sequence 155, App
862	7	1.0	151	16	US-10-424-599-212242	Sequence 212242, A	935	7	1.0	308	17	US-10-962-365-135	Sequence 135, App
863	7	1.0	156	13	US-10-053-200-2	Sequence 2, Appli	936	7	1.0	314	14	US-10-264-049-2827	Sequence 2827, Ap
864	7	1.0	157	15	US-10-424-599-199827	Sequence 199827, A	937	7	1.0	324	15	US-10-264-049-2827	Sequence 2827, Ap
865	7	1.0	157	15	US-10-425-114-49725	Sequence 49725, A	938	7	1.0	330	15	US-10-369-493-15829	Sequence 15829, A
866	7	1.0	158	16	US-10-437-963-203623	Sequence 203623, A	939	7	1.0	330	15	US-10-369-493-16209	Sequence 16209, A
867	7	1.0	164	15	US-10-259-194A-222	Sequence 222, App	940	7	1.0	331	15	US-10-425-114-53205	Sequence 53205, A
868	7	1.0	172	15	US-10-282-122A-67170	Sequence 67170, A	941	7	1.0	332	10	US-09-510-332-101	Sequence 101, App
869	7	1.0	172	16	US-10-437-963-160181	Sequence 160181, A	942	7	1.0	332	15	US-10-369-493-15461	Sequence 15461, A
870	7	1.0	177	16	US-10-437-963-193489	Sequence 193489, A	943	7	1.0	332	17	US-10-962-365-101	Sequence 101, App
871	7	1.0	182	16	US-10-437-963-193489	Sequence 193489, A	944	7	1.0	336	15	US-10-389-566-1548	Sequence 1548, Ap
872	7	1.0	186	15	US-10-425-114-62298	Sequence 62298, A	945	7	1.0	338	15	US-10-389-566-1565	Sequence 1565, Ap
873	7	1.0	192	16	US-10-437-963-104072	Sequence 104072, A	946	7	1.0	345	15	US-10-424-599-268634	Sequence 268634, A
874	7	1.0	194	10	US-09-791-932-104	Sequence 104, App	947	7	1.0	345	15	US-10-275-026A-94	Sequence 94, Appl
875	7	1.0	200	9	US-09-811-284-240	Sequence 240, App	948	7	1.0	375	15	US-10-424-599-160824	Sequence 160824, A
876	7	1.0	204	16	US-10-437-963-178632	Sequence 178632, A	949	7	1.0	383	15	US-10-425-114-50358	Sequence 50358, A
877	7	1.0	206	16	US-10-437-963-105498	Sequence 105498, A	950	7	1.0	386	15	US-10-425-114-50358	Sequence 50358, A
878	7	1.0	206	16	US-10-767-701-57306	Sequence 57306, A	951	7	1.0	409	15	US-10-282-122A-65178	Sequence 65178, A
879	7	1.0	209	15	US-10-425-114-65921	Sequence 65921, A	952	7	1.0	416	10	US-09-976-782-114	Sequence 114, App
880	7	1.0	210	15	US-10-369-493-20095	Sequence 20095, A	953	7	1.0	416	10	US-09-976-782-114	Sequence 117075, A
881	7	1.0	210	15	US-10-289-762-869	Sequence 869, App	954	7	1.0	429	16	US-10-437-963-17075	Sequence 17075, A
882	7	1.0	211	15	US-10-282-122A-55523	Sequence 55523, A	955	7	1.0	433	15	US-10-282-122A-62604	Sequence 62604, A
883	7	1.0	211	15	US-10-282-122A-77886	Sequence 77886, A	956	7	1.0	443	16	US-10-437-963-180424	Sequence 180424, A
884	7	1.0	212	9	US-09-815-242-10149	Sequence 10149, A	957	7	1.0	443	15	US-10-282-122A-44986	Sequence 44986, A
885	7	1.0	212	15	US-10-282-122A-42990	Sequence 42990, A	958	7	1.0	448	15	US-10-424-599-199828	Sequence 199828, A
886	7	1.0	212	15	US-10-282-122A-59410	Sequence 59410, A	959	7	1.0	456	10	US-10-425-114-48669	Sequence 48669, A
887	7	1.0	212	15	US-10-282-122A-73395	Sequence 73395, A	960	7	1.0	456	14	US-09-932-227-64	Sequence 64, Appl
888	7	1.0	212	15	US-10-282-122A-73395	Sequence 73395, A	961	7	1.0	461	15	US-10-183-708-64	Sequence 64, Appl
889	7	1.0	213	15	US-10-282-122A-75987	Sequence 75987, A	962	7	1.0	461	15	US-10-282-122A-61657	Sequence 61657, A
890	7	1.0	213	15	US-10-282-122A-68483	Sequence 68483, A	963	7	1.0	462	16	US-10-282-122A-64914	Sequence 64914, A
891	7	1.0	214	15	US-10-425-114-71387	Sequence 71387, A	964	7	1.0	463	17	US-10-437-963-185820	Sequence 185820, A
892	7	1.0	218	15	US-10-425-114-64477	Sequence 64477, A	965	7	1.0	463	17	US-10-959-539-8	Sequence 8, Appli
893	7	1.0	218	15	US-10-425-114-66277	Sequence 66277, A	966	7	1.0	464	16	US-10-437-963-109962	Sequence 109962, A
894	7	1.0	218	15	US-10-425-114-67294	Sequence 67294, A	967	7	1.0	465	15	US-10-389-566-2016	Sequence 2016, Ap
895	7	1.0	218	15	US-10-425-114-69657	Sequence 69657, A	968	7	1.0	470	14	US-10-369-493-3738	Sequence 3738, Ap
896	7	1.0	222	15	US-10-424-599-215367	Sequence 215367, A	969	7	1.0	470	14	US-10-355-430-34	Sequence 34, Appl
897	7	1.0	223	16	US-10-437-963-178810	Sequence 178810, A	970	7	1.0	471	16	US-10-437-963-118377	Sequence 118377, A
			225	16	US-10-437-963-143960	Sequence 143960, A				477	15	US-10-425-114-65737	Sequence 65737, A



971	7	1.0	492	9	US-09-801-368-192	Sequence 192, App	1044	7	1.0	3972	14	US-10-156-761-8476	Sequence 8476, Ap
972	7	1.0	493	10	US-09-976-782-115	Sequence 115, App	1045	7	1.0	3972	16	US-10-204-862A-4	Sequence 4, Appli
973	7	1.0	494	10	US-09-820-843A-32	Sequence 32, Appl	1046	7	1.0	3972	16	US-10-204-862A-8	Sequence 8, Appli
974	7	1.0	498	9	US-09-764-864-1122	Sequence 1122, Ap	1047	7	1.0	11877	9	US-09-861-289-6	Sequence 6, Appli
975	7	1.0	500	15	US-10-369-493-20424	Sequence 20424, A	1048	7	1.0	11877	9	US-09-860-846-6	Sequence 6, Appli
976	7	1.0	502	16	US-10-474-776-295	Sequence 295, App	1049	7	1.0	11877	10	US-09-836-821-6	Sequence 6, Appli
977	7	1.0	502	17	US-10-472-928-1880	Sequence 1880, Ap	1050	7	1.0	11877	10	US-09-836-821-6	Sequence 6, Appli
978	7	1.0	503	9	US-09-071-035-360	Sequence 360, App	1051	7	1.0	12199	10	US-09-988-384B-6	Sequence 49, Appl
979	7	1.0	503	14	US-10-206-576-360	Sequence 360, App	1052	6	0.8	9	15	US-10-013-312-45	Sequence 45, Appl
980	7	1.0	503	17	US-10-912-362-360	Sequence 360, App	1053	6	0.8	9	15	US-10-013-312-111	Sequence 111, App
981	7	1.0	509	15	US-10-114-270-94	Sequence 94, Appl	1054	6	0.8	9	15	US-10-013-312-420	Sequence 420, App
982	7	1.0	513	15	US-10-369-493-11240	Sequence 11240, A	1055	6	0.8	9	15	US-10-013-312-521	Sequence 523, App
983	7	1.0	517	15	US-10-381-598A-4	Sequence 4, Appli	1056	6	0.8	9	15	US-10-013-312-646	Sequence 646, App
984	7	1.0	519	15	US-10-424-599-216138	Sequence 216138, A	1057	6	0.8	9	15	US-10-013-312-1328	Sequence 1328, Ap
985	7	1.0	543	15	US-10-369-493-3712	Sequence 3712, Ap	1058	6	0.8	9	15	US-10-013-312-1353	Sequence 1353, Ap
986	7	1.0	553	9	US-09-815-242-13391	Sequence 13391, A	1059	6	0.8	9	15	US-10-013-312-1369	Sequence 1369, Ap
987	7	1.0	553	15	US-10-282-122A-73854	Sequence 73854, A	1060	6	0.8	9	15	US-10-013-312-1451	Sequence 1451, Ap
988	7	1.0	553	17	US-10-472-928-1116	Sequence 1116, Ap	1061	6	0.8	9	15	US-10-013-312-1495	Sequence 1495, Ap
989	7	1.0	556	9	US-09-795-691-2	Sequence 2, Appli	1062	6	0.8	9	15	US-10-013-312-1842	Sequence 1842, Ap
990	7	1.0	556	14	US-10-229-662-2	Sequence 2, Appli	1063	6	0.8	9	15	US-10-013-312-1590	Sequence 1590, Ap
991	7	1.0	556	15	US-10-426-776-2	Sequence 2, Appli	1064	6	0.8	9	15	US-10-013-312-1591	Sequence 1591, Ap
992	7	1.0	560	16	US-10-437-963-185707	Sequence 185707, A	1065	6	0.8	9	15	US-10-013-312-1591	Sequence 1591, Ap
993	7	1.0	571	16	US-10-437-963-111762	Sequence 111762, A	1066	6	0.8	9	15	US-10-013-312-1686	Sequence 1686, Ap
994	7	1.0	573	15	US-10-282-122A-46569	Sequence 46569, A	1067	6	0.8	9	15	US-10-013-312-1712	Sequence 1712, Ap
995	7	1.0	588	15	US-10-369-493-17841	Sequence 17841, A	1068	6	0.8	9	15	US-10-013-312-1731	Sequence 1731, Ap
996	7	1.0	593	16	US-10-437-963-122654	Sequence 122654, A	1069	6	0.8	9	15	US-10-013-312-1795	Sequence 1795, Ap
997	7	1.0	600	14	US-10-156-761-8406	Sequence 8406, Ap	1070	6	0.8	9	15	US-10-013-312-1821	Sequence 1821, Ap
998	7	1.0	622	14	US-10-020-141-8	Sequence 8, Appli	1071	6	0.8	9	15	US-10-013-312-1922	Sequence 1922, Ap
999	7	1.0	622	14	US-10-017-631-2	Sequence 2, Appli	1072	6	0.8	10	15	US-10-013-312-178	Sequence 178, App
1000	7	1.0	622	14	US-10-214-932-116	Sequence 116, App	1073	6	0.8	10	15	US-10-013-312-375	Sequence 375, App
1001	7	1.0	622	14	US-10-172-712-23	Sequence 23, Appl	1074	6	0.8	10	15	US-10-013-312-478	Sequence 478, App
1002	7	1.0	622	16	US-10-872-198-149	Sequence 149, App	1075	6	0.8	10	15	US-10-013-312-573	Sequence 573, App
1003	7	1.0	639	17	US-10-792-498-16	Sequence 16, Appl	1076	6	0.8	10	15	US-10-013-312-683	Sequence 683, App
1004	7	1.0	639	17	US-10-792-498-17	Sequence 17, Appl	1077	6	0.8	10	15	US-10-013-312-683	Sequence 683, App
1005	7	1.0	713	15	US-10-282-122A-50120	Sequence 50120, A	1078	6	0.8	10	15	US-10-013-312-2091	Sequence 2091, Ap
1006	7	1.0	716	16	US-10-437-963-147102	Sequence 147102, A	1079	6	0.8	10	15	US-10-013-312-2098	Sequence 2098, Ap
1007	7	1.0	772	16	US-10-437-963-152918	Sequence 152918, A	1080	6	0.8	10	15	US-10-013-312-2183	Sequence 2183, Ap
1008	7	1.0	776	15	US-10-320-797-3297	Sequence 3297, Ap	1081	6	0.8	10	15	US-10-013-312-2200	Sequence 2200, Ap
1009	7	1.0	783	15	US-10-389-647-553	Sequence 553, App	1082	6	0.8	10	15	US-10-013-312-2280	Sequence 2280, Ap
1010	7	1.0	784	15	US-10-259-194A-178	Sequence 178, App	1083	6	0.8	10	15	US-10-013-312-2300	Sequence 2300, Ap
1011	7	1.0	790	14	US-10-174-677-17	Sequence 17, Appl	1084	6	0.8	10	15	US-10-013-312-2346	Sequence 2346, Ap
1012	7	1.0	799	9	US-09-738-626-4131	Sequence 4131, Ap	1085	6	0.8	10	15	US-10-013-312-2367	Sequence 2367, Ap
1013	7	1.0	799	16	US-10-494-672-142	Sequence 142, App	1086	6	0.8	10	15	US-10-013-312-2390	Sequence 2390, Ap
1014	7	1.0	859	8	US-08-945-749-1	Sequence 1, Appli	1087	6	0.8	11	9	US-09-987-844-2	Sequence 2, Appli
1015	7	1.0	859	16	US-10-437-963-166508	Sequence 166508, A	1088	6	0.8	11	14	US-10-062-710-168	Sequence 168, App
1016	7	1.0	878	16	US-10-437-963-158328	Sequence 158328, A	1089	6	0.8	12	14	US-09-933-767-304	Sequence 304, App
1017	7	1.0	950	16	US-10-437-963-115663	Sequence 115663, A	1090	6	0.8	12	14	US-10-004-860-304	Sequence 304, App
1018	7	1.0	984	17	US-10-211-028-25	Sequence 25, Appl	1091	6	0.8	12	14	US-10-023-282-304	Sequence 304, App
1019	7	1.0	986	9	US-09-850-048A-4	Sequence 4, Appli	1093	6	0.8	14	14	US-10-014-340-139	Sequence 139, App
1020	7	1.0	1074	9	US-09-071-035-358	Sequence 358, App	1095	6	0.8	14	16	US-10-712-447-198	Sequence 198, App
1021	7	1.0	1074	9	US-09-071-035-394	Sequence 394, App	1096	6	0.8	14	16	US-10-712-447-198	Sequence 198, App
1022	7	1.0	1074	14	US-10-206-576-358	Sequence 358, App	1097	6	0.8	15	14	US-10-062-710-167	Sequence 167, App
1023	7	1.0	1074	14	US-10-206-576-358	Sequence 358, App	1098	6	0.8	15	15	US-10-013-312-2625	Sequence 2625, Ap
1024	7	1.0	1074	17	US-10-912-362-358	Sequence 358, App	1099	6	0.8	15	15	US-10-013-312-2658	Sequence 2658, Ap
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1032	7	1.0	1346	14	US-10-201-365-5	Sequence 5, Appli	1107	6	0.8	15	15	US-10-013-312-2886	Sequence 2886, Ap
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1037	7	1.0	1592	16	US-10-437-963-188419	Sequence 188419, A	1112	6	0.8	21	14	US-10-062-710-47	Sequence 47, Appl
1038	7	1.0	2306	15	US-10-015-115-60	Sequence 60, Appl	1113	6	0.8	21	14	US-10-062-710-169	Sequence 169, App
1039	7	1.0	2910	16	US-10-322-696-18	Sequence 18, Appl	1114	6	0.8	21	14	US-10-084-813-286	Sequence 286, App
1040	7	1.0	2911	10	US-09-825-751A-68	Sequence 68, Appl	1115	6	0.8	21	14	US-10-084-813-287	Sequence 287, App
1041	7	1.0	2911	15	US-10-295-027-162	Sequence 162, App	1116	6	0.8	21	14	US-10-084-813-288	Sequence 288, App
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1119	6	0.8	22	17	US-10-794-774-36	Sequence 36, Appl	1192	6	0.8	51	9	US-09-984-245-236	Sequence 236, App
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1122	6	0.8	25	13	US-10-062-624-28	Sequence 28, Appl	1195	6	0.8	51	14	US-10-059-395-236	Sequence 236, App
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1135	6	0.8	35	14	US-10-289-660-62	Sequence 62, Appl	1208	6	0.8	54	15	US-10-424-599-171307	Sequence 171307,
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1145	6	0.8	37	14	US-10-687-361-14	Sequence 14, Appl	1218	6	0.8	56	14	US-10-080-170-237	Sequence 237, App
1146	6	0.8	37	16	US-10-716-379-14	Sequence 14, Appl	1219	6	0.8	56	15	US-10-424-599-172883	Sequence 172883,
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1271	6	0.8	66	14	US-10-040-862-1109	Sequence 1109, App	1344	74	15	US-10-319-745-130	Sequence 130, App
1272	6	0.8	66	14	US-10-040-862-1122	Sequence 1122, App	1345	74	15	US-10-319-745-137	Sequence 137, App
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1285	6	0.8	66	15	US-10-424-599-156756	Sequence 156756, App	1358	76	13	US-10-125-540-519	Sequence 519, App
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GenCore version 5.1.6  
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 OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: May 9, 2005, 22:33:58 ; Search time 981 Seconds  
 (without alignments)  
 4344.764 Million cell updates/sec

Title: US-10-063-692-38  
 Perfect score: 3945  
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 Scoring table: BLOSUM62

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Delop 6.0	Delext 7.0	

Searched: 4390206 seqs, 2959870667 residues  
 Total number of hits satisfying chosen parameters: 8780412  
 Minimum DB seq length: 0  
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 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

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 11: Geneseqn2003ds:  
 12: Geneseqn2004as:  
 13: Geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	ID	Description
SUMMARIES				
RESULT 1				
ID	ADA00368	standard; cDNA; 2843 BP.		
DE	Human secreted/transmembrane polypeptide PRO 1344	cDNA.		
PN	US2003027992-A1.			
PD	06-FEB-2003.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 2				
ID	AAZ65034	standard; cDNA; 2846 BP.		
DE	Membrane-bound protein PRO1344	encoding cDNA.		
PN	WO9663088-A2.			
PD	09-DEC-1999.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 3				
ID	AAS46009	standard; cDNA; 2846 BP.		
DE	Human DNA encoding PRO polypeptide	sequence #85.		
PN	WO200168848-A2.			
PD	02-JAN-2003.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 4				
ID	AAF92076	standard; cDNA; 2846 BP.		
DE	Human PRO1344	cDNA.		
PN	WO200116318-A2.			
PD	08-MAR-2001.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 5				
ID	AAF44180	standard; cDNA; 2846 BP.		
DE	Human PRO1344 (UNQ699)	nucleotide sequence SEQ ID NO:230.		
PN	WO200073454-A1.			
PD	07-DEC-2000.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 6				
ID	ABS74396	standard; cDNA; 2846 BP.		
DE	Human cDNA encoding secreted/transmembrane protein PRO1344.			
PN	US2002119130-A1.			
PD	29-AUG-2002.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 7				
ID	ACA89459	standard; cDNA; 2846 BP.		
DE	cDNA encoding human PRO polypeptide #85.			
PN	US2003036141-A1.			
PD	20-FEB-2003.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 8				
ID	ACA73469	standard; cDNA; 2846 BP.		
DE	Human secreted/transmembrane protein (PRO)	cDNA #85.		
PN	US2003036146-A1.			
PD	20-FEB-2003.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 9				
ID	ACA05784	standard; cDNA; 2846 BP.		
DE	Human secreted/transmembrane protein (PRO)	cDNA #85.		
PN	US2003036162-A1.			
PD	20-FEB-2003.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 10				
ID	ACA66618	standard; cDNA; 2846 BP.		
DE	cDNA encoding human PRO protein #85.			
PN	US2003036137-A1.			
PD	20-FEB-2003.			
PA	(GETH ) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 11				
ID	ACA64316	standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344	cDNA.		
PN	US2003003531-A1.			
PD	02-JAN-2003.			
PA	(GETH ) GENENTECH INC.			

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 12  
ID ACA91182 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 13  
ID ACD81559 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 14  
ID ACF20193 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 15  
ID ACF19579 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 16  
ID ACD21867 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 17  
ID ACF13032 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 18  
ID ACD25135 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 19  
ID ACF00184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 20  
ID ACA60381 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 21  
ID ACA72241 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 22  
ID ACD04765 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 23  
ID ACD18226 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 24  
ID ACD08233 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 25  
ID ACA88667 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 26  
ID ACA70109 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 27  
ID ACD12331 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 28  
ID ACC74246 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 29  
ID ACD15874 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003027324-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 30  
ID ACD25442 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 31  
ID ACD17919 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 32  
ID ACC88206 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 33  
ID ACD21560 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 34  
ID ACD18627 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 35  
ID ACA58828 standard; cDNA; 2846 BP.  
DE cDNA encoding human secreted polypeptide PRO1344.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 36  
ID ABX98237 standard; cDNA; 2846 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 169.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 37  
ID ACD13988 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 38  
ID ACD09768 standard; cDNA; 2846 BP.

DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 39  
ID ACC88513 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 40  
ID ACD21253 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 41  
ID ABX75625 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 42  
ID ACA64004 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 43  
ID ABX97828 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 44  
ID ACA97304 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 45  
ID ACA57767 standard; cDNA; 2846 BP.  
DE Human PRO1344 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 46  
ID ACD14295 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indel: 0  
RESULT 47



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ID ACC91078 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 48
ID ACC88820 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036132-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 49
ID ACD07017 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 50
ID ACA67468 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003017542-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 51
ID ACC81523 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032137-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 52
ID ACA91268 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #19.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 53
ID ACC89127 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027269-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 54
ID ACC86483 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027268-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 55
ID ACC89741 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027274-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 56
ID ACC92920 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 57
ID ABX80775 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 58
ID ACA72548 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003022295-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 59
ID ACA89066 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003022297-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 60
ID ACA69802 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032105-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 61
ID ACA96945 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 62
ID ACA90941 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 63
ID ACA70723 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032111-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 64
ID ACA95233 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
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Best Local Similarity: 100.00% Mismatches: 0 Indels: 0  
Query Match: 100.00%  
RESULT 65  
ID ACD44284 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 66  
ID ACC86176 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 67  
ID ACD45167 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO1344 cDNA.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 68  
ID ACC90048 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 69  
ID ACD12656 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 70  
ID ACF19886 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 71  
ID ABX76830 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 72  
ID ACA73162 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 73  
ID ACA68705 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 74  
ID ACA74549 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 75  
ID ACA70416 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 76  
ID ACD14602 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 77  
ID ACA93715 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 78  
ID ACA68274 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 79  
ID ABX98739 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 80  
ID ACC81216 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 81  
ID ACA95540 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 82  
ID ACD04458 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.

```
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ACC87899 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ACF12561 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040058-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ACH66262 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ABX79455 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein cDNA, #94.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ACA96276 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003017540-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ACA65050 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032106-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ACA73776 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032129-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ACA74188 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003032131-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ACA96583 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003032131-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ACD10689 standard; cDNA; 2846 BP.
DE CDNA encoding human PRO polypeptide #85.
PN US2003032107-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ACC91385 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032139-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ACA93476 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003022187-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 95
ID ACD02720 standard; cDNA; 2846 BP.
DE CDNA encoding human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 96
ID ACC87285 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 97
ID ACC85869 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027262-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 98
ID ABX81158 standard; cDNA; 2846 BP.
DE Human secreted or transmembrane protein related PCR primer #50.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ACA65357 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032110-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ACA94174 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032110-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
```

PN US2003036142-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 101  
ID ACA97918 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 102  
ID ACA91420 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 103  
ID ACA90634 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 104  
ID ACD16181 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 105  
ID ACD17342 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 106  
ID ACC91999 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 107  
ID ACD02316 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 108  
ID ACA74856 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 109  
ID ACA91727 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.

PN US2003032128-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 110  
ID ACA71371 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 111  
ID ACC90771 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 112  
ID ACA65781 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO protein #85.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 113  
ID ACA68944 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 114  
ID ACA92974 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 115  
ID ACA94926 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 116  
ID ACD16488 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 117  
ID ACD15567 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 118  
ID ACA98466 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.

PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 119  
ID ABX17058 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 120  
ID ABX16670 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein #85.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 121  
ID ACA67913 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 122  
ID ACA63391 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #19.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 123  
ID ACA97611 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 124  
ID ACA99060 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 125  
ID ACC91692 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 126  
ID ACD11103 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 127  
ID ACD14953 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 128  
ID ACA88362 standard; cDNA; 2846 BP.  
DE Human secreted and transmembrane polypeptide PRO1344 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 129  
ID ACD81869 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 130  
ID ACD1117 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 131  
ID ACC95846 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 132  
ID ACF16409 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 133  
ID ACF02527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003045741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 134  
ID ACF02834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003045743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 135  
ID ACP21421 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 136  
ID ACF10105 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 137  
ID ACF77998 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 138  
ID ACD46703 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 139  
ID ACD49466 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 140  
ID ACF28233 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 141  
ID ACD8923 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 142  
ID ACD84318 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 143  
ID ACD99092 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.

PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 144  
ID ADA77921 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 145  
ID ACF48834 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 146  
ID ACD09154 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 147  
ID ACF11947 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 148  
ID ACF41181 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 149  
ID ACF15795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 150  
ID ACF16102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 151  
ID ADB17094 standard; cDNA; 2846 BP.  
DE Human cDNA clone (Segid 37) encoding the transmembrane PRO protein.  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 0  
RESULT 152  
ID ACD99092 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.

Query Match: 100.00% Indels: 0  
RESULT 152  
ID ACF31929 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 153  
ID ACF18737 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 154  
ID ACF09184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 155  
ID ACF78305 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 156  
ID ACF51904 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 157  
ID ACF26391 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 158  
ID ACF24184 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 159  
ID ACF63495 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 160  
ID ACD45475 standard; cDNA; 2846 BP.

ID ACF50369 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 161  
ID ACH07840 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 162  
ID ACF13646 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 163  
ID ACD41572 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 164  
ID ADA37741 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US200308297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 165  
ID ACF31985 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 166  
ID ACF23263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 167  
ID ACF39953 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 168  
ID ACD45475 standard; cDNA; 2846 BP.



DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 169  
ID ACF53132 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 170  
ID ACF27312 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 171  
ID ACF45150 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 172  
ID ACF29768 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 173  
ID ACD89844 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 174  
ID ACD84625 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 175  
ID ACD98785 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 176  
ID ACF77077 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 177  
ID ACF76770 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 178  
ID ACF49755 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 179  
ID ACF50062 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 180  
ID ADA21427 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 181  
ID ACD09461 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 182  
ID ACD08540 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 183  
ID ACH03594 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 184  
ID ACF12254 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 185  
ID ACC94762 standard; cDNA; 2846 BP.

```
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 186
ID ACD22481 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 187
ID ACF15181 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 188
ID ACC97276 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 189
ID ACC92306 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 190
ID ACF13953 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 191
ID ACF14260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 192
ID ADA10214 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1344.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 193
ID ACF09491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 194
ID ACD45782 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 195
ID ACD47931 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 196
ID ACD67662 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 197
ID ACF25470 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 198
ID ACF29154 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 199
ID ACD84932 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 200
ID ACD84011 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 201
ID ACD88002 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
```

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 202  
ID ACF30689 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003069407-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 203  
ID ACF32292 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104555-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 204  
ID ACHI1952 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049768-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 205  
ID ACHI2259 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049771-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 206  
ID ADA19899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003069394-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 207  
ID ACD40651 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032134-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 208  
ID ADB17282 standard; cDNA; 2846 BP.  
DE Human cDNA clone (SeqID 37) encoding the transmembrane PRO protein.  
PN US2003050465-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 209  
ID ADA17758 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003054987-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 210  
ID ADA17758 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2003054987-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0

ID ACF18123 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054481-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 211  
ID ACF08570 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049778-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 212  
ID ACF31371 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049782-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 213  
ID ACF52211 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054476-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 214  
ID ACD50080 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068733-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 215  
ID ACF38783 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068692-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 216  
ID ACF26698 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068709-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 217  
ID ACF24798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068716-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 218  
ID ACF46378 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068716-A1.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0

```
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 219
ID ACF27926 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 220
ID ACD89230 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 221
ID ACF63802 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 222
ID ACF60442 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 223
ID ACHI2566 standard; cDNA; 2846 BP.
DE ACHI2566 standard; cDNA; 2846 BP.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 224
ID ACH09989 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 225
ID ACD03844 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 226
ID ACD10382 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 227
ID ACD12024 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 228
ID ACF42409 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 229
ID ADA27866 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 230
ID ACF18430 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 231
ID ACF02220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 232
ID ACF21728 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 233
ID ACF10412 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 234
ID ACF33864 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 235
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ID ACF44826 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 236  
ID ACD90458 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 237  
ID ACD91071 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 238  
ID ACF30382 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 239  
ID ACD87081 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 240  
ID ACF60135 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 241  
ID ACF46685 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 242  
ID ACF75542 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 243  
ID ADA79713 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073173-A1.

PD 17-APR-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 244  
ID ACF17202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 245  
ID ACF22956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 246  
ID ACF07956 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 247  
ID ACF08263 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 248  
ID ACF40567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003084448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 249  
ID ACF53746 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 250  
ID ACD47010 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 251  
ID ACF47913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID ACF47299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068753-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 253
ID ACF46071 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068742-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 254
ID ACD86160 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068756-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 255
ID ACF52518 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082715-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 01-MAY-2003. Indels: 0
Query Match: 100.00%
RESULT 256
ID ACF52825 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003082716-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 01-MAY-2003. Indels: 0
Query Match: 100.00%
RESULT 257
ID ACF64818 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068737-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 10-APR-2003. Indels: 0
Query Match: 100.00%
RESULT 258
ID ACF76463 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104547-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 05-JUN-2003. Indels: 0
Query Match: 100.00%
RESULT 259
ID ACF61363 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003096359-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 22-MAY-2003. Indels: 0
Query Match: 100.00%
RESULT 260
ID ACF07342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049753-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 13-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 261
ID ACD30701 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032125-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 13-FEB-2003. Indels: 0
Query Match: 100.00%
RESULT 262
ID ACD31622 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054454-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 263
ID ACD32543 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003054477-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 264
ID ADA20071 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003055222-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 265
ID ACD82108 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane polypeptide PRO 1344 cDNA.
PN US2003060601-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 27-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 266
ID ACF17509 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054460-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 20-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 267
ID ADA94446 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 27-MAR-2003. Indels: 0
Query Match: 100.00%
RESULT 268
ID ACF07342 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049753-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
PD 13-MAR-2003. Indels: 0
Query Match: 100.00%
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PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 269  
ID ACF20500 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049763-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 270  
ID ACF20807 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073172-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 271  
ID ACF21114 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073172-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 272  
ID ACD47624 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068700-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 273  
ID ACF47606 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068736-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 274  
ID ACF53439 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068679-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 275  
ID ACD86774 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068767-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 276  
ID ACH05022 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003073182-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

Query Match: 100.00%  
Indels: 0

RESULT 277  
ID ACF44519 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104557-A1.  
PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 278  
ID AUA81440 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003092121-A1.  
PD 15-MAY-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 279  
ID ACD22174 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003027276-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 280  
ID ACD24521 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044920-A1.  
PD 06-MAR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 281  
ID ACD39724 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003027265-A1.  
PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 282  
ID ACD40031 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054461-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 283  
ID ACF13339 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064446-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 284  
ID ACF03141 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049744-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 285  
ID ACF78612 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.



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PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 286
ID ACD90151 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 295
ID ACD83704 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 296
ID ACF49141 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 297
ID ACH07226 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 298
ID ACH07533 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 299
ID ACH08147 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 300
ID ACH11338 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 301
ID ACH11645 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 287
ID ACF50676 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 288
ID ACF34171 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 289
ID ACD46396 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 290
ID ACD48238 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 291
ID ACF27619 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 292
ID ACF24491 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 0
RESULT 293
ID ACD85546 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
RESULT 302
ID ACH10296 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 303
ID ACF01299 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 304
ID ACF40874 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 305
ID ACD24214 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 306
ID ACD31315 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 307
ID ACF17816 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054462-A1.
PD 28-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 308
ID ADA38671 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 309
ID ACF32599 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 310
ID ACF40260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064449-A1.
Query Match: 100.00% Indels: 0
RESULT 311
ID ACF48220 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 312
ID ACF38169 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 313
ID ACF25105 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 314
ID ACF27005 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 315
ID ACF29461 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 316
ID ACD87695 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 317
ID ACF76156 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 318
ID ACF49448 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104541-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 319
ID ACF40260 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064449-A1.
```

Query Match: 100.00% Indels: 0  
RESULT 319  
ID ACF43905 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 320  
ID ACH06250 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 321  
ID ACH06557 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 322  
ID ADA83238 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 323  
ID ACC92613 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 324  
ID ACC93227 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 325  
ID ACF19272 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 326  
ID ACD12963 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 327  
ID ACF06421 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040057-A1.

PD 27-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 328  
ID ACC94455 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 329  
ID ACC97883 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 330  
ID ACC94148 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 331  
ID ACF42102 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 332  
ID ACD31008 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 333  
ID ACD43037 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 334  
ID ACD43344 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 335  
ID ACF14874 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 336  
ID ACF06421 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040057-A1.

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RESULT 336
ID ACD92792 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 337
ID ACF01606 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049738-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 338
ID ACF31678 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064469-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 339
ID ACD67355 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064453-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 340
ID ACD48545 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064466-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 341
ID ACD48852 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003064468-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 342
ID ACF51290 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068760-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 343
ID ACF54053 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068769-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 344
ID ACF25777 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068769-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 345
ID ACF39090 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068698-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 346
ID ACF28847 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068759-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 347
ID ACD90764 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049748-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 348
ID ACD86467 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003068765-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 349
ID ACH05329 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049754-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 350
ID ACF65125 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068698-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 351
ID ADB20281 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003082767-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 352
ID ACF43598 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104552-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 353
ID ACF43598 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104552-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
```

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 353  
ID ACH09068 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 354  
ID ACH09375 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 355  
ID ADA78533 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 356  
ID ACF09798 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 357  
ID ACF50983 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 358  
ID ACF23877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 359  
ID ACD88309 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 360  
ID ACH09682 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 361  
ID ACH10603 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 362  
ID ACD11410 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 363  
ID ACC96460 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 364  
ID ACC98490 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 365  
ID ACF41795 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 366  
ID ACF16716 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 367  
ID ACD32236 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 368  
ID ACD30394 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 369  
ID ACD41265 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064467-A1.

```
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 370
ID ACF07649 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 371
ID ACF31064 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 372
ID ACF77384 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 373
ID ACF11026 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 374
ID ACF32906 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 375
ID ACF26084 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 376
ID ACD83397 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 377
ID ACF23570 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 378
ID ACF42984 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 379
ID ACF43291 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 380
ID ACH05943 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO polypeptide #85.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 381
ID ACH08761 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 382
ID ACC90355 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 383
ID ACF10719 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 384
ID ACC93534 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 385
ID ACC96153 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 386
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ID ACD24828 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 387  
ID ACF01913 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 388  
ID ACF22035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 389  
ID ACF22649 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 390  
ID ACF08877 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 391  
ID ACF33213 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 392  
ID ACF54667 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 393  
ID ACF48527 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 394  
ID ACD47317 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.

PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 395  
ID ACD49159 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 396  
ID ACF37862 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 397  
ID ACF30075 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 398  
ID ACD87388 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 399  
ID ACF61977 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 400  
ID ACH10910 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 401  
ID ACD10075 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 402  
ID ACD16800 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 403  
ID ACD47317 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.



Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 403  
ID ACH65430 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 404  
ID ACC99097 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 405  
ID ACF00491 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 406  
ID ACD40958 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 407  
ID ACF14567 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 408  
ID ACF22342 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 409  
ID ACF78919 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 410  
ID ACF11640 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 411  
ID ADA22353 standard; cDNA; 2846 BP.

DE Human cDNA encoding secreted/transmembrane polypeptide PRO1344.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 412  
ID ACF51597 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 413  
ID ACF33520 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 414  
ID ACD49773 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 415  
ID ACF37555 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 416  
ID ACF28540 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 417  
ID ACD88616 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 418  
ID ACF75235 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 419  
ID ACF61056 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 420  
ID ACF44212 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 421  
ID ACH08454 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 422  
ID ACD39420 standard; DNA; 2846 BP.  
DE Human PRO 1344 PCR primer #1.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 423  
ID ACC93841 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 424  
ID ACD20946 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 425  
ID ACF06728 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 426  
ID ACD20639 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 427  
ID ACD22788 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 428  
ID ACF41488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 429  
ID ADA06519 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #65.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 430  
ID ADA39212 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 431  
ID ACF07035 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 432  
ID ACF77691 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 433  
ID ACD46089 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 434  
ID ACF46992 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 435  
ID ACF54360 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 436  
ID ACF45764 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 437  
ID ACF41488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 437  
ID ACF45457 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 438  
ID ACF38476 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 439  
ID ACD89537 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 440  
ID ACD85239 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 441  
ID ACD85853 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 442  
ID ACF75849 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 443  
ID ACF60749 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 444  
ID ACH05636 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

Query Match: 100.00% Indels: 0  
RESULT 445  
ID ADA82604 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 446  
ID ADB85610 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 447  
ID ADB96238 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 448  
ID ACF55895 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 449  
ID ACF55281 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 450  
ID ADB85912 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 451  
ID ACF56202 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 452  
ID ACF56509 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 453  
ID ADB68289 standard; cDNA; 2846 BP.

```
DE Human PRO1344 cDNA.
PN US2003065161-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 454
ID ADB68096 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060600-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 455
ID ACF55588 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068761-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 456
ID ACF54974 standard; cDNA; 2846 BP.
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.
PN US2003068771-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 457
ID ADB90913 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003083473-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 458
ID ADC57710 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003027754-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 459
ID ADC55074 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003045463-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 460
ID ADC11941 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003049681-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 461
ID ADC06993 standard; cDNA; 2846 BP.
DE Human PRO1344 cDNA.
PN US2003060602-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 462
ID ADC56363 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
PN US2003064375-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 463
ID ADC17172 standard; cDNA; 2846 BP.
DE cDNA sequence encoding a PRO polypeptide (SeqID 37).
PN US2003065143-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 464
ID ADC07418 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003068647-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 465
ID ADC11408 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003059403-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 466
ID ADC14870 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003073208-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 467
ID ADC52365 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003138882-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 468
ID ADC14530 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003082546-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 469
ID ADD08062 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003068623-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match:
RESULT 470
ID ADC81887 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #65.
```

PN US2003083461-A1.  
PD 01-MAY-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 471  
ID ADD07529 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 472  
ID ADC82420 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 473  
ID ADD05642 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 474  
ID ADD08600 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 475  
ID ADD05649 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 476  
ID ADC83096 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 477  
ID ADD55203 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003077593-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 478  
ID ADD36041 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 479  
ID ADD56161 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003077594-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 480  
ID ADD54599 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 481  
ID ADE26753 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 482  
ID ADE26220 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 483  
ID ADF67157 standard; cDNA; 2846 BP.  
DE Human PRO1344 nucleotide sequence SEQ ID NO:230.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 484  
ID ADG01042 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 485  
ID ADG08595 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 486  
ID ADG02637 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Conservative: 0  
Mismatches: 0

RESULT 487  
ID ADG01344 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207399-A1.

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PD 06-NOV-2003
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 488
ID ADF95519 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 489
ID ADF95216 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 490
ID ADG12334 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 491
ID ADH24069 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 492
ID ADH34095 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 493
ID ADH29928 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 494
ID ADH23899 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 495
ID ADH08994 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 496
ID ADG85303 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 497
ID ADH24579 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 498
ID ADH37435 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 499
ID ADH02024 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 500
ID ADH37605 standard; cDNA; 2846 BP.
DE Human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 501
ID ADG85643 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 502
ID ADH24239 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 503
ID ADH38533 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
```

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 504			
ID	ADG83654 standard; cDNA; 2846 BP.		
DE	Human PRO polynucleotide #19.		
PN	US2003180794-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 505			
ID	ADH29462 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003180860-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 506			
ID	ADH27578 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003180906-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 507			
ID	ADH37775 standard; cDNA; 2846 BP.		
DE	Human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181647-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 508			
ID	ADH37952 standard; cDNA; 2846 BP.		
DE	Human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181649-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 509			
ID	ADH57372 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003180920-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 510			
ID	ADH53514 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181636-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 511			
ID	ADH53684 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181641-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 512			
ID	ADH52020 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181638-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 513			
ID	ADH49675 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181639-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 514			
ID	ADI25385 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181696-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 515			
ID	ADH90178 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181698-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 516			
ID	ADI25555 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181669-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 517			
ID	ADH97729 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181672-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 518			
ID	ADI35411 standard; cDNA; 2846 BP.		
DE	Human PRO polynucleotide #65.		
PN	US2003050457-A1.		
PD	13-MAR-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 519			
ID	ADI03577 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181656-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 520			
ID	ADH53684 standard; cDNA; 2846 BP.		
DE	Novel human secreted and transmembrane protein PRO1344 cDNA.		
PN	US2003181641-A1.		
PD	25-SEP-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0



ID ADI11934 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 521  
ID ADH90008 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 522  
ID ADH99903 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 523  
ID ADH98409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 524  
ID ADI11084 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 525  
ID ADI11594 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 526  
ID ADH98239 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 527  
ID ADH98579 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 528  
ID ADH98069 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 529  
ID ABX78612 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 530  
ID ACA75584 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 531  
ID ACA71064 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 532  
ID ACC87592 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 533  
ID ACC86978 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 534  
ID ACD04151 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 535  
ID ABX77859 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #65.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 536  
ID AXH80271 standard; DNA; 2846 BP.  
DE Human secreted or transmembrane protein related PCR primer #50.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Query Match:  
RESULT 537  
ID ACA69177 standard; cDNA; 2846 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 538  
ID ACA69482 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO polypeptide #85.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 539  
ID ACA90327 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US200303036147-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 540  
ID ACC89434 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 541  
ID ABX90248 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein cDNA, #94.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 542  
ID ACA98225 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 543  
ID ACA93867 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 544  
ID ACD15260 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 545  
ID ACD08847 standard; cDNA; 2846 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #85.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 546  
ID ACC96767 standard; cDNA; 2846 BP.

DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 547  
ID ACF15488 standard; cDNA; 2846 BP.  
DE Human secreted polypeptide PRO1344-encoding cDNA, SEQ ID NO:169.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 548  
ID ABX64094 standard; cDNA; 2846 BP.  
DE cDNA encoding human PRO1344 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 549  
ID ACA72855 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 550  
ID ACD03027 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US200303153-A1.  
PD 16-JAN-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 551  
ID ACD01842 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 552  
ID ACA92034 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 553  
ID ADI05057 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 554  
ID ADI03407 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 555  
ID ACC96767 standard; cDNA; 2846 BP.

Query Match: 100.00% Indels: 0

RESULT 555  
ID ADI04802 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 556  
ID ADH78256 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 557  
ID ADI19600 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 558  
ID ADH90348 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 559  
ID ADI03067 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 560  
ID ADH77916 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 561  
ID ADH97899 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 562  
ID ADI01284 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 563  
ID ADI01979 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 564  
ID ADI03237 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 565  
ID ADI11424 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 566  
ID ADI02326 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 567  
ID ADI11764 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 568  
ID ADI05401 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 569  
ID ADH79473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 570  
ID ADI19430 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

RESULT 571  
ID ADI19430 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0

ID ADI05231 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 572  
ID ADH79643 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 573  
ID ADI01469 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 574  
ID ADI01639 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 575  
ID ADI01809 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 576  
ID ADH79813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 577  
ID ADI04631 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 578  
ID ADI02767 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 579  
ID ADH78086 standard; cDNA; 2846 BP.

DE Human PRO polynucleotide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 580  
ID ADI25725 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 581  
ID ADI25895 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 582  
ID ADH98749 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 583  
ID ADH79990 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 584  
ID ADL32775 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 585  
ID ADM30309 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 586  
ID ADL93721 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Query Match: 100.00%  
RESULT 587  
ID ADC52175 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.

```
PN US2003130483-AL.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 588
ID ADE74306 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211572-AL.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 589
ID ADE74918 standard; cDNA; 2846 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #85.
PN US2003211574-AL.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 590
ID ADF35356 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003194760-AL.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 591
ID ADG11606 standard; cDNA; 2846 BP.
DE cDNA encoding human PRO1344 polypeptide.
PN US2003228655-AL.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 592
ID ADF96131 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215909-AL.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 593
ID ADG04402 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215912-AL.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 594
ID ADG00562 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003215911-AL.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 595
ID ADH06607 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180852-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 596
ID ADH06437 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180853-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 597
ID ADG68858 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180855-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 598
ID ADH27748 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180912-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 599
ID ADH25089 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180913-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 600
ID ADH33721 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003181645-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 601
ID ADG82818 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #85.
PN US2003215910-AL.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 602
ID ADH02364 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180839-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 603
ID ADH07971 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180845-AL.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Indels: 0
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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RESULT 604  
ID ADG69368 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 605  
ID ADH39189 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 606  
ID ADH26099 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 607  
ID ADG83929 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 608  
ID ADH19476 standard; cDNA; 2846 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 609  
ID ADG85473 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US200316848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 610  
ID ADH06267 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 611  
ID ADH30097 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 612  
ID ADH01101 standard; cDNA; 2846 BP.

ID ADH24409 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 613  
ID ADH33068 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 614  
ID ADG69538 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 615  
ID ADH07801 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 616  
ID ADG85813 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 617  
ID ADH39359 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 618  
ID ADH33551 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 619  
ID ADH33891 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 620  
ID ADH01101 standard; cDNA; 2846 BP.

```
DE Human PRO polynucleotide #19.
PN US2003180838-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 621
ID ADG69708 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180843-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 622
ID ADH20969 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003224359-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 623
ID ADH02194 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180841-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 624
ID ADG66919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180847-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 625
ID ADG85983 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180862-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 626
ID ADH24919 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180909-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 627
ID ADH39536 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180915-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 628
ID ADH20009 standard; cDNA; 2846 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1344.
PN US2003219856-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 629
ID ADH02534 standard; cDNA; 2846 BP.
DE Human PRO polynucleotide #19.
PN US2003180840-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 630
ID ADG69028 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180849-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 631
ID ADH07631 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180850-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 632
ID ADG86153 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180863-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 633
ID ADH24749 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180908-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 634
ID ADH25797 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180911-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 635
ID ADH38363 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003180922-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 636
ID ADH57202 standard; cDNA; 2846 BP.
DE Novel human secreted and transmembrane protein PRO1344 cDNA.
PN US2003181642-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
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PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 637  
ID ADH52190 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 638  
ID ADH9556 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 639  
ID ADH90518 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 640  
ID ADH11254 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 641  
ID ADH98919 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 642  
ID ADI02149 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 643  
ID ADH90688 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 644  
ID ADJ54807 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 645  
ID ADJ98563 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181797-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 646  
ID ADJ98733 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 647  
ID ADH78892 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 648  
ID ADJ99126 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 649  
ID ADJ99296 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 650  
ID ADJ98914 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 651  
ID ADH79062 standard; cDNA; 2846 BP.  
DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 652  
ID ADK00922 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Conservative: 0  
Mismatch: 0  
Indels: 0  
RESULT 653  
ID ADJ54807 standard; cDNA; 2846 BP.  
DE Human PRO polynucleotide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0 Indels: 0  
 Query Match: 100.00%  
 RESULT 653  
 ID ADK1443 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003187229-A1.  
 PD 02-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 654  
 ID ADJ64578 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #85.  
 PN US2004038337-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 655  
 ID ADM31474 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2004048334-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 656  
 ID ADM38521 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2004053358-A1.  
 PD 18-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 657  
 ID ADM40326 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2004048335-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 658  
 ID ADM80892 standard; cDNA; 2846 BP.  
 DE Human PRO polynucleotide #19.  
 PN US2004058411-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 659  
 ID ADN37934 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2004091959-A1.  
 PD 13-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 660  
 ID ADK65407 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003073821-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 99.86%  
 Best Local Similarity: 99.86%

Query Match: 99.87% Indels: 0  
 RESULT 661  
 ID AAF74433 standard; cDNA; 2306 BP.  
 DE Human PRO2 nucleotide sequence SEQ ID NO:3.  
 PN WO200110902-A2.  
 PD 15-FEB-2001.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 99.72%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 662  
 ID AAS01222 standard; cDNA; 2306 BP.  
 DE DNA encoding human secreted protein, POLY13.  
 PN WO200119856-A2.  
 PD 22-MAR-2001.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 99.72%  
 Mismatches: 0  
 Indels: 0  
 Query Match:  
 RESULT 663  
 ID AAA39952 standard; cDNA; 2163 BP.  
 DE Human TANGO 215 coding sequence cDNA.  
 PN WO200018904-A2.  
 PD 06-APR-2000.  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 Percent Similarity: 99.86%  
 Best Local Similarity: 99.72%  
 Mismatches: 1  
 Indels: 0  
 Query Match:  
 RESULT 664  
 ID AAA39951 standard; cDNA; 2747 BP.  
 DE Human TANGO 215 cDNA.  
 PN WO200018904-A2.  
 PD 06-APR-2000.  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 Percent Similarity: 99.86%  
 Best Local Similarity: 99.72%  
 Mismatches: 1  
 Indels: 0  
 Query Match:  
 RESULT 665  
 ID ABZ3533 standard; cDNA; 2845 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 644.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 99.86%  
 Best Local Similarity: 99.86%  
 Mismatches: 0  
 Indels: 1  
 Query Match:  
 RESULT 666  
 ID ACA67289 standard; cDNA; 2848 BP.  
 DE cDNA encoding human secreted polypeptide PRO1344.  
 PN US2003027212-A1.  
 PD 08-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 99.86%  
 Best Local Similarity: 99.86%  
 Mismatches: 0  
 Indels: 1  
 Query Match:  
 RESULT 667  
 ID ACA89307 standard; cDNA; 2846 BP.  
 DE Novel human secreted and transmembrane protein PRO1344 cDNA.  
 PN US2003036634-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 99.72%  
 Best Local Similarity: 99.72%  
 Mismatches: 2  
 Indels: 0  
 Query Match:  
 RESULT 668  
 ID AAH47258 standard; cDNA; 2289 BP.  
 DE Human serine protease-like protein coding sequence.  
 PN WO200109349-A1.  
 PD 08-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 97.56%  
 Best Local Similarity: 97.56%  
 Mismatches: 1  
 Indels: 17  
 Query Match:

RESULT 669  
ID AAH47256 standard; cDNA; 2784 BP.  
DE Human serine protease-like protein encoding cDNA (hc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 97.56%  
Best Local Similarity: 97.56%  
Query Match: 99.40%  
Conservative: 0  
Mismatch: 1  
Indels: 17  
RESULT 670  
ID AAH15142 standard; cDNA; 2784 BP.  
DE Human cDNA sequence SEQ ID NO:13201.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 97.56%  
Best Local Similarity: 97.56%  
Query Match: 99.40%  
Conservative: 0  
Mismatch: 1  
Indels: 17  
RESULT 671  
ID ADN04639 standard; cDNA; 2784 BP.  
DE Antipeptidic cDNA sequence #529.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 97.56%  
Best Local Similarity: 97.56%  
Query Match: 99.40%  
Conservative: 0  
Mismatch: 1  
Indels: 17  
RESULT 672  
ID ADS85021 standard; DNA; 2784 BP.  
DE Human atopic dermatitis-related gene sequence SeqID23.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 97.56%  
Best Local Similarity: 97.56%  
Query Match: 99.40%  
Conservative: 0  
Mismatch: 1  
Indels: 17  
RESULT 673  
ID ADS85033 standard; DNA; 2784 BP.  
DE Human atopic dermatitis-related gene sequence SeqID35.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (UYJU-) UNIV JUNTENDO.  
Percent Similarity: 97.56%  
Best Local Similarity: 97.56%  
Query Match: 99.40%  
Conservative: 0  
Mismatch: 1  
Indels: 17  
RESULT 674  
ID ADH99027 standard; cDNA; 2305 BP.  
DE Human POLYX polynucleotide #13.  
PN US2003198959-A1.  
PD 23-OCT-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (PERN/) FERNANDES E.  
PA (HERR/) HERRMANN J L.  
PA (LIUX/) LIU X.  
PA (YANG/) YANG M.  
PA (BOLD/) BOLD OG F L.  
PA (SMIT/) SMITHSON G.  
PA (RASI/) RASTELLI L.  
Percent Similarity: 99.86%  
Best Local Similarity: 99.58%  
Query Match: 99.11%  
Conservative: 2  
Mismatch: 1  
Indels: 1  
RESULT 675  
ID ADL06663 standard; DNA; 2650 BP.  
DE Human 3T3 cell conversion promoter FP938 DNA.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Percent Similarity: 99.86%  
Best Local Similarity: 99.86%  
Query Match: 96.65%  
Conservative: 0  
Mismatch: 0  
Indels: 1  
RESULT 676  
ID ADL06661 standard; cDNA; 2650 BP.  
DE Human 3T3 cell conversion promoter FP938 cDNA.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Percent Similarity: 99.86%  
Best Local Similarity: 99.86%  
Query Match: 96.65%  
Conservative: 0  
Mismatch: 0  
Indels: 1  
RESULT 677  
ID AAA39985 standard; cDNA; 2823 BP.  
DE Murine TANGO 215 cDNA.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Percent Similarity: 94.86%  
Best Local Similarity: 90.28%  
Query Match: 91.69%  
Conservative: 33  
Mismatch: 37  
Indels: 0  
RESULT 678  
ID AAH47257 standard; cDNA; 2244 BP.  
DE Murine serine protease-like protein encoding cDNA (mC-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 94.72%  
Best Local Similarity: 90.14%  
Query Match: 91.56%  
Conservative: 33  
Mismatch: 38  
Indels: 0  
RESULT 679  
ID AAD30584 standard; cDNA; 2632 BP.  
DE Human protease, PRPS-17 cDNA.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 90.00%  
Best Local Similarity: 90.00%  
Query Match: 88.73%  
Conservative: 0  
Mismatch: 1  
Indels: 71  
RESULT 680  
ID ABK30334 standard; cDNA; 2886 BP.  
DE Human G-protein-coupled protease #104.  
PN US6331427-B1.  
PD 18-DEC-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 94.45%  
Best Local Similarity: 94.19%  
Query Match: 87.47%  
Conservative: 2  
Mismatch: 5  
Indels: 37  
RESULT 681  
ID AAF74432 standard; cDNA; 1867 BP.  
DE Human PRQ1 nucleotide sequence SEQ ID NO:1.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 99.31%  
Best Local Similarity: 99.31%  
Query Match: 79.40%  
Conservative: 0  
Mismatch: 3  
Indels: 2  
RESULT 682  
ID AAC90025 standard; cDNA; 2259 BP.  
DE Clone HPEY75 coding sequence.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 96.84%  
Best Local Similarity: 96.84%  
Query Match: 74.69%  
Conservative: 0  
Mismatch: 1  
Indels: 17  
RESULT 683  
ID ADR41309 standard; cDNA; 2311 BP.  
DE Human CD-like molecule HSXDF41 cDNA, SEQ ID NO:108.  
PN WO200228930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 99.27%  
Best Local Similarity: 99.27%  
Query Match: 74.63%  
Conservative: 0  
Mismatch: 4  
Indels: 0  
RESULT 684  
ID AAI59113 standard; cDNA; 2142 BP.

```
DE Human polynucleotide SEQ ID NO 1316.
PN WO200153312-A1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 685
ID AAD33261 standard; cDNA; 2142 BP.
DE DNA encoding human GPCR-like protein seqid 1006.
PN US6569662-B1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 686
ID ADB49096 standard; cDNA; 2142 BP.
DE Novel human cDNA SEQ ID NO 1006.
PN US2003104529-A1.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 687
ID AAI59076 standard; cDNA; 2144 BP.
DE Human polynucleotide SEQ ID NO 1279.
PN WO200153312-A1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 688
ID ADQ99299 standard; cDNA; 2144 BP.
DE DNA encoding human GPCR-like protein seqid 969.
PN US6569662-B1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 689
ID ADB49059 standard; cDNA; 2144 BP.
DE Novel human cDNA SEQ ID NO 969.
PN US2003104529-A1.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R.
Percent Similarity: 96.72%
Best Local Similarity: 96.72%
Query Match: 67.90%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 690
ID AAI60862 standard; cDNA; 2040 BP.
DE Human polynucleotide SEQ ID NO 4851.
PN WO200153312-A1.
PA (HYSE-) HYSQ INC.
Percent Similarity: 96.59%
Best Local Similarity: 96.59%
Query Match: 65.34%
Conservative: 0
Mismatch: 0
Indels: 17
RESULT 691
ID AAD33261 standard; cDNA; 2022 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:35.
PN WO200218435-A1.
PD 07-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 99.34%
Best Local Similarity: 99.34%
Query Match: 61.17%
Conservative: 0
Mismatch: 3
Indels: 0
RESULT 692
ID AAD33241 standard; cDNA; 1101 BP.
DE Human secreted protein-encoding gene 5 cDNA clone HSLGU75, SEQ ID NO:15.
PN WO200218435-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 94.12%
Best Local Similarity: 94.12%
Query Match: 43.31%
Conservative: 0
Mismatch: 2
Indels: 17
RESULT 693
ID AAH99144 standard; cDNA; 1058 BP.
DE Human EST-derived coding sequence SEQ ID NO: 1001.
PN WO200154477-A2.
PA (HYSE-) HYSQ INC.
Percent Similarity: 92.00%
Best Local Similarity: 90.80%
Query Match: 31.24%
Conservative: 3
Mismatch: 16
Indels: 4
RESULT 694
ID AAS86826 standard; cDNA; 1058 BP.
DE DNA encoding novel human diagnostic protein #22630.
PN WO200175067-A2.
PA (HYSE-) HYSQ INC.
Percent Similarity: 92.00%
Best Local Similarity: 90.80%
Query Match: 31.24%
Conservative: 3
Mismatch: 16
Indels: 4
RESULT 695
ID AAH08069 standard; cDNA; 705 BP.
DE Human cDNA clone (5'-primer) SEQ ID NO:4904.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Percent Similarity: 97.25%
Best Local Similarity: 97.25%
Query Match: 30.19%
Conservative: 0
Mismatch: 5
Indels: 1
RESULT 696
ID ABK30409 standard; cDNA; 505 BP.
DE Human G-protein-coupled protease #179.
PN US6331427-B1.
PD 18-DEC-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 98.81%
Best Local Similarity: 98.81%
Query Match: 22.64%
Conservative: 0
Mismatch: 1
Indels: 2
RESULT 697
ID AEN74148 standard; cDNA; 997 BP.
DE Bovine embryonic germ (EG) cell cDNA EST #199.
PN WO200194550-A2.
PD 13-DEC-2001.
PA (INFI-) INFING INC.
Percent Similarity: 86.63%
Best Local Similarity: 80.21%
Query Match: 20.82%
Conservative: 12
Mismatch: 24
Indels: 1
RESULT 698
ID AAI60899 standard; cDNA; 438 BP.
DE Human polynucleotide SEQ ID NO 4888.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSQ INC.
Percent Similarity: 97.92%
Best Local Similarity: 97.22%
Query Match: 19.04%
Conservative: 1
Mismatch: 3
Indels: 1
RESULT 699
ID ABZ58473 standard; cDNA; 3467 BP.
DE Horseshoe crab Factor C coding sequence.
PN WO2003002976-A2.
PD 09-JAN-2003.
```



PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 Percent Similarity: 94.38%  
 Best Local Similarity: 93.26%  
 Query Match: 11.99%  
 Indels: 0  
 Conservative: 1  
 Mismatches: 5

RESULT 716  
 ID AAF83985 standard; DNA; 3895 BP.  
 DE Human serine protease MASP-3 encoding DNA.  
 PN WO200140451-A2.  
 PD 07-JUN-2001.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 25.03%  
 Query Match: 11.94%  
 Indels: 214  
 Conservative: 97  
 Mismatches: 228

RESULT 717  
 ID ACN42374 standard; cDNA; 5269 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1249.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 38.76%  
 Best Local Similarity: 24.75%  
 Query Match: 11.77%  
 Indels: 214  
 Conservative: 99  
 Mismatches: 219

RESULT 718  
 ID AAH43512 standard; cDNA; 3863 BP.  
 DE cDNA encoding protease PRPS-1.  
 PN WO200171004-A2.  
 PD 27-SEP-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 38.39%  
 Best Local Similarity: 24.90%  
 Query Match: 11.69%  
 Indels: 214  
 Conservative: 97  
 Mismatches: 229

RESULT 719  
 ID AAD37042 standard; DNA; 369 BP.  
 DE Mouse limulus-clotting factor protease-like EST gene.  
 PN WO200203787-A2.  
 PD 17-JAN-2002.  
 PA (DEL-) DELTAGEN INC.  
 PA (DEL-) DELTAGEN INC.  
 Percent Similarity: 92.59%  
 Best Local Similarity: 84.26%  
 Query Match: 11.65%  
 Indels: 2  
 Conservative: 9  
 Mismatches: 8

RESULT 720  
 ID ABZ35488 standard; cDNA; 3064 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 599.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 23.01%  
 Query Match: 10.35%  
 Indels: 245  
 Conservative: 95  
 Mismatches: 259

RESULT 721  
 ID AAD24224 standard; cDNA; 2472 BP.  
 DE Human MASP-2 cDNA clone phl-4.  
 PN WO200206460-A2.  
 PD 24-JAN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 33.16%  
 Best Local Similarity: 22.98%  
 Query Match: 10.30%  
 Indels: 266  
 Conservative: 78  
 Mismatches: 246

RESULT 722  
 ID ABS52737 standard; cDNA; 2475 BP.  
 DE cDNA encoding human MASP-2 protein.  
 PN US2002082208-A1.  
 PD 27-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 33.16%  
 Best Local Similarity: 22.98%  
 Query Match: 10.27%  
 Indels: 265  
 Conservative: 78  
 Mismatches: 247

RESULT 723  
 ID AAF83985 standard; DNA; 3895 BP.  
 DE Human serine protease MASP-3 encoding DNA.  
 PN WO200140451-A2.  
 PD 07-JUN-2001.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 25.03%  
 Query Match: 11.94%  
 Indels: 214  
 Conservative: 97  
 Mismatches: 228

ID ADP65502 standard; DNA; 2386 BP.  
 DE Human mRNA for complement component C1r DNA.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Percent Similarity: 34.64%  
 Best Local Similarity: 22.59%  
 Query Match: 10.23%  
 Indels: 265  
 Conservative: 95  
 Mismatches: 250

RESULT 724  
 ID ADP65013 standard; DNA; 2386 BP.  
 DE Human complement component 1, r subcomponent (C1R) DNA sequence.  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Percent Similarity: 34.64%  
 Best Local Similarity: 22.59%  
 Query Match: 10.23%  
 Indels: 265  
 Conservative: 95  
 Mismatches: 250

RESULT 725  
 ID ADR24793 standard; DNA; 2386 BP.  
 DE Breast cancer prognosis marker #654.  
 PN WO2004055545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Percent Similarity: 34.64%  
 Best Local Similarity: 22.59%  
 Query Match: 10.23%  
 Indels: 265  
 Conservative: 95  
 Mismatches: 250

RESULT 726  
 ID AAX24297 standard; cDNA; 2492 BP.  
 DE Human complement component 1, subcomponent r (c1r) cDNA.  
 PN WO9907896-A2.  
 PD 18-FEB-1999.  
 PA (CURA-) CURAGEN CORP.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 22.88%  
 Query Match: 10.23%  
 Indels: 245  
 Conservative: 96  
 Mismatches: 259

RESULT 727  
 ID ABA83114 standard; DNA; 2493 BP.  
 DE Complement component 1 r ovarian tumour marker gene, SEQ ID NO:65.  
 PN WO200175177-A2.  
 PD 11-OCT-2001.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 22.88%  
 Query Match: 10.23%  
 Indels: 245  
 Conservative: 96  
 Mismatches: 259

RESULT 728  
 ID AEN95758 standard; DNA; 2493 BP.  
 DE Gene #2256 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 22.88%  
 Query Match: 10.23%  
 Indels: 245  
 Conservative: 96  
 Mismatches: 259

RESULT 729  
 ID ABX63613 standard; cDNA; 2555 BP.  
 DE Human cDNA #613 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 PA (BAND/) BANDMAN O.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 22.88%  
 Query Match: 10.23%  
 Indels: 245  
 Conservative: 96  
 Mismatches: 259

RESULT 730  
 ID ADJ56217 standard; cDNA; 2555 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 23.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA/) STUART S G.  
 PA (NUCH/) NUCHTERN J G.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 22.88%  
 Query Match: 10.23%  
 Indels: 245  
 Conservative: 96  
 Mismatches: 259

RESULT 731  
 ID AAF83985 standard; DNA; 3895 BP.  
 DE Human serine protease MASP-3 encoding DNA.  
 PN WO200140451-A2.  
 PD 07-JUN-2001.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 25.03%  
 Query Match: 11.94%  
 Indels: 214  
 Conservative: 97  
 Mismatches: 228

RESULT 732  
 ID AAF83985 standard; DNA; 3895 BP.  
 DE Human serine protease MASP-3 encoding DNA.  
 PN WO200140451-A2.  
 PD 07-JUN-2001.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 25.03%  
 Query Match: 11.94%  
 Indels: 214  
 Conservative: 97  
 Mismatches: 228

RESULT 733  
 ID AAF83985 standard; DNA; 3895 BP.  
 DE Human serine protease MASP-3 encoding DNA.  
 PN WO200140451-A2.  
 PD 07-JUN-2001.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 38.53%  
 Best Local Similarity: 25.03%  
 Query Match: 11.94%  
 Indels: 214  
 Conservative: 97  
 Mismatches: 228

Best Local Similarity: 22.88% Mismatches: 259  
 Query Match: 10.23% Indels: 245  
 RESULT 731  
 ID ADQ27012 standard; cDNA; 2061 BP.  
 DE Human MASP-2 polypeptide cDNA sequence.  
 PN WO2004050907-A2.  
 PD 17-JUN-2004.  
 PA (UYAA-) UNIV AARHUS.  
 PA (AARH) AARHUS AMT.  
 Percent Similarity: 33.03%  
 Best Local Similarity: 22.67%  
 Query Match: 10.18%  
 Indels: 267  
 RESULT 732  
 ID ABK90781 standard; cDNA; 2476 BP.  
 DE cDNA encoding Mannan-binding lectin associated serine protease-2.  
 PN US2002082209-A1.  
 PD 27-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 PA (THIE/) THIEL S.  
 Percent Similarity: 32.63%  
 Best Local Similarity: 22.80%  
 Query Match: 10.14%  
 Indels: 259  
 RESULT 733  
 ID ADQ21819 standard; DNA; 286 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4638.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 80.61%  
 Best Local Similarity: 79.59%  
 Query Match: 10.05%  
 Indels: 15  
 RESULT 734  
 ID ABN95607 standard; DNA; 2647 BP.  
 DE Gene #2105 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 32.95%  
 Best Local Similarity: 21.77%  
 Query Match: 8.90%  
 Indels: 301  
 RESULT 735  
 ID ADJ74872 standard; DNA; 2647 BP.  
 DE Marker gene SEQ ID NO:124.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Percent Similarity: 32.95%  
 Best Local Similarity: 21.77%  
 Query Match: 8.90%  
 Indels: 301  
 RESULT 736  
 ID ADR24794 standard; DNA; 2647 BP.  
 DE Breast cancer prognosis marker #655.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Percent Similarity: 32.95%  
 Best Local Similarity: 21.77%  
 Query Match: 8.90%  
 Indels: 301  
 RESULT 737  
 ID ACN39359 standard; cDNA; 2647 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA88114, SEQ ID NO:3452.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.95%  
 Best Local Similarity: 21.77%  
 Query Match: 8.90%  
 Indels: 301  
 RESULT 738  
 ID ABX63472 standard; cDNA; 2659 BP.  
 DE Human cDNA #472 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.

PA (BAND/) BANDMAN O.  
 Percent Similarity: 33.14%  
 Best Local Similarity: 21.90%  
 Query Match: 8.87%  
 Indels: 308  
 RESULT 739  
 ID ADJ56209 standard; cDNA; 2659 BP.  
 DE Human cDNA differentially expressed in MYCN activated cells SeqID 15.  
 PN US2003119009-A1.  
 PD 26-JUN-2003.  
 PA (STUA/) STUART S G.  
 PA (NUCH/) NUCHTERN J G.  
 PA (PLOW/) PLOW S E.  
 PA (SHOH/) SHOHET J M.  
 Percent Similarity: 33.14%  
 Best Local Similarity: 21.90%  
 Query Match: 8.87%  
 Indels: 308  
 RESULT 740  
 ID ADQ85290 standard; cDNA; 2648 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2104.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 33.03%  
 Best Local Similarity: 21.90%  
 Query Match: 8.85%  
 Indels: 308  
 RESULT 741  
 ID ADQ84481 standard; cDNA; 2648 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #1295.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 33.03%  
 Best Local Similarity: 21.90%  
 Query Match: 8.85%  
 Indels: 308  
 RESULT 742  
 ID ADE53754 standard; cDNA; 7149 BP.  
 DE Human prostate cancer cDNA #101.  
 PN US2003190640-A1.  
 PD 09-OCT-2003.  
 PA (FARI/) FARIS M.  
 PA (PEAR/) PEARSON C I.  
 Percent Similarity: 32.83%  
 Best Local Similarity: 21.89%  
 Query Match: 8.83%  
 Indels: 305  
 RESULT 743  
 ID AAH99569 standard; cDNA; 3115 BP.  
 DE Human protein encoding cDNA sequence SEQ ID NO:404.  
 PN WO200153455-A2.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 36.16%  
 Best Local Similarity: 24.21%  
 Query Match: 8.80%  
 Indels: 169  
 RESULT 744  
 ID ABA08672 standard; cDNA; 3115 BP.  
 DE Human membrane-type Ser kinase homologue cDNA, SEQ ID NO:448.  
 PN WO200157188-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 36.16%  
 Best Local Similarity: 24.21%  
 Query Match: 8.80%  
 Indels: 169  
 RESULT 745  
 ID ADL64960 standard; DNA; 2647 BP.  
 DE DNA encoding human complement component 1 protein, CIS.  
 PN US2004033582-A1.  
 PD 19-FEB-2004.  
 PA (EDMO/) EDMONDS M.  
 PA (HUIL/) HUI L.



PA (PERE/) PERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAMA/) RAMANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERB/) ZERBA K.  
Percent Similarity: 33.22%  
Best Local Similarity: 21.76%  
Query Match: 8.77%  
Conservative: 99  
Mismatches: 284  
Indels: 293  
RESULT 746  
ID AAC77788 standard; cDNA; 2725 BP.  
DE Human cancer associated gene sequence SEQ ID NO:182.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 32.45%  
Best Local Similarity: 21.33%  
Query Match: 8.67%  
Conservative: 97  
Mismatches: 286  
Indels: 303  
RESULT 747  
ID ABK63441 standard; cDNA; 2908 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1348.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.71%  
Best Local Similarity: 21.34%  
Query Match: 8.63%  
Conservative: 98  
Mismatches: 248  
Indels: 278  
RESULT 748  
ID ADB58967 standard; DNA; 2908 BP.  
DE Toxicity-related gene, SEQ ID 3993.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.71%  
Best Local Similarity: 21.34%  
Query Match: 8.63%  
Conservative: 98  
Mismatches: 248  
Indels: 278  
RESULT 749  
ID ADB53715 standard; DNA; 2908 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4257.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.71%  
Best Local Similarity: 21.34%  
Query Match: 8.63%  
Conservative: 98  
Mismatches: 248  
Indels: 278  
RESULT 750  
ID APT41719 standard; DNA; 2908 BP.  
DE Toxicity modelling related rat gene SEQ ID No 1421.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.71%  
Best Local Similarity: 21.34%  
Query Match: 8.63%  
Conservative: 98  
Mismatches: 248  
Indels: 278  
RESULT 751  
ID AAS92433 standard; cDNA; 2358 BP.  
DE DNA encoding novel human diagnostic protein #28237.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 35.86%  
Best Local Similarity: 22.85%  
Query Match: 8.57%  
Conservative: 103  
Mismatches: 288  
Indels: 221  
RESULT 752  
ID AAA88492 standard; cDNA; 2955 BP.  
DE Human matrixase (truncated form) cDNA.  
PN WO200053232-A1.  
PD 14-SEP-2000.  
PA (GEOU) UNIV GEORGETOWN.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 753

ID AAF28099 standard; cDNA; 3142 BP.  
DE Human membrane-type serine protease MT-SPI coding sequence.  
PN WO200123524-A2.  
PD 05-APR-2001.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 754  
ID AAA88493 standard; cDNA; 3149 BP.  
DE Human matrixase cDNA.  
PN WO200053232-A1.  
PD 14-SEP-2000.  
PA (GEOU) UNIV GEORGETOWN.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 755  
ID ADN39650 standard; cDNA; 3149 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C22.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 756  
ID ADR24296 standard; DNA; 3149 BP.  
DE Breast cancer prognosis marker #157.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 757  
ID AAH57431 standard; cDNA; 3152 BP.  
DE Human intestine cell specific cDNA sequence SEQ ID NO:271.  
PN WO200132927-A2.  
PD 10-MAY-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 758  
ID AAA37657 standard; DNA; 3159 BP.  
DE Human peptidase, HPEP-1 coding sequence.  
PN WO200042201-A2.  
PD 20-JUL-2000.  
PA (INCY-) INCYTE PHARM INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 759  
ID ADN04753 standard; cDNA; 3269 BP.  
DE Antipsoriatic cDNA sequence #590.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 760  
ID ADP23333 standard; cDNA; 3269 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:427.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatches: 238  
Indels: 170  
RESULT 761

ID ADR66212 standard; DNA; 3269 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 66 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatch: 238  
Indels: 170  
RESULT 762  
ID ADR66554 standard; DNA; 3269 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 66 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.33%  
Query Match: 8.53%  
Conservative: 75  
Mismatch: 238  
Indels: 170  
RESULT 763  
ID ADI16507 standard; cDNA; 2838 BP.  
DE Human NOVX cDNA to treat human pathological conditions SeqID43.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 764  
ID ADF90776 standard; DNA; 3128 BP.  
DE Human hepatic-fibrosis disease marker SEQ ID 238.  
PN JP2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU-) SUMITOMO SEIYAKU KK.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 765  
ID AAX87815 standard; cDNA; 3147 BP.  
DE Tumour antigen derived gene-15 (TAGD-15) cDNA.  
PN WO942120-A1.  
PD 26-AUG-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 766  
ID AAH23609 standard; RNA; 3147 BP.  
DE Human TAGD-15 antisense RNA sequence.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 767  
ID AAH23601 standard; DNA; 3147 BP.  
DE Human TAGD-15 coding sequence.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 768  
ID AAD13155 standard; DNA; 3147 BP.  
DE Human membrane-type serine protease (MTSP) 1 protease domain DNA.

PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 769  
ID AAD13113 standard; DNA; 3147 BP.  
DE Human membrane-type serine protease (MTSP) 1 DNA.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 770  
ID AAL53444 standard; DNA; 3147 BP.  
DE Type II transmembrane serine protease 1 coding DNA SEQ ID No 1.  
PN WO200272786-A2.  
PD 19-SEP-2002.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 771  
ID AAL53445 standard; DNA; 3147 BP.  
DE Type II transmembrane serine protease 1 domain DNA SEQ ID No 3.  
PN WO200272786-A2.  
PD 19-SEP-2002.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 772  
ID ABZ22450 standard; cDNA; 3147 BP.  
DE Human membrane-type serine protease MTSP1 encoding cDNA SEQ ID NO:1.  
PN WO200292841-A2.  
PD 21-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 773  
ID ABZ22451 standard; cDNA; 3147 BP.  
DE Human MTSP1 protease domain encoding cDNA SEQ ID NO:3.  
PN WO200292841-A2.  
PD 21-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 774  
ID AAL60793 standard; DNA; 3147 BP.  
DE Human membrane-type serine protease MTSP1 protease domain DNA.  
PN WO2003044179-A2.  
PD 30-MAY-2003.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 775  
ID AAL60792 standard; DNA; 3147 BP.  
DE Human membrane-type serine protease MTSP1 DNA.  
PN WO2003044179-A2.  
PD 30-MAY-2003.  
PA (CORV-) CORVAS INT INC.  
Percent Similarity: 36.11%  
Best Local Similarity: 24.49%  
Query Match: 8.50%  
Conservative: 74  
Mismatch: 238  
Indels: 170  
RESULT 776  
ID RAD47225 standard; DNA; 3147 BP.  
DE Human membrane-type serine protease 1 (MTSP1) DNA.  
PN WO200277267-A2.

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PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
RESULT 777
ID AAD47181 standard; DNA; 3147 BP.
DE Human membrane-type serine protease (MTSP1) protease domain DNA.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
RESULT 778
ID AAD47180 standard; DNA; 3147 BP.
DE Human membrane-type serine protease, MTSP1 DNA.
PN WO200277263-A2.
PD 03-OCT-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 779
ID ABZ58500 standard; cDNA; 3147 BP.
DE Transmembrane serine protease 1 (MTSP1) cDNA.
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 780
ID ABZ58501 standard; cDNA; 3147 BP.
DE Transmembrane serine protease 1 (MTSP1) protein domain cDNA.
PN WO2003004681-A2.
PD 16-JAN-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 781
ID ADB97550 standard; DNA; 3147 BP.
DE Human MTSP1-encoding DNA, SEQ ID NO:1.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 782
ID ADB97552 standard; DNA; 3147 BP.
DE Human MTSP1 protease domain-encoding DNA, SEQ ID NO:3.
PN WO2003031585-A2.
PD 17-APR-2003.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 783
ID ADI10370 standard; DNA; 3147 BP.
DE Human cell surface protease coding sequence #1.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 784
ID ADG65325 standard; cDNA; 3147 BP.
DE Human MTSP1 coding sequence.
PN WO2003104394-A2.
PD 18-DEC-2003.
PA (DEND-) DENDREON SAN DIEGO LLC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Indels: 170
RESULT 785
ID ADI28860 standard; cDNA; 3147 BP.
DE Human matriptase (MTSP1) nucleotide sequence.
PN WO2004005471-A2.
PD 15-JAN-2004.
PA (DEND-) DENDREON SAN DIEGO LLC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 786
ID ADJ46894 standard; cDNA; 3147 BP.
DE Human transmembrane serine protease (MTSP) cDNA #1.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 36.11%
Best Local Similarity: 24.49%
Query Match: 8.50%
Conservative: 74
Mismatch: 238
Indels: 170
RESULT 787
ID ADE53755 standard; cDNA; 3145 BP.
DE Human prostate cancer cDNA #102.
PN US2003190640-A1.
PD 09-OCT-2003.
PA (FARI/) FARIS M.
PA (PEAR/) PEARSON C I.
Percent Similarity: 34.47%
Best Local Similarity: 22.66%
Query Match: 8.48%
Conservative: 97
Mismatch: 309
Indels: 230
RESULT 788
ID RAD13165 standard; DNA; 3696 BP.
DE Human enterokinase DNA.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 789
ID ADA83984 standard; DNA; 3696 BP.
DE Human PRSS7 gene.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 790
ID ADI10399 standard; DNA; 3696 BP.
DE Human cell surface protease coding sequence #16.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 791
ID ADJ46923 standard; cDNA; 3696 BP.
DE Human transmembrane serine protease (MTSP)-related cDNA #6.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 38.05%
Best Local Similarity: 22.90%
Query Match: 8.40%
Conservative: 90
Mismatch: 225
Indels: 143
RESULT 792
ID ADH72215 standard; DNA; 10989 BP.
DE Human gene of the invention NOV54b SEQ ID NO:1111.
PN WO2003102155-A2.
PD 11-DEC-2003.

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PA (CURA-) CURAGEN CORP.	Conservative: 93	PA (ROSE/) ROSEN C A.	Conservative: 68
Percent Similarity: 32.74%	Mismatches: 239	Best Local Similarity: 35.13%	Mismatches: 196
Best Local Similarity: 20.84%	Indels: 287	Query Match: 8.30%	Indels: 177
Query Match: 8.35%		RESULT 801	
RESULT 793		ID ADH71143 standard; DNA; 10466 BP.	
ID ABS58378 standard; DNA; 4506 BP.		DE Human gene of the invention NOV4e	SEQ ID NO:39.
DE Protein modification and maintenance molecule #11.		PN WO2003102155-A2.	
PD 08-AUG-2002.		PD 11-DEC-2003.	
PA (INCY-) INCYTE GENOMICS INC.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.26%	Indels: 293
Query Match: 8.33%		RESULT 802	
RESULT 794		ID ADH71135 standard; DNA; 10655 BP.	
ID AAS18801 standard; cDNA; 5598 BP.		DE Human gene of the invention NOV4a	SEQ ID NO:31.
DE DNA encoding cancer and neurogenesis associated gene.		PN WO2003102155-A2.	
PD 29-NOV-2001.		PD 11-DEC-2003.	
PA (UYLE-) UNIV LEEDS.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.26%	Indels: 293
Query Match: 8.33%		RESULT 803	
RESULT 795		ID ADH71145 standard; DNA; 12900 BP.	
ID AAS18804 standard; cDNA; 5667 BP.		DE Human gene of the invention NOV4f	SEQ ID NO:41.
DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V3.		PN WO2003102155-A2.	
PD 29-NOV-2001.		PD 11-DEC-2003.	
PA (UYLE-) UNIV LEEDS.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.26%	Indels: 293
Query Match: 8.33%		RESULT 804	
RESULT 796		ID AAH23602 standard; DNA; 2900 BP.	
ID AAS18802 standard; cDNA; 6145 BP.		DE Human gene of the invention NOV4i	SEQ ID NO:41.
DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V1.		PN WO200129056-A1.	
PD 29-NOV-2001.		PD 26-APR-2001.	
PA (UYLE-) UNIV LEEDS.		PA (UYAR-) UNIV ARKANSAS.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 37.93%	Conservative: 79
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 25.55%	Mismatches: 225
Query Match: 8.33%	Indels: 287	Query Match: 8.21%	Indels: 174
Query Match: 8.33%		RESULT 805	
RESULT 797		ID ABK84260 standard; cDNA; 2900 BP.	
ID AAS18803 standard; cDNA; 6409 BP.		DE Human cDNA differentially expressed in granulocytic cells #831.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5G-3V2.		PN WO200228999-A2.	
PD 29-NOV-2001.		PD 11-APR-2002.	
PA (UYLE-) UNIV LEEDS.		PA (GENE-) GENE LOGIC INC.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 37.93%	Conservative: 79
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 25.55%	Mismatches: 225
Query Match: 8.33%	Indels: 287	Query Match: 8.21%	Indels: 174
Query Match: 8.33%		RESULT 806	
RESULT 798		ID AAD33319 standard; cDNA; 12525 BP.	
ID AAS18805 standard; cDNA; 7323 BP.		DE Rat C3b/C4b complement receptor like cDNA.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5R-3V2.		PN WO200210199-A2.	
PD 29-NOV-2001.		PD 07-FEB-2002.	
PA (UYLE-) UNIV LEEDS.		PA (AMGE-) AMGEN INC.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 32.94%	Conservative: 94
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 20.50%	Mismatches: 222
Query Match: 8.33%	Indels: 287	Query Match: 8.21%	Indels: 286
Query Match: 8.33%		RESULT 807	
RESULT 799		ID ABS64376 standard; DNA; 8010 BP.	
ID AAS18806 standard; cDNA; 8034 BP.		DE Human cub and sushi domain containing gene #2.	
DE DNA encoding cancer and neurogenesis associated gene, variant 5R23V2.		PN WO200264791-A2.	
PD 29-NOV-2001.		PD 22-AUG-2002.	
PA (UYLE-) UNIV LEEDS.		PA (CURA-) CURAGEN CORP.	
Percent Similarity: 32.74%	Conservative: 93	Percent Similarity: 31.76%	Conservative: 78
Best Local Similarity: 20.84%	Mismatches: 239	Best Local Similarity: 22.30%	Mismatches: 270
Query Match: 8.33%	Indels: 287	Query Match: 8.19%	Indels: 293
Query Match: 8.33%		RESULT 808	
RESULT 800		ID ADH71139 standard; DNA; 8010 BP.	
ID AAF18150 standard; DNA; 2063 BP.		DE Human gene of the invention NOV4c	SEQ ID NO:35.
DE Lung cancer associated polynucleotide sequence SEQ ID 169.		PN WO2003102155-A2.	
PD 21-SEP-2000.		PD 11-DEC-2003.	
PA (HUMA-) HUMAN GENOME SCI INC.		PA (CURA-) CURAGEN CORP.	

Percent Similarity: 31.76% Conservative: 78  
Best Local Similarity: 22.30% Mismatches: 270  
Query Match: 8.19% Indels: 293  
RESULT 809  
ID ADH71141 standard; DNA; 9951 BP.  
DE Human gene of the invention NOV4d SEQ ID NO:37.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 31.76% Conservative: 78  
Best Local Similarity: 22.30% Mismatches: 270  
Query Match: 8.19% Indels: 293  
RESULT 810  
ID ABS64375 standard; DNA; 10136 BP.  
DE Human cub and sushi domain containing gene #1.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 31.76% Conservative: 78  
Best Local Similarity: 22.30% Mismatches: 270  
Query Match: 8.19% Indels: 293  
RESULT 811  
ID ADH71165 standard; DNA; 10136 BP.  
DE Human gene of the invention NOV4p SEQ ID NO:61.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 31.76% Conservative: 78  
Best Local Similarity: 22.30% Mismatches: 270  
Query Match: 8.19% Indels: 293  
RESULT 812  
ID ADH71137 standard; DNA; 10136 BP.  
DE Human gene of the invention NOV4b SEQ ID NO:33.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 31.76% Conservative: 78  
Best Local Similarity: 22.30% Mismatches: 270  
Query Match: 8.19% Indels: 293  
RESULT 813  
ID ADH71167 standard; DNA; 10136 BP.  
DE Human gene of the invention NOV4q SEQ ID NO:63.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 31.76% Conservative: 78  
Best Local Similarity: 22.30% Mismatches: 270  
Query Match: 8.19% Indels: 293  
RESULT 814  
ID AAD33320 standard; cDNA; 10433 BP.  
DE Human C3b/C4b complement receptor like cDNA #2.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Percent Similarity: 32.48% Conservative: 92  
Best Local Similarity: 20.72% Mismatches: 241  
Query Match: 8.12% Indels: 287  
RESULT 815  
ID AAD33318 standard; cDNA; 10673 BP.  
DE Human C3b/C4b complement receptor like cDNA #1.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Percent Similarity: 32.48% Conservative: 92  
Best Local Similarity: 20.72% Mismatches: 241  
Query Match: 8.12% Indels: 287  
RESULT 816  
ID ADG83835 standard; cDNA; 1401 BP.  
DE Rough scale snake venom protease coding sequence.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU-) UNIV QUEENSLAND.  
Percent Similarity: 37.66% Conservative: 79

Best Local Similarity: 23.42% Mismatches: 183  
Query Match: 8.10% Indels: 163  
RESULT 817  
ID AAC77957 standard; cDNA; 2756 BP.  
DE Human cancer associated gene sequence SEQ ID NO:351.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.89% Conservative: 82  
Best Local Similarity: 24.02% Mismatches: 233  
Query Match: 8.07% Indels: 171  
RESULT 818  
ID AAD37039 standard; DNA; 3106 BP.  
DE Epithin gene.  
PN WO200203787-A2.  
PD 17-JAN-2002.  
PA (DELT-) DELTAGEN INC.  
Percent Similarity: 34.74% Conservative: 81  
Best Local Similarity: 22.92% Mismatches: 245  
Query Match: 8.07% Indels: 204  
RESULT 819  
ID AAQ70104 standard; cDNA; 2581 BP.  
DE Bovine enterokinase.  
PN WO9416083-A1.  
PD 21-JUL-1994.  
PA (GEMY-) GENETICS INST INC.  
Percent Similarity: 38.05% Conservative: 80  
Best Local Similarity: 24.58% Mismatches: 225  
Query Match: 8.05% Indels: 143  
RESULT 820  
ID ADG83831 standard; cDNA; 1365 BP.  
DE Red belly black snake venom protease coding sequence.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU-) UNIV QUEENSLAND.  
Percent Similarity: 36.25% Conservative: 73  
Best Local Similarity: 22.95% Mismatches: 189  
Query Match: 7.97% Indels: 161  
RESULT 821  
ID ADG83833 standard; cDNA; 1395 BP.  
DE Mainland tiger snake venom protease coding sequence.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU-) UNIV QUEENSLAND.  
Percent Similarity: 37.07% Conservative: 78  
Best Local Similarity: 22.97% Mismatches: 187  
Query Match: 7.97% Indels: 161  
RESULT 822  
ID AAQ12680 standard; DNA; 1529 BP.  
DE PAP-I-protein C fusion construct.  
PN WO9109953-A.  
PD 11-JUL-1991.  
PA (ZYMO-) ZYMOGENETICS INC.  
Percent Similarity: 35.98% Conservative: 68  
Best Local Similarity: 23.99% Mismatches: 182  
Query Match: 7.93% Indels: 182  
RESULT 823  
ID AAA54035 standard; DNA; 1843 BP.  
DE Human protein C coding sequence.  
PN WO200054787-A1.  
PD 21-SEP-2000.  
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.  
Percent Similarity: 34.99% Conservative: 68  
Best Local Similarity: 24.42% Mismatches: 220  
Query Match: 7.92% Indels: 199  
RESULT 824  
ID AAF54050 standard; DNA; 1843 BP.  
DE Human protein C gene, SEQ ID NO:49.  
PN WO200075279-A2.  
PD 14-DEC-2000.  
PA (UNMI-) UNIV MICHIGAN.  
Percent Similarity: 34.99% Conservative: 68

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Best Local Similarity: 24.42% Mismatches: 220
Query Match: 7.92% Indels: 199
RESULT 825
ID AHN97175 standard; DNA; 1843 BP.
DE Gene #3673 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 34.99% Conservative: 68
Best Local Similarity: 24.42% Mismatches: 220
Query Match: 7.92% Indels: 199
RESULT 826
ID ADN42161 standard; cDNA; 2838 BP.
DE Human cDNA encoding NOV 8.
PN US2004033493-A1.
PD 19-FEB-2004.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELDI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
Percent Similarity: 36.26% Conservative: 72
Best Local Similarity: 24.96% Mismatches: 238
Query Match: 7.92% Indels: 170
RESULT 827
ID AAH26365 standard; cDNA; 1386 BP.
DE DNA encoding human protein C derivative.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.36% Conservative: 64
Best Local Similarity: 24.96% Mismatches: 176
Query Match: 7.91% Indels: 182
RESULT 828
ID ABO86158 standard; DNA; 3096 BP.
DE Novel human gene. SEQ ID 29.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK/) SMITHKLINE BEECHAM CORP.
PA (SMIK/) SMITHKLINE BEECHAM PLC.
PA (GLAX/) GLAXO GROUP LTD.
Percent Similarity: 34.63% Conservative: 87
Best Local Similarity: 22.58% Mismatches: 278
Query Match: 7.91% Indels: 194
RESULT 829
ID AAN81563 standard; cDNA; 1756 BP.
DE cDNA sequence encoding protein C.
PN EP266190-A.
PD 04-MAY-1988.
PA (ZYMO/) ZYMOGENETICS INC.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.90% Indels: 181
RESULT 830
ID ADB63780 standard; cDNA; 2580 BP.
DE

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DE Human cDNA encoding clone UTERU20087070.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 34.49% Conservative: 110
Best Local Similarity: 21.32% Mismatches: 258
Query Match: 7.90% Indels: 258
RESULT 831
ID AAH26363 standard; cDNA; 1386 BP.
DE DNA encoding human protein C derivative.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.36% Conservative: 64
Best Local Similarity: 24.96% Mismatches: 176
Query Match: 7.88% Indels: 182
RESULT 832
ID AAH26366 standard; cDNA; 1386 BP.
DE DNA encoding human protein C derivative.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.36% Conservative: 64
Best Local Similarity: 24.96% Mismatches: 176
Query Match: 7.88% Indels: 182
RESULT 833
ID AAZ46750 standard; DNA; 1245 BP.
DE Truncated human protein C polypeptide encoding DNA.
PN WO9963070-A1.
PD 09-DEC-1999.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 834
ID AAK86039 standard; DNA; 1257 BP.
DE Synthetic DNA encoding zymogen protein C.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 835
ID ADO18784 standard; DNA; 1257 BP.
DE Mature human zymogen-like protein C coding sequence.
PN WO2004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 836
ID AAN60001 standard; DNA; 1260 BP.
DE Sequence encoding polypeptide with human protein C activity.
PN EP191606-A.
PD 20-AUG-1986.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181
RESULT 837
ID AAH26361 standard; cDNA; 1260 BP.
DE DNA encoding human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL/) LILLY & CO ELI.
Percent Similarity: 36.12% Conservative: 61
Best Local Similarity: 25.05% Mismatches: 172
Query Match: 7.87% Indels: 181

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RESULT 838
ID AAC83311 standard; DNA; 1260 BP.
DE DNA encoding human protein C derivative 1.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 839
ID AAD15223 standard; DNA; 1260 BP.
DE Human mature wild type protein C encoding DNA.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 840
ID AAK86038 standard; DNA; 1383 BP.
DE Synthetic DNA encoding protein C precursor protein.
PN WO200232461-A2.
PD 25-APR-2002.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 841
ID ADM77501 standard; DNA; 1383 BP.
DE Human protein C wild-type gene sequence.
PN WO2003106666-A2.
PD 24-DEC-2003.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 842
ID ADO18785 standard; DNA; 1383 BP.
DE Human zymogen-like protein C coding sequence.
PN WO2004044190-A2.
PD 27-MAY-2004.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 843
ID AAN81408 standard; DNA; 1386 BP.
DE DNA encoding human protein C.
PN JP63263083-A.
PD 31-OCT-1988.
PA (FARH ) HOECHST JAPAN LTD.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 844
ID AAN90187 standard; DNA; 1386 BP.
DE DNA encoding zymogen form of human protein C.
PN EP323149-A.
PD 05-JUL-1989.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 845
ID AAR79724 standard; DNA; 1386 BP.
DE Human protein C cdna.
PN WO9720043-A1.
PD 05-JUN-1997.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 846
ID AAH26362 standard; cDNA; 1386 BP.
DE DNA encoding human protein C.
PN WO200157193-A2.
PD 09-AUG-2001.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 847
ID RAC83313 standard; DNA; 1386 BP.
DE DNA encoding human protein C derivative 3.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 848
ID AAC83312 standard; DNA; 1386 BP.
DE DNA encoding human protein C derivative 2.
PN WO200066754-A1.
PD 09-NOV-2000.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 849
ID RAD15224 standard; DNA; 1386 BP.
DE Human wild type protein C encoding DNA.
PN WO200159084-A1.
PD 16-AUG-2001.
PA (ELIL ) LILLY & CO ELI.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 850
ID RAQ13357 standard; cDNA; 1754 BP.
DE Human protein C gene.
PN WO9112320-A.
PD 22-AUG-1991.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 851
ID AAQ12649 standard; cDNA; 1754 BP.
DE Protein C precursor gene.
PN WO9109951-A.
PD 11-JUL-1991.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 852
ID AAQ12678 standard; cDNA; 1755 BP.
DE Human protein C.
PN WO9109953-A.
PD 11-JUL-1991.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 36.12%
Best Local Similarity: 36.12%
Conservative: 61
Query Match: 25.05%
Mismatch: 172
Indels: 181
RESULT 853
ID AAR32795 standard; cDNA; 1755 BP.
DE Human protein C cdna.
PN US5516650-A.
PD 14-MAY-1996.
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Best Local Similarity: 22.85%  
Query Match: 7.63%  
Mismatches: 211  
Indels: 205

RESULT 870  
ID AAN60598 standard; DNA; 2459 BP.  
DE Sequence encoding plasmid pDPAP3.  
PN JP61139386-A.  
PD 26-JUN-1986.  
PA (TOYU ) TOYO SODA MFG CO LTD.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (CENG ) CENTRAL GLASS CO LTD.  
PA (HODO ) HODOGAYA CHEM IND CO LTD.  
Percent Similarity: 35.31%  
Best Local Similarity: 22.81%  
Query Match: 7.62%  
Conservative: 80  
Mismatches: 212  
Indels: 205

RESULT 871  
ID AAN70389 standard; DNA; 2459 BP.  
DE CDNA encoding human tissue plasminogen activator (TPA) in plasmid pDPAP3.  
PN EP231883-A.  
PD 12-AUG-1987.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (NIPS ) NIPPON SODA CO.  
PA (CENG ) CENTRAL GLASS CO LTD.  
PA (TOYU ) TOYO SODA MFG CO LTD.  
PA (NISC ) NISSAN CHEM IND LTD.  
PA (NISC ) NISSAN CHEMICAL INDS KK.  
Percent Similarity: 35.31%  
Best Local Similarity: 22.81%  
Query Match: 7.62%  
Conservative: 80  
Mismatches: 212  
Indels: 205

RESULT 872  
ID AAQ03218 standard; DNA; 1389 BP.  
DE DNA sequence encoding human protein C mutant.  
PN EP352651-A.  
PD 31-JAN-1990.  
PA (FARH ) HOECHST JAPAN LTD.  
Percent Similarity: 34.78%  
Best Local Similarity: 23.73%  
Query Match: 7.59%  
Conservative: 61  
Mismatches: 178  
Indels: 183

RESULT 873  
ID AAQ24121 standard; DNA; 2550 BP.  
DE Encodes tPA analogue KK2A.  
PN US5106741-A.  
PD 21-APR-1992.  
PA (UPJO ) UPJOHN CO.  
Percent Similarity: 38.66%  
Best Local Similarity: 23.91%  
Query Match: 7.58%  
Conservative: 95  
Mismatches: 235  
Indels: 161

RESULT 874  
ID AAQ03581 standard; DNA; 1614 BP.  
DE Glycosylated plasminogen activator sequence.  
PN JP02042981-A.  
PD 13-FEB-1990.  
PA (KANF ) KANEGAFUCHI CHEM KK.  
Percent Similarity: 35.62%  
Best Local Similarity: 22.88%  
Query Match: 7.57%  
Conservative: 78  
Mismatches: 196  
Indels: 201

RESULT 875  
ID ADE06939 standard; DNA; 2145 BP.  
DE Novel coding sequence (useful for identifying genetic disorders) #5.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 36.84%  
Best Local Similarity: 24.42%  
Query Match: 7.54%  
Conservative: 85  
Mismatches: 226  
Indels: 207

RESULT 876  
ID ADD18497 standard; DNA; 2198 BP.  
DE Human prostate cancer diagnosis related DNA sequence SeqID69.  
PN WO2003012067-A2.  
PD 13-FEB-2003.  
PA (UNMI ) UNIV MICHIGAN.  
Percent Similarity: 35.54%  
Best Local Similarity: 22.43%  
Query Match: 7.54%  
Conservative: 93  
Mismatches: 236  
Indels: 222

RESULT 877  
ID ABX77617 standard; cDNA; 2641 BP.  
DE Differentially expressed breast cancer associated cDNA #112.  
PN US2002156263-A1.  
PD 24-OCT-2002.  
PA (CHEN/) CHEN H.  
Percent Similarity: 35.70%  
Best Local Similarity: 21.93%  
Query Match: 7.54%  
Conservative: 93  
Mismatches: 208  
Indels: 227

RESULT 878  
ID ACN41469 standard; cDNA; 3112 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:344.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 34.52%  
Best Local Similarity: 21.28%  
Query Match: 7.52%  
Conservative: 112  
Mismatches: 265  
Indels: 293

RESULT 879  
ID AAN70779 standard; DNA; 2550 BP.  
DE Sequence encoding tissue plasminogen (TPA) analogue.  
PN WO8703906-A.  
PD 02-JUL-1987.  
PA (UPJO ) UPJOHN CO.  
PA (MARO/) MAROTTI K R.  
Percent Similarity: 34.28%  
Best Local Similarity: 21.86%  
Query Match: 7.50%  
Conservative: 83  
Mismatches: 229  
Indels: 211

RESULT 880  
ID AAQ71243 standard; cDNA; 1554 BP.  
DE Serine protease for fusion protein cleavage.  
PN WO9418227-A2.  
PD 18-AUG-1994.  
PA (DENZ-) DENZYME APS.  
Percent Similarity: 37.30%  
Best Local Similarity: 23.78%  
Query Match: 7.49%  
Conservative: 75  
Mismatches: 198  
Indels: 152

RESULT 881  
ID AAQ12073 standard; DNA; 2091 BP.  
DE T-PA variant contg. fibronectin for thrombosis lysis (1).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.06%  
Best Local Similarity: 21.98%  
Query Match: 7.49%  
Conservative: 83  
Mismatches: 217  
Indels: 239

RESULT 882  
ID ABK63668 standard; cDNA; 1543 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1575.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 37.08%  
Best Local Similarity: 24.66%  
Query Match: 7.47%  
Conservative: 74  
Mismatches: 181  
Indels: 194

RESULT 883  
ID ADB59220 standard; DNA; 1543 BP.  
DE Toxicity-related gene, SEQ ID 4246.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 37.08%  
Best Local Similarity: 24.66%  
Query Match: 7.47%  
Conservative: 74  
Mismatches: 181  
Indels: 194

RESULT 884  
ID ADB52603 standard; DNA; 1543 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3145.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 37.08%  
Best Local Similarity: 24.66%  
Query Match: 7.47%  
Conservative: 74  
Mismatches: 181  
Indels: 194

RESULT 885  
ID AAT41842 standard; DNA; 1543 BP.  
DE Toxicity modelling related rat gene SEQ ID No 1544.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 37.08%  
Best Local Similarity: 24.66%  
Query Match: 7.47%  
Conservative: 74  
Mismatch: 181  
Indels: 194  
RESULT 886  
ID ADP72980 standard; DNA; 1543 BP.  
DE Renal toxin progression gene marker #1569.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 37.08%  
Best Local Similarity: 24.66%  
Query Match: 7.47%  
Conservative: 74  
Mismatch: 181  
Indels: 194  
RESULT 887  
ID AAQ04903 standard; DNA; 1689 BP.  
DE Part of tPA024 gene encoding precursor protein.  
PN EP373896-A.  
PD 20-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Percent Similarity: 35.89%  
Best Local Similarity: 23.00%  
Query Match: 7.43%  
Conservative: 74  
Mismatch: 185  
Indels: 186  
RESULT 888  
ID ARX5285 standard; DNA; 3121 BP.  
DE Human NOVI2a CG92293-01 DNA SEQ ID 49.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 34.31%  
Best Local Similarity: 21.76%  
Query Match: 7.43%  
Conservative: 90  
Mismatch: 271  
Indels: 200  
RESULT 889  
ID AAN70778 standard; DNA; 2543 BP.  
DE Sequence encoding tissue plasminogen (TPA) analogue.  
PN WO8703906-A.  
PD 02-JUL-1987.  
PA (UPJO ) UPJOHN CO.  
Percent Similarity: 35.41%  
Best Local Similarity: 21.78%  
Query Match: 7.41%  
Conservative: 92  
Mismatch: 210  
Indels: 227  
RESULT 890  
ID ACN41472 standard; cDNA; 2877 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:347.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 32.21%  
Best Local Similarity: 21.68%  
Query Match: 7.41%  
Conservative: 84  
Mismatch: 268  
Indels: 276  
RESULT 891  
ID ADG83825 standard; cDNA; 1407 BP.  
DE Brown snake venom protease coding sequence.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU ) UNIV QUEENSLAND.  
Percent Similarity: 35.68%  
Best Local Similarity: 22.34%  
Query Match: 7.40%  
Conservative: 74  
Mismatch: 197  
Indels: 160  
RESULT 892  
ID AAN81086 standard; DNA; 1738 BP.  
DE Pre-pro tissue plasminogen activator coding sequence.  
PN EP293934-A.  
PD 07-DEC-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
Percent Similarity: 35.68%  
Best Local Similarity: 22.34%  
Query Match: 7.40%  
Conservative: 74  
Mismatch: 197  
Indels: 160  
RESULT 893  
ID AAN81068 standard; cDNA; 1740 BP.  
DE Synthetic pre-pro tissue plasminogen activator homologue.  
PN EP292009-A.  
PD 23-NOV-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
Percent Similarity: 36.82%  
Best Local Similarity: 22.86%  
Query Match: 7.38%  
Conservative: 80  
Mismatch: 181  
Indels: 182  
RESULT 894  
ID AAN91476 standard; DNA; 1557 BP.  
DE Sequence of des 1-44E275 t-PA mutant encoded by plasmid p1179.  
PN WO8909266-A.  
PD 05-OCT-1989.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.62%  
Best Local Similarity: 22.71%  
Query Match: 7.36%  
Conservative: 79  
Mismatch: 198  
Indels: 199  
RESULT 895  
ID AAQ12076 standard; DNA; 2100 BP.  
DE T-PA variant having Lys416 substituted (3).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.59%  
Best Local Similarity: 21.75%  
Query Match: 7.36%  
Conservative: 85  
Mismatch: 209  
Indels: 227  
RESULT 896  
ID AAL60580 standard; DNA; 2280 BP.  
DE Human tissue plasminogen activator (tPA) DNA.  
PN WO2003044050-A1.  
PD 30-MAY-2003.  
PA (PARK/) PARK H.  
Percent Similarity: 34.47%  
Best Local Similarity: 21.75%  
Query Match: 7.36%  
Conservative: 86  
Mismatch: 215  
Indels: 231  
RESULT 897  
ID AAQ87370 standard; DNA; 2162 BP.  
DE Human tPA clone.  
PN WO9507351-A1.  
PD 16-MAR-1995.  
PA (HARD ) HARVARD COLLEGE.  
Percent Similarity: 34.47%  
Best Local Similarity: 21.75%  
Query Match: 7.34%  
Conservative: 86  
Mismatch: 215  
Indels: 231  
RESULT 898  
ID AAV37294 standard; DNA; 2162 BP.  
DE Human tissue plasminogen activator gene sequence.  
PN US5780272-A.  
PD 14-JUL-1998.  
PA (HARD ) HARVARD COLLEGE.  
Percent Similarity: 34.47%  
Best Local Similarity: 21.75%  
Query Match: 7.34%  
Conservative: 86  
Mismatch: 215  
Indels: 231

Percent Similarity: 35.81%  
Best Local Similarity: 22.84%  
Query Match: 7.40%  
Conservative: 75  
Mismatch: 180  
Indels: 192  
RESULT 893  
ID AAQ12071 standard; DNA; 2097 BP.  
DE T-PA with -ve charged finger and/or kringle domain (1).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.78%  
Best Local Similarity: 21.95%  
Query Match: 7.40%  
Conservative: 83  
Mismatch: 199  
Indels: 226  
RESULT 894  
ID ACN41473 standard; cDNA; 2827 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:348.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 32.37%  
Best Local Similarity: 21.58%  
Query Match: 7.40%  
Conservative: 86  
Mismatch: 252  
Indels: 292  
RESULT 895  
ID AAN81068 standard; cDNA; 1740 BP.  
DE Synthetic pre-pro tissue plasminogen activator homologue.  
PN EP292009-A.  
PD 23-NOV-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
Percent Similarity: 36.82%  
Best Local Similarity: 22.86%  
Query Match: 7.38%  
Conservative: 80  
Mismatch: 181  
Indels: 182  
RESULT 896  
ID AAN91476 standard; DNA; 1557 BP.  
DE Sequence of des 1-44E275 t-PA mutant encoded by plasmid p1179.  
PN WO8909266-A.  
PD 05-OCT-1989.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.62%  
Best Local Similarity: 22.71%  
Query Match: 7.36%  
Conservative: 79  
Mismatch: 198  
Indels: 199  
RESULT 897  
ID AAQ12076 standard; DNA; 2100 BP.  
DE T-PA variant having Lys416 substituted (3).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.59%  
Best Local Similarity: 21.75%  
Query Match: 7.36%  
Conservative: 85  
Mismatch: 209  
Indels: 227  
RESULT 898  
ID AAL60580 standard; DNA; 2280 BP.  
DE Human tissue plasminogen activator (tPA) DNA.  
PN WO2003044050-A1.  
PD 30-MAY-2003.  
PA (PARK/) PARK H.  
Percent Similarity: 34.47%  
Best Local Similarity: 21.75%  
Query Match: 7.36%  
Conservative: 86  
Mismatch: 215  
Indels: 231  
RESULT 899  
ID AAQ87370 standard; DNA; 2162 BP.  
DE Human tPA clone.  
PN WO9507351-A1.  
PD 16-MAR-1995.  
PA (HARD ) HARVARD COLLEGE.  
Percent Similarity: 34.47%  
Best Local Similarity: 21.75%  
Query Match: 7.34%  
Conservative: 86  
Mismatch: 215  
Indels: 231  
RESULT 900  
ID AAV37294 standard; DNA; 2162 BP.  
DE Human tissue plasminogen activator gene sequence.  
PN US5780272-A.  
PD 14-JUL-1998.  
PA (HARD ) HARVARD COLLEGE.  
Percent Similarity: 34.47%  
Best Local Similarity: 21.75%  
Query Match: 7.34%  
Conservative: 86  
Mismatch: 215  
Indels: 231

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Best Local Similarity: 21.75%      Mismatches: 215
Query Match: 7.34%                Indels: 231
RESULT 901
ID AAN70248 standard; DNA; 2170 BP.
DE Sequence encoding human tissue plasminogen activator (t-PA) produced by
DE normal human cells.
PN EP225177-A.
PD 10-JUN-1987.
PA (MITK ) MITSUI TOATSU CHEM INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 902
ID AAQ86576 standard; cDNA; 2170 BP.
DE Human tissue plasminogen activator cDNA.
PN JP07046983-A.
PD 21-FEB-1995.
PA (MITK ) MITSUI TOATSU CHEM INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 903
ID AAN90508 standard; cDNA; 2509 BP.
DE cDNA of human tissue plasminogen activator.
PN JP01174388-A.
PD 10-JUL-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 904
ID AAD56135 standard; DNA; 2509 BP.
DE Human tissue-type plasminogen activator (t-PA) DNA.
PN WO2003033009-A2.
PD 24-APR-2003.
PA (OMNI-) OMNITO AB.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 905
ID ABL59544 standard; cDNA; 2519 BP.
DE Human tissue type plasminogen activator (t-PA) cDNA SEQ ID NO:44.
PN WO200227028-A1.
PD 04-APR-2002.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 906
ID ABK52545 standard; DNA; 2519 BP.
DE Human tissue plasminogen activator (t-PA) DNA sequence.
PN WO200232446-A2.
PD 25-APR-2002.
PA (PFIZ ) PFIZER LTD.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 907
ID ADR24679 standard; DNA; 2519 BP.
DE Breast cancer prognosis marker #540.
PN WO2004065545-A2.
PD 05-AUG-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 908
ID AAN90542 standard; cDNA; 2560 BP.
DE Plasmid pKG12 contg. DNA encoding human melanoma t-PA.
PN EP297066-A.
PD 28-DEC-1988.
PA (NECA-) NETHERLANDS CANCER INST.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 909
ID ADN95625 standard; DNA; 2653 BP.
DE Human BEC/LEC-related gene sequence SeqID548.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 910
ID ADO28678 standard; cDNA; 2653 BP.
DE Human tPA encoding cDNA SEQ ID NO:107.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 911
ID ACN38795 standard; cDNA; 2653 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325090, SEQ ID NO:2534.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 912
ID AAD13117 standard; cDNA; 2672 BP.
DE Human membrane-type serine protease (MTSP) 4-S splice variant cDNA.
PN WO200157194-A2.
PD 09-AUG-2001.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 35.06%
Best Local Similarity: 22.70%      Mismatches: 74
Query Match: 7.34%                Indels: 175
RESULT 913
ID ADI10378 standard; DNA; 2672 BP.
DE Human cell surface protease coding sequence #5.
PN WO200295007-A2.
PD 28-NOV-2002.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 35.06%
Best Local Similarity: 22.70%      Mismatches: 74
Query Match: 7.34%                Indels: 175
RESULT 914
ID ADJ46902 standard; cDNA; 2672 BP.
DE Human transmembrane serine protease (MTSP) cDNA #5.
PN US2004001801-A1.
PD 01-JAN-2004.
PA (CORV-) CORVAS INT INC.
Percent Similarity: 35.06%
Best Local Similarity: 22.70%      Mismatches: 74
Query Match: 7.34%                Indels: 175
RESULT 915
ID ADL46102 standard; DNA; 2859 BP.
DE Human ovarian cancer DNA marker #19992.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Percent Similarity: 34.47%
Best Local Similarity: 21.75%      Mismatches: 86
Query Match: 7.34%                Indels: 215
RESULT 916
ID AAD13116 standard; cDNA; 3104 BP.
DE Human membrane-type serine protease (MTSP) 4-L splice variant cDNA.
PN WO200157194-A2.
PD 09-AUG-2001.

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Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 933  
ID ADA12368 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO618.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 934  
ID ACD29162 standard; cDNA; 3143 BP.  
DE Novel human secreted and transmembrane polypeptide cDNA #37.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 935  
ID ADB73674 standard; cDNA; 3143 BP.  
DE Human PRO polynucleotide sequence #37.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 936  
ID ADB76390 standard; cDNA; 3143 BP.  
DE Human PRO polynucleotide sequence #37.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 937  
ID ADC43816 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 938  
ID ADC61576 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 939  
ID ADC63540 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 940  
ID ADC66640 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175

RESULT 941  
ID ADC68764 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 942  
ID ADC62824 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 943  
ID ADC67889 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 944  
ID ADC41209 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 945  
ID ADC67264 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 946  
ID ADC62200 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 947  
ID ADC41833 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 948  
ID ADE49202 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175  
RESULT 949  
ID ADE49202 standard; cDNA; 3143 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.89% Conservative: 73  
Best Local Similarity: 22.70% Mismatches: 215  
Query Match: 7.31% Indels: 175

ID ADE35256 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003203434-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 950  
 ID ADE16370 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003203435-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 951  
 ID ADD72985 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003203436-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 952  
 ID ADD72343 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003194781-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 953  
 ID ADE16994 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003203433-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 954  
 ID ADF47008 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003195333-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 955  
 ID ADG52765 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003216561-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 956  
 ID ADG60085 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003206915-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 957  
 ID ADI60845 standard; cDNA; 3143 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003077700-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 958  
 ID ACD42566 standard; cDNA; 3143 BP.  
 DE Novel human secreted and transmembrane protein PRO618 cDNA.  
 PN US2003050239-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 959  
 ID ADE48502 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003104536-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 960  
 ID ADE89603 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003130181-A1.  
 PD 10-JUL-2003.  
 PA (ASHK/) ASHKENAZI A J.  
 PA (BAKE/) BAKER K P.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERK/) FERRARA N.  
 PA (FILN/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERE/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GIRM/) GIRMALDI J C.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (KUOS/) KUO S S.  
 PA (NAPI/) NAPIER M A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (SHEL/) SHELTON D L.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 961  
 ID ADF61243 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003195345-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Mismatches: 215  
 Indels: 175  
 Query Match:  
 RESULT 962  
 ID ADF39935 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003198994-A1.



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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 963
ID ADF45731 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 964
ID ADF24127 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 965
ID ADF40559 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 966
ID ADF23503 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 967
ID ADF33486 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 968
ID ADF26953 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 969
ID ADF27589 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 970
ID ADF41183 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 971
ID ADF32862 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 972
ID ADF25228 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 973
ID ADF26329 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 974
ID ADF34118 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 975
ID ADF46355 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 976
ID ADG50341 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 977
ID ADG49717 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.89%
Best Local Similarity: 22.70%
Query Match: 7.31%
Conservative: 73
Mismatch: 215
Indels: 175
RESULT 978
ID ADG51589 standard; cDNA; 3143 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO618.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
```

Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 979  
 ID ADG49093 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003216305-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 980  
 ID ADG48469 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2003216560-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 981  
 ID ADG50965 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 982  
 ID ADG58909 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2004005657-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 983  
 ID ADG62365 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2004006219-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 984  
 ID ADH25390 standard; cDNA; 3143 BP.  
 DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:168.  
 PN EP1386931-A1.  
 PD 04-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 985  
 ID ADM17167 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2004048332-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 986  
 ID ADL07001 standard; cDNA; 3143 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO618.  
 PN US2004063921-A1.  
 PD 01-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%

Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 987  
 ID ADT91614 standard; cDNA; 3143 BP.  
 DE Human PRO618 cDNA sequence.  
 PN AU2002317529-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.89%  
 Best Local Similarity: 22.70%  
 Query Match: 7.31%  
 RESULT 988  
 ID AAZ29663 standard; cDNA; 3547 BP.  
 DE Mouse Serine protease, Corin cDNA.  
 PN WO9964608-A1.  
 PD 16-DEC-1999.  
 PA (SCHD ) SCHERING AG.  
 Percent Similarity: 36.24%  
 Best Local Similarity: 21.99%  
 Query Match: 7.31%  
 RESULT 989  
 ID AAN60659 standard; DNA; 2547 BP.  
 DE Sequence encoding human pre-tissue plasminogen activator (pre-t-PA).  
 PN GB2173804-A.  
 PD 22-OCT-1986.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.58%  
 Best Local Similarity: 21.76%  
 Query Match: 7.30%  
 RESULT 990  
 ID AAN60736 standard; DNA; 2547 BP.  
 DE Sequence encoding modified human tissue plasminogen activator (t-PA).  
 PN FR2581652-A.  
 PD 14-NOV-1986.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.58%  
 Best Local Similarity: 21.76%  
 Query Match: 7.30%  
 RESULT 991  
 ID ABQ61196 standard; cDNA; 2801 BP.  
 DE Human PRO618 encoding sequence.  
 PN WO200231111-A2.  
 PD 18-APR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.13%  
 Best Local Similarity: 20.97%  
 Query Match: 7.30%  
 RESULT 992  
 ID AAZ32168 standard; DNA; 1366 BP.  
 DE Human low density lipoprotein receptor exon 2 nucleotide sequence.  
 PN WO9950454-A2.  
 PD 07-OCT-1999.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 Percent Similarity: 35.22%  
 Best Local Similarity: 25.10%  
 Query Match: 7.29%  
 RESULT 993  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 994  
 ID ACF05074 standard; cDNA; 1917 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 995  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 996  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 997  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 998  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 999  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%  
 RESULT 1000  
 ID ACF05072 standard; cDNA; 1755 BP.  
 DE Bovine recombinant prothrombin nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 35.12%  
 Best Local Similarity: 24.10%  
 Query Match: 7.29%

Query Match: 7.29% Indels: 217  
 RESULT 995  
 ID ADG83827 standard; cDNA; 1404 BP.  
 DE Taipan snake venom protease coding sequence.  
 PN WO2003082914-A1.  
 PD 09-OCT-2003.  
 PA (UYQU ) UNIV QUEENSLAND.  
 Percent Similarity: 36.15%  
 Best Local Similarity: 22.48%  
 Query Match: 7.28% Indels: 162  
 RESULT 996  
 ID AAN30001 standard; cDNA; 2547 BP.  
 DE Sequence encoding full length tissue plasminogen activator (t-Pa).  
 PN EP93619-A.  
 PD 09-NOV-1983.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 34.58%  
 Best Local Similarity: 21.61%  
 Query Match: 7.28% Indels: 234  
 RESULT 997  
 ID ADQ38420 standard; DNA; 2933 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 83.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 34.37%  
 Best Local Similarity: 21.78%  
 Query Match: 7.28% Indels: 231  
 RESULT 998  
 ID AAN70741 standard; DNA; 1598 BP.  
 DE Sequence of synthetic gene for mature human tissue plasminogen activator (tPA).  
 PN WO8705934-A.  
 PD 08-OCT-1987.  
 PA (CREA/) CREA R.  
 Percent Similarity: 36.31%  
 Best Local Similarity: 22.90%  
 Query Match: 7.25% Indels: 154  
 RESULT 999  
 ID AAQ04904 standard; DNA; 1689 BP.  
 DE Part of tPA023 gene encoding precursor protein.  
 PN EP373896-A.  
 PD 20-JUN-1990.  
 PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1000  
 ID AAQ13379 standard; DNA; 1689 BP.  
 DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.  
 PN US5041376-A.  
 PD 20-AUG-1991.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1001  
 ID ASK52546 standard; DNA; 1689 BP.  
 DE Human tissue plasminogen activator (t-PA) coding sequence.  
 PN WO200232446-A2.  
 PD 25-APR-2002.  
 PA (PFIZ ) PFIZER LTD.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1002  
 ID ACC78881 standard; DNA; 1726 BP.  
 DE Human tissue-type plasminogen activator (TPA) encoding DNA.  
 PN WO2003031464-A2.  
 PD 17-APR-2003.

PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1003  
 ID ADN49697 standard; DNA; 1726 BP.  
 DE Human tissue type plasminogen activator TPA DNA SeqID 25.  
 PN WO2004033651-A2.  
 PD 22-APR-2004.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1004  
 ID AAT27585 standard; DNA; 1740 BP.  
 DE Full-length tissue plasminogen activator DNA clone.  
 PN US5504001-A.  
 PD 02-APR-1996.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1005  
 ID AAZ31998 standard; cDNA; 1955 BP.  
 DE Human tissue plasminogen activator coding sequence.  
 PN US5985607-A.  
 PD 16-NOV-1999.  
 PA (CANG-) CANGENE CORP.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1006  
 ID AAN91111 standard; DNA; 1974 BP.  
 DE BgIII fragment of mutant tPA plasmid pTPAL02.  
 PN EP302456-A.  
 PD 08-FEB-1989.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1007  
 ID AAN91119 standard; DNA; 2100 BP.  
 DE Sequence of native tPA in plasmid pST112.  
 PN EP302456-A.  
 PD 08-FEB-1989.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1008  
 ID AAQ05932 standard; DNA; 2100 BP.  
 DE Plasmid pST112 encoding novel N-terminal for tissue plasminogen activator (tPA).  
 PN EP373890-A.  
 PD 01-AUG-1990.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Percent Similarity: 35.71%  
 Best Local Similarity: 22.82%  
 Query Match: 7.25% Indels: 186  
 RESULT 1009  
 ID AAQ05944 standard; DNA; 2313 BP.  
 DE Sequence encoding thrombomodulin analogue / t-PA fusion protein.  
 PN WO9010081-A.  
 PD 07-SEP-1990.  
 PA (CODO-) CODON.  
 Percent Similarity: 37.00%  
 Best Local Similarity: 22.86%  
 Query Match: 7.25% Indels: 182  
 RESULT 1010  
 ID AAN60146 standard; cDNA; 2457 BP.  
 DE cDNA sequence encoding active human uterine tissue plasminogen activator (UTPA).  
 PN EP178105-A.

PD 16-APR-1986.  
PA (INTE-) INTEG GENETICS INC.  
Percent Similarity: 35.71%  
Best Local Similarity: 22.82%  
Query Match: 7.25%  
RESULT 1011  
ID ADR24680 standard; DNA; 2461 BP.  
DE Breast cancer prognosis marker #541.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Percent Similarity: 35.71%  
Best Local Similarity: 22.82%  
Query Match: 7.25%  
RESULT 1012  
ID AAN70491 standard; cDNA; 7533 BP.  
DE Entire sequence of high level expression vector pEmpl-tpa for tissue  
DE Plasmid pEmpl-tpa.  
PN EP237157-A.  
PD 16-SEP-1987.  
PA (DAMO-) DAMON BIOTECH INC.  
PA (ABBO-) ABBOTT BIOTECH INC.  
Percent Similarity: 35.71%  
Best Local Similarity: 22.82%  
Query Match: 7.25%  
RESULT 1013  
ID AAN81970 standard; DNA; 7533 BP.  
DE Plasmid pEmpl-tpa.  
PN WO8800242-A.  
PD 14-JAN-1988.  
PA (DAMO-) DAMON BIOTECH INC.  
Percent Similarity: 35.71%  
Best Local Similarity: 22.82%  
Query Match: 7.25%  
RESULT 1014  
ID ABL52893 standard; DNA; 1686 BP.  
DE Tissue type plasminogen activator, tPA, coding sequence.  
PN KR141262-B1.  
PD 15-JUN-1998.  
PA (GLDS) LG CHEM LTD.  
Percent Similarity: 35.71%  
Best Local Similarity: 22.65%  
Query Match: 7.22%  
RESULT 1015  
ID AAN91216 standard; DNA; 1689 BP.  
DE Mutated cDNA coding sequence of tissue plasminogen activator (t-PA).  
PN AU8817430-A.  
PD 08-DEC-1988.  
PA (NOVO) NOVO IND AS.  
PA (ZYMO) ZYMOGENETICS INC.  
PA (EISA) EISAI CO LTD.  
Percent Similarity: 37.52%  
Best Local Similarity: 23.91%  
Query Match: 7.22%  
RESULT 1016  
ID AAO05177 standard; DNA; 1689 BP.  
DE Sequence encoding thrombolytic protein with secondary structure of human  
DE tissue plasminogen activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA) YAMANOUCHI PHARM CO LTD.  
Percent Similarity: 36.88%  
Best Local Similarity: 23.05%  
Query Match: 7.22%  
RESULT 1017  
ID AAO05531 standard; DNA; 1974 BP.  
DE Plasmid pTPA102 encoding novel tissue plasminogen activator (t-PA).  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Percent Similarity: 35.71%  
Best Local Similarity: 22.82%

Query Match: 7.22%  
RESULT 1018  
ID AAO08500 standard; cDNA; 2547 BP.  
DE Sequence encoding tissue plasminogen activator (t-PA) mutant Thr 478.  
PN WO8912680-A.  
PD 28-DEC-1989.  
PA (UNIW) UNIV WASHINGTON.  
Percent Similarity: 34.58%  
Best Local Similarity: 21.61%  
Query Match: 7.22%  
RESULT 1019  
ID AAO61733 standard; cDNA; 1149 BP.  
DE cDNA encoding human serine protease BSSP5 (hBSSP5) SEQ ID NO:1.  
PN WO2000031243-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Percent Similarity: 44.00%  
Best Local Similarity: 28.00%  
Query Match: 7.21%  
RESULT 1020  
ID AAO53318 standard; cDNA to mRNA; 1800 BP.  
DE Human tPA (R129W) coding sequence.  
PN JP05304992-A.  
PD 19-NOV-1993.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Percent Similarity: 34.32%  
Best Local Similarity: 21.75%  
Query Match: 7.21%  
RESULT 1021  
ID AAO40654 standard; DNA; 1800 BP.  
DE tPA mutein DNA.  
PN JP05076361-A.  
PD 30-MAR-1993.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Percent Similarity: 34.32%  
Best Local Similarity: 21.75%  
Query Match: 7.21%  
RESULT 1022  
ID AAO12074 standard; DNA; 2100 BP.  
DE T-PA variant having Lys416 substituted (1).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.57%  
Best Local Similarity: 21.76%  
Query Match: 7.21%  
RESULT 1023  
ID AAO12075 standard; DNA; 2105 BP.  
DE T-PA variant having Lys416 substituted (2).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.72%  
Best Local Similarity: 21.76%  
Query Match: 7.21%  
RESULT 1024  
ID AAO12867 standard; cDNA; 2512 BP.  
DE JM1-229 cell line t-PA.  
PN WO9110447-A.  
PD 25-JUL-1991.  
PA (PORT-) PORTON PROD LTD.  
PA (PUBL-) PUBLIC HEALTH LAB SERVIC.  
PA (UNLO) UNIV COLLEGE LONDON.  
Percent Similarity: 39.29%  
Best Local Similarity: 26.07%  
Query Match: 7.21%  
RESULT 1025  
ID ADR29370 standard; DNA; 4864 BP.  
DE Murine Lrp4 dopaminergic neuronal marker DNA SEQ ID NO:1.  
PN WO2004065599-A1.  
PD 05-AUG-2004.  
PA (EISA) EISAI CO LTD.  
Percent Similarity: 36.24%  
Conservative: 117  
Mismatch: 218  
Indels: 110

Best Local Similarity: 21.87% Mismatches: 282  
Query Match: 7.21% Indels: 238  
RESULT 1026  
ID AAN82177 standard; DNA; 1689 BP.  
DE Tissue plasminogen activator with G-183 and S-186 substd for S and T.  
PN JP63230083-A.  
PD 26-SEP-1988.  
PA (EISA) EISA CO LTD.  
Percent Similarity: 36.82% Conservative: 81  
Best Local Similarity: 22.69% Mismatches: 181  
Query Match: 7.20% Indels: 182  
RESULT 1027  
ID ADB58261 standard; DNA; 1497 BP.  
DE Toxicity-related gene, SEQ ID 3287.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 35.30% Conservative: 70  
Best Local Similarity: 22.76% Mismatches: 206  
Query Match: 7.19% Indels: 155  
RESULT 1028  
ID ADB52793 standard; DNA; 1497 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3335.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 35.30% Conservative: 70  
Best Local Similarity: 22.76% Mismatches: 206  
Query Match: 7.19% Indels: 155  
RESULT 1029  
ID ABI9227 standard; cDNA; 2519 BP.  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:40.  
PN WO200108188-A2.  
PD 22-NOV-2001.  
PA (YUNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Percent Similarity: 38.20% Conservative: 72  
Best Local Similarity: 25.23% Mismatches: 199  
Query Match: 7.19% Indels: 146  
RESULT 1030  
ID ADR12597 standard; DNA; 2519 BP.  
DE Gene vaccine nucleic acid #30.  
PN WO2004067040-A1.  
PD 12-AUG-2004.  
PA (KYUS-) KYUSHU TLO CO LTD.  
Percent Similarity: 38.20% Conservative: 72  
Best Local Similarity: 25.23% Mismatches: 199  
Query Match: 7.19% Indels: 146  
RESULT 1031  
ID AAQ01358 standard; DNA; 1780 BP.  
DE Sequence encoding wild type tissue plasminogen activator (t-PA).  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO) NOVO-NORDISK AS.  
Percent Similarity: 35.61% Conservative: 74  
Best Local Similarity: 22.63% Mismatches: 192  
Query Match: 7.17% Indels: 176  
RESULT 1032  
ID AAQ04354 standard; DNA; 1780 BP.  
DE Sequence encoding tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO) NOVO-NORDISK AS.  
Percent Similarity: 35.61% Conservative: 74  
Best Local Similarity: 22.63% Mismatches: 192  
Query Match: 7.17% Indels: 176  
RESULT 1033  
ID AAQ04353 standard; DNA; 1780 BP.  
DE Sequence encoding tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residues 419 and 420.  
PN EP351246-A.

PD 17-JAN-1990.  
PA (NOVO) NOVO-NORDISK AS.  
Percent Similarity: 35.44% Conservative: 73  
Best Local Similarity: 22.63% Mismatches: 193  
Query Match: 7.17% Indels: 176  
RESULT 1034  
ID AAN70088 standard; DNA; 1836 BP.  
DE Hybrid plasminogen activator (PA) contg. urokinase kringle (UKK) 1-131 and tissue plasminogen activator (tPA) 92-527.  
PN EP213794-A.  
PD 11-MAR-1987.  
PA (AMHP) AMERICAN HOME PROD CORP.  
Percent Similarity: 36.90% Conservative: 90  
Best Local Similarity: 22.95% Mismatches: 208  
Query Match: 7.17% Indels: 200  
RESULT 1035  
ID AAQ42718 standard; DNA; 2544 BP.  
DE Sequence encoding tissue plasminogen activator (t-PA).  
PN WO9312225-A1.  
PD 24-JUN-1993.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 34.32% Conservative: 86  
Best Local Similarity: 21.60% Mismatches: 216  
Query Match: 7.16% Indels: 231  
RESULT 1036  
ID AAN60813 standard; cDNA; 1630 BP.  
DE Sequence encoding tissue plasminogen activator (TPA) in pUCH.  
PN DB3537176-A.  
PD 10-JUL-1986.  
PA (ZYMO) ZYMOGENETICS INC.  
Percent Similarity: 35.54% Conservative: 73  
Best Local Similarity: 22.82% Mismatches: 187  
Query Match: 7.15% Indels: 186  
RESULT 1037  
ID AAN81090 standard; DNA; 1689 BP.  
DE Mutated t-PA analogue coding sequence in plasmid ZEM99-9100.  
PN EP293934-A.  
PD 07-DEC-1988.  
PA (ZYMO) ZYMOGENETICS INC.  
Percent Similarity: 35.37% Conservative: 72  
Best Local Similarity: 22.82% Mismatches: 188  
Query Match: 7.15% Indels: 186  
RESULT 1038  
ID AAN82179 standard; DNA; 1689 BP.  
DE Tissue plasminogen activator with S-119 substd for M and QGI96-98 substd for NGT.  
PN JP63230083-A.  
PD 26-SEP-1988.  
PA (EISA) EISA CO LTD.  
Percent Similarity: 36.06% Conservative: 74  
Best Local Similarity: 23.17% Mismatches: 184  
Query Match: 7.15% Indels: 186  
RESULT 1039  
ID AAZ41406 standard; cDNA; 901 BP.  
DE Human normal pancreas tissue derived cDNA 21.  
PN DE19818598-A1.  
PD 21-OCT-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Percent Similarity: 42.72% Conservative: 48  
Best Local Similarity: 27.18% Mismatches: 102  
Query Match: 7.14% Indels: 75  
RESULT 1040  
ID AAH19462 standard; DNA; 1221 BP.  
DE Mutant blood coagulant factor VII (FVII-30) coding sequence.  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
Percent Similarity: 35.41% Conservative: 65  
Best Local Similarity: 22.76% Mismatches: 149  
Query Match: 7.14% Indels: 183

ID	AAQ06317 standard; DNA; 1605 BP.		
DE	Synthetic gene encoding t-PA, used to prepare pJS023.		
PN	US4963357-A.		
PD	16-OCT-1990.		
PA	(MONS ) MONSANTO CO.		
Percent Similarity:	36.77%	Conservative:	77
Best Local Similarity:	23.09%	Mismatches:	192
Query Match:	7.12%	Indels:	164
RESULT 1050			
ID	AAQ46260 standard; DNA; 1605 BP.		
DE	Synthetic tPA gene with optimum yeast codons.		
PN	US5244676-A.		
PD	14-SEP-1993.		
PA	(MONS ) MONSANTO CO.		
Percent Similarity:	36.70%	Conservative:	77
Best Local Similarity:	23.05%	Mismatches:	193
Query Match:	7.12%	Indels:	164
RESULT 1051			
ID	ABL70002 standard; DNA; 1184 BP.		
DE	Pancreas cancer related gene sequence SEQ ID NO:8339.		
PN	WO200194629-A2.		
PD	13-DEC-2001.		
PA	(AVAL-) AVALON PHARM.		
Percent Similarity:	43.67%	Conservative:	47
Best Local Similarity:	28.00%	Mismatches:	112
Query Match:	7.11%	Indels:	57
RESULT 1052			
ID	AD884828 standard; DNA; 1184 BP.		
DE	Farnesyl transferase inhibitor modulated leukemia associated gene #47.		
PN	WO2003038129-A2.		
PD	08-MAY-2003.		
PA	(ORTH ) ORTH CLINICAL DIAGNOSTICS INC.		
Percent Similarity:	43.67%	Conservative:	47
Best Local Similarity:	28.00%	Mismatches:	112
Query Match:	7.11%	Indels:	57
RESULT 1053			
ID	ACN40045 standard; cDNA; 1184 BP.		
DE	Tumour-associated antigenic target (TAT) cDNA DNA88261, SEQ ID NO:4579.		
PN	WO2004030615-A2.		
PD	15-APR-2004.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	43.67%	Conservative:	47
Best Local Similarity:	28.00%	Mismatches:	112
Query Match:	7.11%	Indels:	57
RESULT 1054			
ID	AAN60065 standard; DNA; 2438 BP.		
DE	Factor IX/Factor VII cDNA fusion.		
PN	EP200421-A.		
PD	10-DEC-1986.		
PA	(ZYMO ) ZYMOGENETICS INC.		
Percent Similarity:	33.18%	Conservative:	73
Best Local Similarity:	21.75%	Mismatches:	188
Query Match:	7.11%	Indels:	239
RESULT 1055			
ID	AAN60597 standard; cDNA; 1446 BP.		
DE	Sequence encoding polypeptide with plasminogen activator activity.		
PN	JP61139385-A.		
PD	26-JUN-1986.		
PA	(TOYJ ) TOYO SODA MFG CO LTD.		
Percent Similarity:	36.70%	Conservative:	77
Best Local Similarity:	23.05%	Mismatches:	193
Query Match:	7.10%	Indels:	164
RESULT 1056			
ID	AAO23498 standard; DNA; 1605 BP.		
DE	Encoded t-PA variant MB1005 with two K2 kringle regions.		
PN	US5100666-A.		
PD	31-MAR-1992.		
PA	(MONS ) MONSANTO CO.		
Percent Similarity:	36.70%	Conservative:	77
Best Local Similarity:	23.05%	Mismatches:	193
Query Match:	7.10%	Indels:	164

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Query Match: 7.10% Indels: 164
RESULT 1057
ID AAN90742 standard; DNA; 1609 BP.
DE Chemically synthesised gene coding for tissue plasminogen activator (t-
DE PA).
PN BP311589-A.
PD 12-APR-1989.
PA (MONS ) MONSANTO CO.
Percent Similarity: 36.70%
Best Local Similarity: 23.05%
Indels: 164
Query Match: 7.10%
RESULT 1058
ID AAOQ5675 standard; cDNA; 2137 BP.
DE V-PA beta.
PN BP383417-A.
PD 22-AUG-1990.
PA (SCHD ) SCHERING AG.
Percent Similarity: 37.32%
Best Local Similarity: 25.36%
Indels: 163
Query Match: 7.10%
RESULT 1059
ID AAN60700 standard; DNA; 1989 BP.
DE Sequence encoding tissue plasminogen activator (t-PA) on plasmid pTPA25.
PN WO8601538-A.
PD 13-MAR-1986.
PA (BIOJ ) BIOGEN NV.
Percent Similarity: 35.54%
Best Local Similarity: 22.65%
Indels: 186
Query Match: 7.08%
RESULT 1060
ID ADJ57514 standard; cDNA; 2106 BP.
DE Human FVII-IgG1 Fc domain fusion protein encoding cDNA.
PN WO2004006962-A2.
PD 22-JAN-2004.
PA (NOVO ) NOVO NORDISK AS.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Indels: 231
Query Match: 7.08%
RESULT 1061
ID AAF29715 standard; DNA; 2138 BP.
DE HEV11asm immunocjugate coding sequence.
PN WO200102439-A1.
PD 11-JAN-2001.
PA (UYVA ) UNIV YALE.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Indels: 231
Query Match: 7.08%
RESULT 1062
ID ABS76526 standard; cDNA; 3112 BP.
DE cDNA encoding human ovarian cancer marker OV82.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL ) MILLENNIUM PHARM INC.
Percent Similarity: 31.02%
Best Local Similarity: 20.84%
Indels: 207
Query Match: 7.08%
RESULT 1063
ID ADJ57515 standard; cDNA; 7494 BP.
DE Human FVII-IgG1 Fc domain fusion protein encoding cDNA.
PN WO2004006962-A2.
PD 22-JAN-2004.
PA (NOVO ) NOVO NORDISK AS.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Indels: 231
Query Match: 7.08%
RESULT 1064
ID AAH19464 standard; DNA; 1206 BP.
DE Mutant blood coagulant factor VII (FVII-39) coding sequence.
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Percent Similarity: 35.21%
Best Local Similarity: 22.76%
Indels: 145
Query Match: 7.07% Indels: 188
RESULT 1065
ID AAN82178 standard; DNA; 1689 BP.
DE Tissue plasminogen activator with S-119 subatd for M.
PN JP63230083-A.
PD 26-SEP-1988.
PA (EISA ) EISAI CO LTD.
Percent Similarity: 36.25%
Best Local Similarity: 23.21%
Indels: 156
Query Match: 7.07%
RESULT 1066
ID ABK31785 standard; DNA; 2913 BP.
DE DNA encoding novel human protease #42.
PN WO200200860-A2.
PD 03-JAN-2002.
PA (SUGE-) SUGEN INC.
Percent Similarity: 36.67%
Best Local Similarity: 23.43%
Indels: 142
Query Match: 7.07%
RESULT 1067
ID ADR43735 standard; cDNA; 3522 BP.
DE Human protease PRTS-6 coding sequence, SEQ ID 23.
PN WO200220736-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 36.67%
Best Local Similarity: 23.43%
Indels: 142
Query Match: 7.07%
RESULT 1068
ID ABZ76262 standard; cDNA; 877 BP.
DE Human GENSET cDNA clone name VCTRL-1.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST ) GENSET SA.
Percent Similarity: 41.75%
Best Local Similarity: 27.18%
Indels: 75
Query Match: 7.06%
RESULT 1069
ID AAH19460 standard; DNA; 1221 BP.
DE Mutant blood coagulant factor VII (FVII-5) coding sequence.
PN JP2001061479-A.
PD 13-MAR-2001.
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
Percent Similarity: 36.63%
Best Local Similarity: 22.97%
Indels: 165
Query Match: 7.06%
RESULT 1070
ID AAO62299 standard; cDNA; 1440 BP.
DE Factor VIII.
PN WO9323074-A1.
PD 25-NOV-1993.
PA (OKLA-) OKLAHOMA MED RES FOUND.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Indels: 231
Query Match: 7.06%
RESULT 1071
ID AAV40389 standard; cDNA; 1440 BP.
DE Human Factor VIIa encoding cDNA.
PN WO9831394-A2.
PD 23-JUL-1998.
PA (TEXA ) UNIV TEXAS SYSTEM.
Percent Similarity: 34.23%
Best Local Similarity: 22.03%
Indels: 231
Query Match: 7.06%
RESULT 1072
ID AAQ12072 standard; DNA; 2100 BP.
DE T-PA with -ve charged finger and/or kringle domain (2).
PN JF03061483-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Percent Similarity: 36.12%
Best Local Similarity: 22.24%
Indels: 197
Query Match: 7.06%

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RESULT 1073  
 ID AAX15425 standard; DNA; 2462 BP.  
 DE DNA encoding coagulation factor VII/VIIa.  
 PN US5877289-A.  
 PD 02-MAR-1999.  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1074  
 ID AAA12968 standard; DNA; 2462 BP.  
 DE DNA encoding Factor VII/VIIa, SEQ ID NO:25.  
 PN US6036955-A.  
 PD 14-MAR-2000.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (SCRI ) SCRIPPS RES INST.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1075  
 ID AAZ56118 standard; DNA; 2462 BP.  
 DE Vitamin-K-dependent coagulation factor VII/VIIa coding sequence.  
 PN US6004555-A.  
 PD 21-DEC-1999.  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1076  
 ID AAA54032 standard; DNA; 2462 BP.  
 DE Human factor VII coding sequence.  
 PN WO200054787-A1.  
 PD 21-SEP-2000.  
 PA (CHIL-) CHILDRENS HOSPITAL, PHILADELPHIA.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1077  
 ID AAA89784 standard; DNA; 2462 BP.  
 DE DNA encoding coagulation factor VII/VIIa.  
 PN US6093399-A.  
 PD 25-JUL-2000.  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1078  
 ID ABL67255 standard; DNA; 2462 BP.  
 DE Thyroid cancer related gene sequence SEQ ID NO:5592.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1079  
 ID ABN95753 standard; DNA; 2462 BP.  
 DE Gene #2251 used to diagnose liver cancer.  
 PN WO200229103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1080  
 ID ADG71756 standard; DNA; 2462 BP.  
 DE Vitamin K dependent coagulation factor VII/VIIa.  
 PN US2003219441-A1.  
 PD 27-NOV-2003.

PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (SCRI ) SCRIPPS RES INST.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1081  
 ID AAN60064 standard; DNA; 2483 BP.  
 DE Factor VII cDNA of lambda VII2463.  
 PN EP200421-A.  
 PD 10-DEC-1986.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Percent Similarity: 34.23%  
 Best Local Similarity: 22.03%  
 Query Match: 7.06%  
 Indels: 231  
 Conservative: 77  
 Mismatches: 184

RESULT 1082  
 ID AAA54031 standard; DNA; 1507 BP.  
 DE Human factor X coding sequence.  
 PN WO200054787-A1.  
 PD 21-SEP-2000.  
 PA (CHIL-) CHILDRENS HOSPITAL, PHILADELPHIA.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 Percent Similarity: 37.50%  
 Best Local Similarity: 23.99%  
 Query Match: 7.05%  
 Indels: 120  
 Conservative: 67  
 Mismatches: 191

RESULT 1083  
 ID ABZ35322 standard; cDNA; 1507 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 433.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 37.50%  
 Best Local Similarity: 23.99%  
 Query Match: 7.05%  
 Indels: 120  
 Conservative: 67  
 Mismatches: 191

RESULT 1084  
 ID ADE84862 standard; DNA; 1507 BP.  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #81.  
 PN WO2003038129-A2.  
 PD 08-MAY-2003.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 37.50%  
 Best Local Similarity: 23.99%  
 Query Match: 7.05%  
 Indels: 120  
 Conservative: 67  
 Mismatches: 191

RESULT 1085  
 ID ABL29871 standard; DNA; 1569 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41086.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 38.99%  
 Best Local Similarity: 25.23%  
 Query Match: 7.05%  
 Indels: 116  
 Conservative: 60  
 Mismatches: 150

RESULT 1086  
 ID ADQ22168 standard; DNA; 1570 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4988.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 37.50%  
 Best Local Similarity: 23.99%  
 Query Match: 7.05%  
 Indels: 120  
 Conservative: 67  
 Mismatches: 191

RESULT 1087  
 ID AAH57469 standard; cDNA; 1887 BP.  
 DE Human liver cell specific cDNA sequence SEQ ID NO:309.  
 PN WO200132927-A2.  
 PD 10-MAY-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.50%  
 Best Local Similarity: 23.99%  
 Query Match: 7.05%  
 Indels: 120  
 Conservative: 67  
 Mismatches: 191

RESULT 1088  
 ID ADE85980 standard; cDNA; 1996 BP.  
 DE Human tissue urokinase plasminogen activator coding sequence.  
 PN WO2003087393-A2.

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PD 23-OCT-2003.
PA (GLOB-) GLOBAL BIOTECH INC.
Percent Similarity: 34.49%
Best Local Similarity: 22.31%
Query Match: 7.05%
RESULT 1089
ID ACN42307 standard; cDNA; 1783 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1182.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INC-) INCYTE CORP.
Percent Similarity: 33.18%
Best Local Similarity: 22.42%
Query Match: 7.03%
RESULT 1090
ID ACN41281 standard; cDNA; 2227 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:156.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INC-) INCYTE CORP.
Percent Similarity: 31.82%
Best Local Similarity: 21.35%
Query Match: 7.03%
RESULT 1091
ID AAQ05674 standard; cDNA; 2257 BP.
DE v-PA alpha2.
PN EP383417-A.
PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Percent Similarity: 38.40%
Best Local Similarity: 26.12%
Query Match: 7.03%
RESULT 1092
ID AAC76693 standard; cDNA; 3623 BP.
DE Human ORFX ORF2248 polynucleotide sequence SEQ ID NO:4495.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.00%
Best Local Similarity: 24.78%
Query Match: 7.03%
RESULT 1093
ID AAZ34034 standard; DNA; 1327 BP.
DE Human EST DNA35597.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1094
ID AAC78495 standard; cDNA; 1327 BP.
DE Human EST DNA35597 nucleotide sequence SEQ ID NO:170.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1095
ID AAC58237 standard; cDNA; 1327 BP.
DE Human EST (expressed sequence tag) DNA35597 SEQ ID NO:25.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1096
ID ACA63602 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein DNA35597.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Conservative: 68
Mismatch: 191
Indel: 156

PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1097
ID ACA71766 standard; cDNA; 1327 BP.
DE Human secreted and transmembrane polypeptide PRO618 EST.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1098
ID ABX92406 standard; cDNA; 1327 BP.
DE Human PRO618 EST polynucleotide sequence.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1099
ID ACA66147 standard; cDNA; 1327 BP.
DE Human secreted/transmembrane protein EST DNA35597.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1100
ID ADA24709 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein EST DNA35597.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1101
ID ACD29748 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein EST DNA35597.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1102
ID ADA12370 standard; cDNA; 1327 BP.
DE Human secreted/transmembrane polypeptide PRO618 EST.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1103
ID ACD29163 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #38.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
RESULT 1104
ID ADB73676 standard; cDNA; 1327 BP.
DE Human PRO polynucleotide sequence #38.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 35.74%
Conservative: 68
Mismatch: 191
Indel: 156
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Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1105					
ID ADB76392 standard; cDNA; 1327 BP.					
DE Human PRO polynucleotide sequence #38.					
PN US2003083248-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1106					
ID ADC43818 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003054986-A1.					
PD 20-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1107					
ID ADC61578 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003049684-A1.					
PD 13-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1108					
ID ADC63542 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003054405-A1.					
PD 20-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1109					
ID ADC66642 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003060406-A1.					
PD 27-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1110					
ID ADC68766 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003064407-A1.					
PD 03-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1111					
ID ADC62826 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003068648-A1.					
PD 10-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1112					
ID ADC67891 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003069178-A1.					
PD 10-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1113					
ID ADC41211 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003072745-A1.					
PD 17-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1114					
ID ADC67266 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003073131-A1.					
PD 17-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1115					
ID ADC62202 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003073624-A1.					
PD 17-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1116					
ID ADC41835 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003104998-A1.					
PD 05-JUN-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1117					
ID ADE49204 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003096744-A1.					
PD 22-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1118					
ID ADE35258 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003203434-A1.					
PD 30-OCT-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1119					
ID ADE16372 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003203435-A1.					
PD 30-OCT-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				
RESULT 1120					
ID ADD72987 standard; cDNA; 1327 BP.					
DE Human EST from secreted/transmembrane protein #1.					
PN US2003203436-A1.					
PD 30-OCT-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity: 35.74%	Conservative: 68				
Best Local Similarity: 23.15%	Mismatches: 191				
Query Match:	Indels: 156				

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RESULT 1121
ID ADD72345 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1122
ID ADE16996 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1123
ID ADF47010 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1124
ID ADG52767 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1125
ID ADG60087 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1126
ID ADI60847 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US200307700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1127
ID ACD42567 standard; cDNA; 1327 BP.
DE Novel human secreted and transmembrane protein EST DNA5597.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1128
ID ADE48504 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1129
ID ADF40561 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1130
ID ADF61245 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1131
ID ADF39937 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1132
ID ADF45733 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156
RESULT 1133
ID ADF24129 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatch: 191
Indels: 156

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PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1135  
ID ADF23505 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1136  
ID ADF33488 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1137  
ID ADF26955 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1138  
ID ADF27591 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1139  
ID ADF41185 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1140  
ID ADF32864 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1141  
ID ADF25230 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1142  
ID ADF6331 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003199674-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1143  
ID ADF34120 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1144  
ID ADF46357 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1145  
ID ADG50343 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1146  
ID ADG49719 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1147  
ID ADG51591 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1148  
ID ADG49095 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1149  
ID ADG48471 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.74%  
Best Local Similarity: 23.15%  
Query Match: 7.02%  
Conservative: 68  
Mismatches: 191  
Indels: 156  
RESULT 1150  
ID ADG50967 standard; cDNA; 1327 BP.  
DE Human EST from secreted/transmembrane protein #1.  
PN US2004005312-A1.  
PD 08-JAN-2004.

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PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1151
ID ADG58911 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1152
ID ADG62367 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1153
ID ADH25392 standard; cDNA; 1327 BP.
DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:170.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1154
ID ADM17169 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1155
ID ADL07003 standard; cDNA; 1327 BP.
DE Human EST from secreted/transmembrane protein #1.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1156
ID ADT91616 standard; cDNA; 1327 BP.
DE Human EST nucleotide DNA35597.
PN AU2002317529-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 35.74%
Best Local Similarity: 23.15%
Query Match: 7.02%
Conservative: 68
Mismatches: 191
Indels: 156
RESULT 1157
ID RAI99982 standard; cDNA; 1338 BP.
DE Human FVII encoding cDNA SEQ ID NO 2.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1158
ID ADF44970 standard; cDNA; 1338 BP.
DE Human Factor VII coding sequence, SEQ ID 1.
PN WO2003093465-A1.
PD 13-NOV-2003.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1159
ID ADO10532 standard; DNA; 1338 BP.
DE Human factor VIIa gene.
PN WO2004029091-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1160
ID ADS12865 standard; DNA; 1338 BP.
DE Human factor VII cDNA SEQ ID NO:1.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1161
ID RAI99983 standard; cDNA; 1357 BP.
DE Human FVII expression cassette SEQ ID NO 4.
PN WO200158935-A2.
PD 16-AUG-2001.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1162
ID ADF44974 standard; DNA; 1357 BP.
DE Human Factor VII-related sequence.
PN WO2003093465-A1.
PD 13-NOV-2003.
PA (MAXY-) MAXYGEN APS.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1163
ID ADS12867 standard; DNA; 1357 BP.
DE Expression optimised human factor VII gene SEQ ID NO:3.
PN WO2004083361-A2.
PD 30-SEP-2004.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
Percent Similarity: 33.08%
Best Local Similarity: 21.54%
Query Match: 7.02%
Conservative: 75
Mismatches: 177
Indels: 259
RESULT 1164
ID AAN81091 standard; DNA; 1689 BP.
DE Mutated t-PA analogue coding sequence in plasmid Zm99-9200.
PN EP293934-A.
PD 07-DEC-1988.
PA (ZYMO ) ZYMOGENETICS INC.
Percent Similarity: 33.08%
Best Local Similarity: 23.38%
Query Match: 7.02%
Conservative: 76
Mismatches: 202
Indels: 148
RESULT 1165
ID ACN41282 standard; cDNA; 2177 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:157.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 31.99%
Best Local Similarity: 21.24%
Query Match: 7.02%
Conservative: 83
Mismatches: 242
Indels: 288

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RESULT 1166  
ID AAO46262 standard; DNA; 1727 BP.  
DE Encodes modified tPA MB1012 with two K2 kringle domains.  
PN US5244676-A.  
PD 14-SEP-1993.  
PA (MONS ) MONSANTO CO.  
Percent Similarity: 36.64%  
Best Local Similarity: 22.64%  
Query Match: 7.01%  
Conservative: 89  
Mismatches: 238  
Indels: 165  
RESULT 1167  
ID ABL65242 standard; DNA; 2036 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3579.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 35.91%  
Best Local Similarity: 24.18%  
Query Match: 7.01%  
Conservative: 79  
Mismatches: 212  
Indels: 222  
RESULT 1168  
ID AEN95114 standard; DNA; 2036 BP.  
DE Gene #1612 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 35.91%  
Best Local Similarity: 24.18%  
Query Match: 7.01%  
Conservative: 79  
Mismatches: 212  
Indels: 222  
RESULT 1169  
ID ADJ57517 standard; cDNA; 2040 BP.  
DE Human FVII-IG1 FC domain fusion protein encoding cDNA.  
PN WO2004006962-A2.  
PD 22-JAN-2004.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 7.01%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1170  
ID ADJ57518 standard; cDNA; 7427 BP.  
DE Human FVII-IG1 FC domain fusion protein encoding cDNA.  
PN WO2004006962-A2.  
PD 22-JAN-2004.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 7.01%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1171  
ID ABS68099 standard; DNA; 1505 BP.  
DE Clotting Factor IX construct PFIXABCD.  
PN WO200264799-A2.  
PD 22-AUG-2002.  
PA (TRAN-) TRANSKARYOTIC THERAPIES INC.  
Percent Similarity: 34.48%  
Best Local Similarity: 21.94%  
Query Match: 7.00%  
Conservative: 80  
Mismatches: 202  
Indels: 217  
RESULT 1172  
ID AAN70249 standard; DNA; 1581 BP.  
DE Sequence encoding wild-type human tissue plasminogen activator (t-PA)  
DE from HeLa cells.  
PN EP225286-A.  
PD 10-JUN-1987.  
PA (CIBA ) CIBA GEIGY AG.  
Percent Similarity: 35.54%  
Best Local Similarity: 22.47%  
Query Match: 7.00%  
Conservative: 75  
Mismatches: 187  
Indels: 186  
RESULT 1173  
ID AAH19459 standard; DNA; 1221 BP.  
DE Wild-type human blood coagulant factor VII (FVII) coding sequence.  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA ) ZH KAGAKU & KESSRI RYOHO KENKYUSHO.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183

RESULT 1174  
ID ACC78872 standard; DNA; 1332 BP.  
DE Human Factor VIIa encoding DNA.  
PN WO2003031464-A2.  
PD 17-APR-2003.  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1175  
ID ADN49679 standard; DNA; 1332 BP.  
DE Human Factor VIIa DNA SeqID 7.  
PN WO2004033651-A2.  
PD 22-APR-2004.  
PA (NEOS-) NEOSE TECHNOLOGIES INC.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1176  
ID ACN42308 standard; cDNA; 1667 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1183.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 35.05%  
Best Local Similarity: 23.12%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 157  
Indels: 198  
RESULT 1177  
ID ADP12869 standard; DNA; 2412 BP.  
DE Reference mRNA sequence #83.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1178  
ID AAO80296 standard; cDNA; 2422 BP.  
DE cDNA encoding Factor VII.  
PN WO9427631-A1.  
PD 08-DEC-1994.  
PA (ZYMO ) ZYMOGENETICS INC.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1179  
ID AAV02230 standard; cDNA; 2422 BP.  
DE Homo sapiens cDNA encoding Ser344Ala modified factor VII.  
PN WO9747651-A1.  
PD 18-DEC-1997.  
PA (NOVO ) NOVO-NORDISK AS.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1180  
ID AAZ57385 standard; cDNA; 2422 BP.  
DE Factor VII encoding cDNA SEQ ID NO:1.  
PN US997864-A.  
PD 07-DEC-1999.  
PA (NOVO ) NOVO-NORDISK AS.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183  
RESULT 1181  
ID AAF57099 standard; cDNA; 2422 BP.  
DE Human Factor VII polypeptide encoding cDNA.  
PN US6183743-B1.  
PD 06-FEB-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Percent Similarity: 35.21%  
Best Local Similarity: 22.57%  
Query Match: 6.98%  
Conservative: 65  
Mismatches: 150  
Indels: 183



Percent Similarity: 35.21% Conservative: 65  
Best Local Similarity: 22.57% Mismatches: 150  
Query Match: 6.98% Indels: 183  
RESULT 1182  
ID ADC24226 standard; cDNA; 2422 BP.  
DE Human NOV8a encoding cDNA SEQ ID NO:33.  
PN WO2003076584-A2.  
PD 18-SEP-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 35.21% Conservative: 65  
Best Local Similarity: 22.57% Mismatches: 150  
Query Match: 6.98% Indels: 183  
RESULT 1183  
ID AAX77712 standard; DNA; 2696 BP.  
DE Murine plasminogen DNA.  
PN WO9926480-A1.  
PD 03-JUN-1999.  
PA (GENE-) GENETIX PHARM INC.  
Percent Similarity: 33.92% Conservative: 98  
Best Local Similarity: 22.38% Mismatches: 272  
Query Match: 6.98% Indels: 292  
RESULT 1184  
ID AAI70086 standard; DNA; 4496 BP.  
DE Plasmid pFN0945 encoding human coagulation Factor IX.  
PN WO200166149-A2.  
PD 13-SEP-2001.  
PA (VALE-) VALENTIS INC.  
Percent Similarity: 32.69% Conservative: 86  
Best Local Similarity: 20.88% Mismatches: 217  
Query Match: 6.98% Indels: 273  
RESULT 1185  
ID ABX14193 standard; DNA; 6098 BP.  
DE Plasmid pLN174 for expressing human coagulation Factor VII.  
PN WO20027218-A1.  
PD 03-OCT-2002.  
PA (NOVO) NOVO NORDISK AS.  
Percent Similarity: 35.21% Conservative: 65  
Best Local Similarity: 22.57% Mismatches: 150  
Query Match: 6.98% Indels: 183  
RESULT 1186  
ID AAL45696 standard; DNA; 1683 BP.  
DE Human blood coagulation factor VII activating protease DNA.  
PN EP1182258-A1.  
PD 27-FEB-2002.  
PA (AVET) AVENTIS BEHRING GMBH.  
Percent Similarity: 40.00% Conservative: 86  
Best Local Similarity: 24.78% Mismatches: 202  
Query Match: 6.97% Indels: 138  
RESULT 1187  
ID AAL45697 standard; DNA; 1683 BP.  
DE Human blood coagulation factor VII activating protease mutant DNA.  
PN EP1182258-A1.  
PD 27-FEB-2002.  
PA (AVET) AVENTIS BEHRING GMBH.  
Percent Similarity: 40.00% Conservative: 86  
Best Local Similarity: 24.78% Mismatches: 202  
Query Match: 6.97% Indels: 138  
RESULT 1188  
ID ABN95170 standard; DNA; 3008 BP.  
DE Gene #1668 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 40.00% Conservative: 86  
Best Local Similarity: 24.78% Mismatches: 202  
Query Match: 6.97% Indels: 138  
RESULT 1189  
ID ACC51204 standard; cDNA; 3008 BP.  
DE Human Plk-1 related cDNA sequence hmft-0306 SEQ ID NO:89.  
PN WO2003018807-A1.  
PD 06-MAR-2003.  
PA (HISM) HISAMITSU PHARM CO LTD.

PA (CHIB-) CHIBA PREFECTURE.  
Percent Similarity: 40.00% Conservative: 86  
Best Local Similarity: 24.78% Mismatches: 202  
Query Match: 6.97% Indels: 138  
RESULT 1190  
ID AAQ11551 standard; DNA; 1659 BP.  
DE Sequence encoding tissue plasminogen activator deriv.  
PN JP03065184-A.  
PD 20-MAR-1991.  
PA (KANF) KANEGAFUCHI CHEM KK.  
Percent Similarity: 35.49% Conservative: 73  
Best Local Similarity: 22.73% Mismatches: 186  
Query Match: 6.95% Indels: 186  
RESULT 1191  
ID AAN70089 standard; DNA; 2009 BP.  
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator  
DE (tPA) 1-91, urokinase kringle (UKK) 50-131 and tPA 92-527.  
PN EP213794-A.  
PD 11-MAR-1987.  
PA (AMP) AMERICAN HOME PROD CORP.  
Percent Similarity: 35.02% Conservative: 81  
Best Local Similarity: 22.24% Mismatches: 197  
Query Match: 6.95% Indels: 216  
RESULT 1192  
ID AAI70087 standard; DNA; 4276 BP.  
DE Codon optimised plasmid pFNI645 for human coagulation Factor IX.  
PN WO200166149-A2.  
PD 13-SEP-2001.  
PA (VALE-) VALENTIS INC.  
Percent Similarity: 32.82% Conservative: 88  
Best Local Similarity: 20.48% Mismatches: 237  
Query Match: 6.95% Indels: 242  
RESULT 1193  
ID AAH19463 standard; DNA; 1206 BP.  
DE Mutant blood coagulant factor VII (FVII-31) coding sequence.  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
Percent Similarity: 35.02% Conservative: 64  
Best Local Similarity: 22.57% Mismatches: 146  
Query Match: 6.92% Indels: 188  
RESULT 1194  
ID AAQ12077 standard; DNA; 2100 BP.  
DE T-PA variant having Lys416 substituted (4).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Percent Similarity: 34.84% Conservative: 74  
Best Local Similarity: 21.95% Mismatches: 191  
Query Match: 6.92% Indels: 186  
RESULT 1195  
ID AAQ13164 standard; DNA; 1721 BP.  
DE Gene encoding t-PA variant MB1023.  
PN US5037752-A.  
PD 06-AUG-1991.  
PA (MONS) MONSANTO CO.  
Percent Similarity: 35.21% Conservative: 88  
Best Local Similarity: 21.80% Mismatches: 220  
Query Match: 6.91% Indels: 205  
RESULT 1196  
ID AAQ63951 standard; cDNA; 2033 BP.  
DE Hepatocyte growth factor converting protease coding sequence.  
PN EP596524-A2.  
PD 11-MAY-1994.  
PA (MITU) MITSUBISHI KASEI CORP.  
Percent Similarity: 36.57% Conservative: 82  
Best Local Similarity: 24.33% Mismatches: 213  
Query Match: 6.91% Indels: 214  
RESULT 1197  
ID AAN60063 standard; cDNA; 2177 BP.  
DE Partial Factor VII cDNA.  
PN EP200421-A.  
PD 10-DEC-1986.

PA (ZYMO ) ZYMOGENETICS INC.  
Percent Similarity: 33.33%  
Best Local Similarity: 22.29%  
Query Match: 6.91%  
RESULT 1198  
ID ABZ33309 standard; cDNA; 1645 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 420.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 38.65%  
Best Local Similarity: 26.52%  
Query Match: 6.89%  
RESULT 1199  
ID AAA62807 standard; DNA; 672 BP.  
DE Neurosin encoding DNA sequence.  
PN WO200031284-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1200  
ID AAQ53487 standard; DNA; 732 BP.  
DE DNA encoding Zyme APP-cleaving protease.  
PN EP576152-A1.  
PD 29-DEC-1993.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1201  
ID AAH19461 standard; DNA; 1221 BP.  
DE Mutant blood coagulant factor VII (FVII-6) coding sequence.  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA ) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.  
Percent Similarity: 35.03%  
Best Local Similarity: 22.31%  
Query Match: 6.88%  
RESULT 1202  
ID ADE53650 standard; cDNA; 1413 BP.  
DE Human kallikrein 6 serine protease encoding cDNA SEQ ID NO:2.  
PN WO200309328-A1.  
PD 04-DEC-2003.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
PA (UYFL ) UNIV FLORIDA STATE.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1203  
ID AAT79126 standard; cDNA to mRNA; 1438 BP.  
DE Human serine protease 59 (SP59) cDNA.  
PN JP09149790-A.  
PD 10-JUN-1997.  
PA (SUNR ) SUNTORY LTD.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1204  
ID ADR72625 standard; DNA; 1451 BP.  
DE Human renal cell carcinoma-related kallikrein 6 (KLK6) DNA 1.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1205  
ID ADR72877 standard; DNA; 1451 BP.  
DE Human ovarian cancer-related tumour marker kallikrein 6 (KLK6) DNA 1.  
PN WO2004075713-A2.  
PD 10-SEP-2004.

PA (MOUN ) MOUNT SINAI HOSPITAL.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1206  
ID ADQ83735 standard; cDNA; 1505 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #549.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1207  
ID ACN40669 standard; cDNA; 1505 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326750, SEQ ID NO:5592.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1208  
ID ABS76453 standard; cDNA; 1506 BP.  
DE cDNA encoding human ovarian cancer marker OV33.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1209  
ID ABL62164 standard; DNA; 1506 BP.  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:501.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1210  
ID ABZ35055 standard; cDNA; 1506 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 167.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1211  
ID ADB80566 standard; DNA; 1506 BP.  
DE Ovarian cancer-associated transcript #66.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1212  
ID AAD63182 standard; DNA; 1506 BP.  
DE Human kallikrein 6 (KLK6) DNA.  
PN US2003190656-A1.  
PD 09-OCT-2003.  
PA (WANG/) WANG Y.  
Percent Similarity: 44.57%  
Best Local Similarity: 31.40%  
Query Match: 6.88%  
RESULT 1213  
ID AAD62783 standard; DNA; 1506 BP.  
DE Human kallikrein 6 (KLK6) DNA.  
PN US2003194733-A1.

PD	16-OCT-2003.
PA	(WANG/) WANG Y.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1214	
ID	ACC80976 standard; cDNA; 1506 BP.
DE	Human 2047 protein encoding cDNA.
PN	WO2003037258-A2.
PD	08-MAY-2003.
PA	(MILL-) MILLENNIUM PHARM INC.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1215	
ID	ADN39211 standard; cDNA; 1506 BP.
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:529.
PN	WO2003042661-A2.
PD	22-MAY-2003.
PA	(BOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1216	
ID	ADP88278 standard; cDNA; 1506 BP.
DE	Ovarian cancer marker gene KLK6, SEQ ID NO:55.
PN	EP1349104-A2.
PD	01-OCT-2003.
PA	(ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1217	
ID	ADN29137 standard; DNA; 1506 BP.
DE	Human kallikrein 6 associated DNA seqid 11.
PN	US2004097452-A1.
PD	20-MAY-2004.
PA	(ISIS-) ISIS PHARM INC.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1218	
ID	ADR24953 standard; DNA; 1506 BP.
DE	Breast cancer prognosis marker #814.
PN	WO2004065545-A2.
PD	05-AUG-2004.
PA	(ROSE-) ROSETTA INPHARMATICS LLC.
PA	(NECA-) NETHERLANDS CANCER INST.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1219	
ID	AQD89075 standard; cDNA; 1506 BP.
DE	Human urological disorder related protein 2047 encoding cDNA SEQ:27.
PN	WO2004065576-A2.
PD	05-AUG-2004.
PA	(MILL-) MILLENNIUM PHARM INC.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1220	
ID	ADR72627 standard; DNA; 1506 BP.
DE	Human renal cell carcinoma-related kallikrein 6 (KLK6) DNA 3.
PN	WO2004077060-A2.
PD	10-SEP-2004.
PA	(MOUN) MOUNT SINAI HOSPITAL.
Percent Similarity:	44.57%
Best Local Similarity:	31.40%
Query Match:	Conservative: 34 Mismatches: 94 Indels: 49
RESULT 1221	
ID	ADR72879 standard; DNA; 1506 BP.
DE	Human ovarian cancer-related tumour marker kallikrein 6 (KLK6) DNA 3.
PN	WO2004075713-A2.

Query Match:	6.84%	Indels:	166
RESULT 1233			
ID AAN70992 standard; DNA; 1323 BP.			
DE Modified tissue plasminogen activator.			
FN AU8661804-A.			
PD 05-MAR-1987.			
PA (ELIL ) LILLY & CO ELI.			
Percent Similarity: 36.86%		Conservative:	66
Best Local Similarity: 23.92%		Mismatches:	177
Query Match:	6.83%	Indels:	145
RESULT 1234			
ID AAN70991 standard; DNA; 1422 BP.			
DE Modified tissue plasminogen activator.			
FN AU8661804-A.			
PD 05-MAR-1987.			
PA (ELIL ) LILLY & CO ELI.			
Percent Similarity: 36.86%		Conservative:	66
Best Local Similarity: 23.92%		Mismatches:	177
Query Match:	6.83%	Indels:	145
RESULT 1235			
ID AAN91217 standard; DNA; 1689 BP.			
DE Mutated cDNA coding sequence of tissue plasminogen activator (t-PA).			
FN AU8817430-A.			
PD 08-DEC-1988.			
PA (NOVO ) NOVO IND AS.			
PA (ZYMO ) ZYMOGENETICS INC.			
PA (EISA ) EISAI CO LTD.			
Percent Similarity: 34.35%		Conservative:	81
Best Local Similarity: 21.98%		Mismatches:	192
Query Match:	6.83%	Indels:	241
RESULT 1236			
ID AAQ06319 standard; DNA; 1721 BP.			
DE Synthetic gene encoding t-PA variant MB1023.			
FN US4963357-A.			
PD 16-OCT-1990.			
PA (MONS ) MONSANTO CO.			
Percent Similarity: 35.21%		Conservative:	89
Best Local Similarity: 21.65%		Mismatches:	220
Query Match:	6.83%	Indels:	205
RESULT 1237			
ID AAQ13165 standard; DNA; 1721 BP.			
DE Gene encoding t-PA variant MB1083 with longer half-life.			
FN US5037752-A.			
PD 06-AUG-1991.			
PA (MONS ) MONSANTO CO.			
Percent Similarity: 35.21%		Conservative:	89
Best Local Similarity: 21.65%		Mismatches:	220
Query Match:	6.83%	Indels:	205
RESULT 1238			
ID ABL06001 standard; cDNA; 1032 BP.			
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12485.			
FN WO200171042-A2.			
PD 27-SEP-2001.			
PA (PEKE ) PE CORP NY.			
Percent Similarity: 40.54%		Conservative:	57
Best Local Similarity: 25.14%		Mismatches:	121
Query Match:	6.82%	Indels:	99
RESULT 1239			
ID ADB58749 standard; DNA; 2737 BP.			
DE Toxicity-related gene, SEQ ID 3775.			
FN WO2003064624-A2.			
PD 07-AUG-2003.			
PA (GENE ) GENE LOGIC INC.			
Percent Similarity: 33.81%		Conservative:	100
Best Local Similarity: 21.99%		Mismatches:	269
Query Match:	6.82%	Indels:	292
RESULT 1240			
ID AAQ00543 standard; cDNA; 1620 BP.			
DE Vampire bat plasminogen activator gene.			
FN EP352119-A.			
PD 24-JAN-1990.			
PA (MERI ) MERCK & CO INC.			
PA (SCHD ) SCHERING AG.			

Percent Similarity:	37.62%	Conservative:	62
Best Local Similarity:	25.54%	Mismatches:	174
Query Match:	6.81%	Indels:	146
RESULT 1241			
ID AAT27588 standard; DNA; 1680 BP.			
DE Novel plasminogen activator DNA.			
PN US5504001-A.			
PD 02-APR-1996.			
PA (ZYMO ) ZYMOGENETICS INC.			
Percent Similarity:	38.38%	Conservative:	81
Best Local Similarity:	23.78%	Mismatches:	194
Query Match:	6.81%	Indels:	149
RESULT 1242			
ID AAN70090 standard; DNA; 2009 BP.			
DE Hybrid plasminogen activator (PA) contg. tissue plasminogen activator			
DE (tPA) 1-261, urokinase kringles (UKK) 50-131 and tPA 262-527.			
PN EP213794-A.			
PD 11-MAR-1987.			
PA (AMHP ) AMERICAN HOME PROD CORP.			
Percent Similarity:	36.12%	Conservative:	78
Best Local Similarity:	23.32%	Mismatches:	225
Query Match:	6.81%	Indels:	166
RESULT 1243			
ID ADH41498 standard; DNA; 3345 BP.			
DE Novel human nucleic acid NOV3s.			
PN WO2003102159-A2.			
PD 11-DEC-2003.			
PA (CURA-) CURAGEN CORP.			
Percent Similarity:	38.76%	Conservative:	69
Best Local Similarity:	24.90%	Mismatches:	180
Query Match:	6.78%	Indels:	126
RESULT 1244			
ID AAL38736 standard; DNA; 1389 BP.			
DE Contiguous DNA of human factor IX.			
PN WO200240544-A2.			
PD 23-MAY-2002.			
PA (TEXA ) UNIV TEXAS SYSTEM.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1245			
ID AAX15426 standard; DNA; 1437 BP.			
DE DNA encoding coagulation factor IX/IXa.			
PN US5877289-A.			
PD 02-MAR-1999.			
PA (SCRI ) SCRIPPS RES INST.			
PA (TEXA ) UNIV TEXAS SYSTEM.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1246			
ID AAA12969 standard; DNA; 1437 BP.			
DE DNA encoding Factor IX/IXa, SEQ ID NO:26.			
PN US6036955-A.			
PD 14-MAR-2000.			
PA (TEXA ) UNIV TEXAS SYSTEM.			
PA (SCRI ) SCRIPPS RES INST.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1247			
ID AAZ56119 standard; DNA; 1437 BP.			
DE Vitamin-K-dependent coagulation factor IX/IXa coding sequence.			
PN US6004555-A.			
PD 21-DEC-1999.			
PA (SCRI ) SCRIPPS RES INST.			
PA (TEXA ) UNIV TEXAS SYSTEM.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1248			
ID AAA89785 standard; DNA; 1437 BP.			
DE DNA encoding coagulation factor IX/IXa.			
PN US6093399-A.			
PD 25-JUL-2000.			
PA (SCRI ) SCRIPPS RES INST.			
PA (TEXA ) UNIV TEXAS SYSTEM.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1249			
ID ADB86697 standard; cDNA; 1437 BP.			
DE Factor IX coding sequence.			
PN WO2003088899-A2.			
PD 30-OCT-2003.			
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1250			
ID ACC78873 standard; DNA; 1437 BP.			
DE Human Factor IX encoding DNA.			
PN WO2003031464-A2.			
PD 17-APR-2003.			
PA (NEOS-) NEOSE TECHNOLOGIES INC.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1251			
ID ADG71757 standard; DNA; 1437 BP.			
DE Vitamin K dependent coagulation factor IX/IXa.			
PN US2003219441-A1.			
PD 27-NOV-2003.			
PA (TEXA ) UNIV TEXAS SYSTEM.			
PA (SCRI ) SCRIPPS RES INST.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1252			
ID ADN49681 standard; DNA; 1437 BP.			
DE Human Factor IX DNA SeqID 9.			
PN WO2004033651-A2.			
PD 22-APR-2004.			
PA (NEOS-) NEOSE TECHNOLOGIES INC.			
Percent Similarity:	35.13%	Conservative:	72
Best Local Similarity:	22.22%	Mismatches:	180
Query Match:	6.77%	Indels:	182
RESULT 1253			
ID ADH41470 standard; DNA; 1368 BP.			
DE Novel human nucleic acid NOV3e.			
PN WO2003102159-A2.			
PD 11-DEC-2003.			
PA (CURA-) CURAGEN CORP.			
Percent Similarity:	38.79%	Conservative:	70
Best Local Similarity:	24.65%	Mismatches:	178
Query Match:	6.76%	Indels:	126
RESULT 1254			
ID ADH41494 standard; DNA; 3345 BP.			
DE Novel human nucleic acid NOV3q.			
PN WO2003102159-A2.			
PD 11-DEC-2003.			
PA (CURA-) CURAGEN CORP.			
Percent Similarity:	38.95%	Conservative:	73
Best Local Similarity:	24.14%	Mismatches:	180
Query Match:	6.76%	Indels:	122
RESULT 1255			
ID AAN81088 standard; DNA; 1680 BP.			
DE Tissue plasminogen activator analogue coding sequence.			
PN EP293934-A.			
PD 07-DEC-1988.			
PA (ZYMO ) ZYMOGENETICS INC.			
PA (NOVO ) NOVO IND AS.			
PA (EISA ) EISA CO LTD.			
Percent Similarity:	38.86%	Conservative:	81
Best Local Similarity:	23.94%	Mismatches:	208
Query Match:	6.74%	Indels:	125

<b>RESULT 1256</b>					
ID	ACN41795 standard; cDNA; 2075 BP.				
DE	Human diagnostic and therapeutic polynucleotide SEQ ID NO:670.				
FN	WO200402373-A2.				
PD	25-MAR-2004.				
PA	(INCY-) INCYTE CORP.				
Percent Similarity:	34.28%	Conservative:	81		
Best Local Similarity:	21.48%	Mismatches:	207		
Query Match:	6.74%	Indels:	211		
<b>RESULT 1257</b>					
ID	ABU18213 standard; DNA; 753 BP.				
DE	Drosophila melanogaster genomic polynucleotide SEQ ID NO 6112.				
FN	WO200171042-A2.				
PD	27-SEP-2001.				
PA	(PEKE ) PE CORP NY.				
Percent Similarity:	45.17%	Conservative:	50		
Best Local Similarity:	25.87%	Mismatches:	111		
Query Match:	6.73%	Indels:	31		
<b>RESULT 1258</b>					
ID	ADH41468 standard; DNA; 1368 BP.				
DE	Novel human nucleic acid NOV3d.				
FN	WO2003102159-A2.				
PD	11-DEC-2003.				
PA	(CURA-) CURAGEN CORP.				
Percent Similarity:	38.79%	Conservative:	69		
Best Local Similarity:	24.85%	Mismatches:	178		
Query Match:	6.73%	Indels:	126		
<b>RESULT 1259</b>					
ID	AA93124 standard; cDNA; 3094 BP.				
DE	Human secreted protein coding sequence SEQ ID NO: 47.				
FN	WO200049134-A1.				
PD	24-AUG-2000.				
PA	(ALPH-) ALPHAGENE INC.				
Percent Similarity:	38.79%	Conservative:	69		
Best Local Similarity:	24.85%	Mismatches:	178		
Query Match:	6.73%	Indels:	126		
<b>RESULT 1260</b>					
ID	ADH41462 standard; DNA; 3345 BP.				
DE	Novel human nucleic acid NOV3a.				
FN	WO2003102159-A2.				
PD	11-DEC-2003.				
PA	(CURA-) CURAGEN CORP.				
Percent Similarity:	38.79%	Conservative:	69		
Best Local Similarity:	24.85%	Mismatches:	178		
Query Match:	6.73%	Indels:	126		
<b>RESULT 1261</b>					
ID	ADH41496 standard; DNA; 3345 BP.				
DE	Novel human nucleic acid NOV3r.				
FN	WO2003102159-A2.				
PD	11-DEC-2003.				
PA	(CURA-) CURAGEN CORP.				
Percent Similarity:	38.79%	Conservative:	69		
Best Local Similarity:	24.85%	Mismatches:	178		
Query Match:	6.73%	Indels:	126		
<b>RESULT 1262</b>					
ID	ADH41492 standard; DNA; 3345 BP.				
DE	Novel human nucleic acid NOV3p.				
FN	WO2003102159-A2.				
PD	11-DEC-2003.				
PA	(CURA-) CURAGEN CORP.				
Percent Similarity:	38.79%	Conservative:	69		
Best Local Similarity:	24.85%	Mismatches:	178		
Query Match:	6.73%	Indels:	126		
<b>RESULT 1263</b>					
ID	ADH41492 standard; DNA; 3345 BP.				
DE	Novel human nucleic acid NOV3p.				
FN	WO2003102159-A2.				
PD	11-DEC-2003.				
PA	(CURA-) CURAGEN CORP.				
Percent Similarity:	38.79%	Conservative:	69		
Best Local Similarity:	24.85%	Mismatches:	178		
Query Match:	6.73%	Indels:	126		
<b>RESULT 1264</b>					
ID	ADC24228 standard; cDNA; 1361 BP.				
DE	Human NOV8b encoding cDNA SEQ ID NO:35.				
FN	WO2003076584-A2.				
PD	18-SEP-2003.				
PA	(CURA-) CURAGEN CORP.				
Percent Similarity:	31.00%	Conservative:	63		
Best Local Similarity:	20.99%	Mismatches:	160		
Query Match:	6.72%	Indels:	274		

ID	AA991220 standard; DNA; 1680 BP.	
DE	Analogue of cDNA coding sequence of tissue plasminogen activator	
FN	AA9817430-A.	
PD	08-DEC-1988.	
PA	(NOVO ) NOVO IND AS.	
PA	(ZYMO ) ZYMOGENETICS INC.	
PA	(EISA ) EISAI CO LTD.	
Percent Similarity:	38.28%	
Best Local Similarity:	24.54%	Conservative: 75
Query Match:	6.72%	Mismatches: 207
RESULT 1265		Indels: 131
ID	AAT27587 standard; DNA; 1680 BP.	
DE	Novel plasminogen activator DNA.	
FN	US5504001-A.	
PD	02-APR-1996.	
PA	(ZYMO ) ZYMOGENETICS INC.	
Percent Similarity:	38.86%	Conservative: 81
Best Local Similarity:	23.94%	Mismatches: 208
Query Match:	6.72%	Indels: 125
RESULT 1266		
ID	AAQ41005 standard; DNA; 5472 BP.	
DE	Sequence of plasmid pN2gpta-FIX.	
FN	AU5221269-A.	
PD	04-MAR-1993.	
PA	(IMMO ) IMMUNO AG.	
Percent Similarity:	34.07%	Conservative: 84
Best Local Similarity:	21.63%	Mismatches: 198
Query Match:	6.72%	Indels: 247
RESULT 1267		
ID	AAA89883 standard; DNA; 5532 BP.	
DE	Plasmid pN2gpta-FIX.	
FN	US6103244-A.	
PD	15-AUG-2000.	
PA	(IMMO ) IMMUNO AG.	
Percent Similarity:	34.07%	Conservative: 84
Best Local Similarity:	21.63%	Mismatches: 198
Query Match:	6.72%	Indels: 247
RESULT 1268		
ID	AAS12901 standard; DNA; 5532 BP.	
DE	Plasmid pN2-gpta-FIX DNA sequence.	
FN	US6265183-B1.	
PD	24-JUL-2001.	
PA	(BAXT ) BAXTER AG.	
Percent Similarity:	34.07%	Conservative: 84
Best Local Similarity:	21.63%	Mismatches: 198
Query Match:	6.72%	Indels: 247
RESULT 1269		
ID	AAQ10170 standard; DNA; 1236 BP.	
DE	Encodes Pro-urokinase derivative	UK-S3 with Asn(153) and Thr(155)
FN	EP405285-A.	
PD	02-JAN-1991.	
PA	(KYOW ) KYOWA HAKKO KOGYO KK.	
Percent Similarity:	37.11%	Conservative: 64
Best Local Similarity:	24.61%	Mismatches: 175
Query Match:	6.70%	Indels: 147
RESULT 1270		
ID	ADH41476 standard; DNA; 1368 BP.	
DE	Novel human nucleic acid NOV3h.	
FN	WO2003102159-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	38.79%	Conservative: 70
Best Local Similarity:	24.65%	Mismatches: 178
Query Match:	6.70%	Indels: 126
RESULT 1271		
ID	ADH41490 standard; DNA; 1479 BP.	
DE	Novel human nucleic acid NOV3o.	
FN	WO2003102159-A2.	
PD	11-DEC-2003.	
PA	(CURA-) CURAGEN CORP.	
Percent Similarity:	38.79%	Conservative: 70
Best Local Similarity:	24.65%	Mismatches: 178
Query Match:	6.70%	Indels: 126

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RESULT 1272
ID AAN91740 standard; DNA; 2303 BP.
DE Sequence of prourokinase cDNA.
PN EP316068-A.
PA (COLB ) COLLABORATIVE RES INC.
Percent Similarity: 37.17%
Best Local Similarity: 23.79%
Query Match: 6.69%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1273
ID AAN30030 standard; cDNA; 2304 BP.
DE Sequence encoding full length urokinase.
PN EP92182-A.
PD 26-OCT-1983.
PA (GETH ) GENENTECH INC.
Percent Similarity: 36.99%
Best Local Similarity: 23.98%
Query Match: 6.69%
Conservative: 70
Mismatch: 185
Indels: 154
RESULT 1274
ID ADE25630 standard; cDNA; 2328 BP.
DE Human cDNA differentially expressed in foam cells #34.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCV-) INCYTE GENOMICS INC.
Percent Similarity: 38.11%
Best Local Similarity: 25.28%
Query Match: 6.69%
Conservative: 68
Mismatch: 190
Indels: 138
RESULT 1275
ID ACH03958 standard; cDNA; 2341 BP.
DE Human cDNA differentially expressed in lung cancer #163.
PN US2003065157-A1.
PD 03-APR-2003.
PA (LASE/) LASEK A W.
Percent Similarity: 38.11%
Best Local Similarity: 25.28%
Query Match: 6.69%
Conservative: 68
Mismatch: 190
Indels: 138
RESULT 1276
ID ADH41478 standard; DNA; 1368 BP.
DE Novel human nucleic acid NOV31.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1277
ID AAV10463 standard; DNA; 1389 BP.
DE Human Factor IX protease genomic DNA.
PN WO9747737-A1.
PD 18-DEC-1997.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
Percent Similarity: 35.17%
Best Local Similarity: 22.24%
Query Match: 6.68%
Conservative: 68
Mismatch: 146
Indels: 195
RESULT 1278
ID AAN50049 standard; cDNA; 1639 BP.
DE Sequence encoding human factor IX.
PN EP162782-A.
PD 27-NOV-1985.
PA (TRGE ) TRANSGENE SA.
Percent Similarity: 34.73%
Best Local Similarity: 22.14%
Query Match: 6.68%
Conservative: 66
Mismatch: 151
Indels: 191
RESULT 1279
ID AAS14091 standard; DNA; 1667 BP.
DE Human FCTR5a DNA sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1280
ID ADB32032 standard; cDNA; 1667 BP.
DE Human FCTR5a cDNA.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1281
ID AAS14092 standard; DNA; 1691 BP.
DE Human FCTR5b DNA sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1282
ID ADB32034 standard; cDNA; 1691 BP.
DE Human FCTR5b cDNA.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
Percent Similarity: 38.79%
Best Local Similarity: 24.65%
Query Match: 6.68%
Conservative: 70
Mismatch: 178
Indels: 126
RESULT 1283
ID AAN40177 standard; cDNA; 2781 BP.
DE Part of the sequence of human factor IX cDNA.
PN GB2125409-A.
PD 07-MAR-1984.
PA (NATR ) NAT RES DEV CORP.
Percent Similarity: 34.76%
Best Local Similarity: 21.75%
Query Match: 6.68%
Conservative: 67
Mismatch: 163
Indels: 173
RESULT 1284
ID AAT02460 standard; mRNA; 2802 BP.
DE Human Factor-IX mRNA.
PN WO9530000-A1.
PD 09-NOV-1995.
PA (BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.
Percent Similarity: 34.76%
Best Local Similarity: 21.55%
Query Match: 6.68%
Conservative: 68
Mismatch: 163
Indels: 173
RESULT 1285
ID AAQ06049 standard; DNA; 1296 BP.
DE plasmid pUK1 pro-urokinase sequence.
PN EP90592-A.
PD 03-OCT-1990.
PA (KYOW ) KYOWA HAKKO KOGYO KK.
PA (EXPE-) CENT INST EXPR ANIMALS.
PA (JIKK-) JIKKEN DOBUTSU CHUO KENK.
Percent Similarity: 37.17%
Best Local Similarity: 23.79%
Query Match: 6.67%
Conservative: 72
Mismatch: 184
Indels: 154
RESULT 1286
ID AAQ55772 standard; cDNA to mRNA; 1296 BP.

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DE Pro-urokinase derivative.  
 PN JF05336985-A.  
 PD 21-DEC-1993.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1287  
 ID ABK86598 standard; cDNA; 1296 BP.  
 DE Human plasminogen activator, urokinase (PLAU) cDNA.  
 PN WO200240503-A2.  
 PD 23-MAY-2002.  
 PA (GENA-) GENAISSANCE PHARM INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1288  
 ID ABA00207 standard; cDNA; 1296 BP.  
 DE sc-uPA coding sequence.  
 PN EP1232755-A2.  
 PD 21-AUG-2002.  
 PA (JCRP-) JCR PHARM CO LTD.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1289  
 ID ADF28768 standard; cDNA; 1296 BP.  
 DE Human urokinase-type plasminogen activator (uPA) encoding cDNA.  
 PN WO2003082072-A2.  
 PD 09-OCT-2003.  
 PA (HARB/) HARBECK N.  
 PA (KATE/) KATES R E.  
 PA (SCHM/) SCHMITT M.  
 PA (FOEK/) FOEKENS J A.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1290  
 ID AAN92037 standard; DNA; 1473 BP.  
 DE Sequence of variant human prourokinase.  
 PN JP01252283-A.  
 PD 06-OCT-1989.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1291  
 ID AAN50138 standard; DNA; 1474 BP.  
 DE Sequence of the signal sequence and noncoding region of the pro-UK  
 DE structural gene (Sequence II).  
 PN EP154272-A.  
 PD 11-SEP-1985.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1292  
 ID AAN81558 standard; DNA; 1475 BP.  
 DE Pro-UK structural gene, signal sequence and non-coding region.  
 PN EP265874-A.  
 PD 04-MAY-1988.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1293  
 ID AAZ24619 standard; cDNA; 1475 BP.  
 DE Human lung tumor associated polynucleotide.  
 PN WO9947674-A2.  
 PD 23-SEP-1999.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%

Query Match: 6.67%  
 RESULT 1294  
 ID AAC65858 standard; cDNA; 1475 BP.  
 DE Human lung cancer-associated cDNA for contig 10.  
 PN WO200061612-A2.  
 PD 19-OCT-2000.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1295  
 ID ABZ35047 standard; cDNA; 1475 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 159.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1296  
 ID ABL49077 standard; cDNA; 1475 BP.  
 DE Human lung tumour cDNA sequence for contig 10 SEQ ID NO:122.  
 PN WO200200174-A2.  
 PD 03-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1297  
 ID ABQ92263 standard; cDNA; 1475 BP.  
 DE Human lung cancer associated cDNA sequence SEQ ID NO:122.  
 PN WO200247534-A2.  
 PD 20-JUN-2002.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1298  
 ID ADA28212 standard; cDNA; 1475 BP.  
 DE Human lung tumour associated cDNA contig 10.  
 PN US2003064947-A1.  
 PD 03-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1299  
 ID ADE33417 standard; cDNA; 1475 BP.  
 DE Human lung tumour protein cDNA sequence #119.  
 PN US2003119763-A1.  
 PD 26-JUN-2003.  
 PA (WANG/) WANG T.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1300  
 ID ADH36776 standard; cDNA; 1475 BP.  
 DE Human lung cancer-related cDNA sequence #119.  
 PN WO2003086175-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1301  
 ID ACC78885 standard; DNA; 1475 BP.  
 DE Human urokinase encoding DNA.  
 PN WO2003031464-A2.  
 PD 17-APR-2003.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1302  
 ID AAN81558 standard; DNA; 1475 BP.  
 DE Pro-UK structural gene, signal sequence and non-coding region.  
 PN EP265874-A.  
 PD 04-MAY-1988.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%  
 RESULT 1303  
 ID AAZ24619 standard; cDNA; 1475 BP.  
 DE Human lung tumor associated polynucleotide.  
 PN WO9947674-A2.  
 PD 23-SEP-1999.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 6.67%

RESULT 1302  
 ID ADM56579 standard; cDNA; 1475 BP.  
 DE Human lung tumour cDNA #119.  
 PN US2003138438-A1.  
 PD 24-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1303  
 ID ADN99623 standard; cDNA; 1475 BP.  
 DE Human lung squamous cell carcinoma cDNA seqid 122.  
 PN US6660838-B1.  
 PD 09-DEC-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1304  
 ID ADN49705 standard; DNA; 1475 BP.  
 DE Human urokinase DNA SeqID 33.  
 PN WO2004033651-A2.  
 PD 22-APR-2004.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1305  
 ID AAN91617 standard; DNA; 1500 BP.  
 DE Sequence of entire prourokinase (PKU) gene from PKU-producing tumour cell  
 DE line ATCC CCL138 clone pUC20.  
 PN EP312941-A.  
 PD 26-APR-1989.  
 PA (BADI) BASF AG.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1306  
 ID AAN91215 standard; cDNA; 1738 BP.  
 DE cDNA coding sequence of tissue plasminogen activator (t-PA).  
 PN AU8817430-A.  
 PD 08-DEC-1988.  
 PA (NOVO) NOVO IND AS.  
 PA (ZYMO) ZYMOGENETICS INC.  
 PA (EISA) EISAI CO LTD.  
 Percent Similarity: 35.65%  
 Best Local Similarity: 35.65%  
 Query Match: 6.67%  
 Indels: 186  
 Conservatives: 74  
 Mismatches: 185

RESULT 1307  
 ID AAH28220 standard; DNA; 1964 BP.  
 DE Nucleotide sequence of urokinase plasminogen activator.  
 PN WO200149309-A2.  
 PD 12-JUL-2001.  
 PA (PFIZ) PFIZER LTD.  
 PA (PFIZ) PFIZER INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1308  
 ID RAD27855 standard; cDNA; 1964 BP.  
 DE Human uPA cDNA.  
 PN WO200196606-A2.  
 PD 20-DEC-2001.  
 PA (NYXT-) NYXTIS NEURO THERAPIES INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1309  
 ID ACN39065 standard; cDNA; 2254 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA325332, SEQ ID NO:2968.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.

Percent Similarity: 38.11%  
 Best Local Similarity: 25.28%  
 Query Match: 6.67%  
 Indels: 138  
 Conservatives: 68  
 Mismatches: 190

RESULT 1310  
 ID AAZ24620 standard; cDNA; 2281 BP.  
 DE Human lung tumor associated polynucleotide.  
 PN WO9947674-A2.  
 PD 23-SEP-1999.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1311  
 ID AAC65859 standard; cDNA; 2294 BP.  
 DE Human lung cancer-associated cDNA for contig 12.  
 PN WO200061612-A2.  
 PD 19-OCT-2000.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1312  
 ID ABL49078 standard; cDNA; 2294 BP.  
 DE Human lung tumour cDNA sequence for contig 12 SEQ ID NO:123.  
 PN WO200200174-A2.  
 PD 03-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1313  
 ID ABQ22264 standard; cDNA; 2294 BP.  
 DE Human lung cancer associated cDNA sequence SEQ ID NO:123.  
 PN WO200247534-A2.  
 PD 20-JUN-2002.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1314  
 ID ADA28213 standard; cDNA; 2294 BP.  
 DE Human lung tumour associated cDNA contig 12.  
 PN US2003064947-A1.  
 PD 03-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1315  
 ID ADE53418 standard; cDNA; 2294 BP.  
 DE Human lung tumour protein cDNA sequence #120.  
 PN US2003119763-A1.  
 PD 26-JUN-2003.  
 PA (WANG/) WANG T.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1316  
 ID ADH36777 standard; cDNA; 2294 BP.  
 DE Human lung cancer-related cDNA sequence #120.  
 PN WO2003086175-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 37.17%  
 Query Match: 6.67%  
 Indels: 154  
 Conservatives: 72  
 Mismatches: 184

RESULT 1317  
 ID ADK61310 standard; DNA; 2294 BP.  
 DE Ovarian cancer-related DNA #465 with altered ovarian cancer expression.  
 PN WO2003068054-A2.  
 PD 21-AUG-2003.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.

Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1318  
 ID ADI31891 standard; cDNA; 2294 BP.  
 DE Human cDNA #1217.  
 PN US6607879-B1.  
 PD 19-AUG-2003.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1319  
 ID ADM56580 standard; cDNA; 2294 BP.  
 DE Human lung tumour cDNA #120.  
 PN US2003138438-A1.  
 PD 24-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1320  
 ID ADN89624 standard; cDNA; 2294 BP.  
 DE Human lung squamous cell carcinoma cDNA seqid 123.  
 PN US660838-B1.  
 PD 09-DEC-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1321  
 ID ACN44243 standard; cDNA; 2297 BP.  
 DE Human mRNA sequence hCT11616.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1322  
 ID AAN80981 standard; DNA; 2298 BP.  
 DE Sequence of the single chain urokinase plasminogen activator (SCU-PA)  
 DE cDNA insert prepared from human Hep3 cells.  
 PN EP288435-A.  
 PD 26-OCT-1988.  
 PA (CIBA) CIBA GEIGY AG.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1323  
 ID AAN60703 standard; DNA; 2299 BP.  
 DE Sequence encoding human urokinase.  
 PN JP61181377-A.  
 PD 14-AUG-1986.  
 PA (NISC) NISSAN CHEM IND LTD.  
 PA (HODO) HODOGAYA CHEM IND CO LTD.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (CENG) CENTRAL GLASS CO LTD.  
 PA (NIPS) NIPPON SODA CO.  
 PA (TOYJ) TOYO SODA MFG CO LTD.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1324  
 ID AAN70390 standard; DNA; 2301 BP.  
 DE cDNA encoding human prourokinase in plasmid pKU22.  
 PN EP231883-A.  
 PD 12-AUG-1987.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (NIPS) NIPPON SODA CO.  
 PA (CENG) CENTRAL GLASS CO LTD.  
 PA (TOYJ) TOYO SODA MFG CO LTD.  
 PA (NISC) NISSAN CHEM IND LTD.

PA (NISC) NISSAN CHEMICAL INDS KK.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1325  
 ID AAN91075 standard; DNA; 2301 BP.  
 DE DNA encoding natural human prourokinase and 5' UTR and 3' UTR.  
 PN WO8901513-A.  
 PD 23-FEB-1989.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (CENG) CENTRAL GLASS CO LTD.  
 PA (HODO) HODOGAYA CHEM KK.  
 PA (NIPS) NIPPON SODA CO.  
 PA (NISC) NISSAN CHEM IND LTD.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1326  
 ID AAQ73483 standard; cDNA; 2303 BP.  
 DE Full length human urokinase protein cDNA.  
 PN EP620279-A1.  
 PD 19-OCT-1994.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1327  
 ID ABL59543 standard; cDNA; 2304 BP.  
 DE Human pro-urokinase (uPA) cDNA SEQ ID NO:43.  
 PN WO200227028-A1.  
 PD 04-APR-2002.  
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1328  
 ID ABX76437 standard; DNA; 2304 BP.  
 DE Lung cancer-associated polynucleotide #301.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1329  
 ID ABX76275 standard; DNA; 2304 BP.  
 DE Lung cancer-associated polynucleotide #140.  
 PN WO200286443-A2.  
 PD 31-OCT-2002.  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1330  
 ID ABX17681 standard; DNA; 2304 BP.  
 DE DNA encoding Human urokinase plasminogen activator #1.  
 PN WO200279515-A1.  
 PD 10-OCT-2002.  
 PA (ISIS-) ISIS PHARM INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1331  
 ID ACF12920 standard; cDNA; 2304 BP.  
 DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:183.  
 PN WO2002101075-A2.  
 PD 19-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.67% Indels: 154  
 RESULT 1332  
 ID ADG89387 standard; DNA; 2304 BP.

DE Cancer detection method related gene #50.  
PN WO2003078662-A1.  
PD 25-SEP-2003.  
PA (GENO-) GENOMIC HEALTH INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1333  
ID ADN39095 standard; cDNA; 2304 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:413.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1334  
ID ADN39740 standard; cDNA; 2304 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C112.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1335  
ID ADN95543 standard; DNA; 2304 BP.  
DE Human BRC/LEC-related gene sequence SeqID466.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1336  
ID ADL70594 standard; cDNA; 2304 BP.  
DE Cervical cancer marker M58, urokinase, cDNA.  
PN WO2004018999-A2.  
PD 04-MAR-2004.  
PA (MILL-) MILLENIUM PHARM INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1337  
ID ADP07333 standard; DNA; 2304 BP.  
DE Human UPA DNA.  
PN DE10255104-A1.  
PD 11-MAR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1338  
ID ADP3870 standard; cDNA; 2304 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1048.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1339  
ID ABZ35347 standard; cDNA; 2336 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 458.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH-) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1340  
ID ADB47346 standard; cDNA; 2336 BP.  
DE Human cDNA upregulated in dendritic cells SEQ ID NO 46.  
PN US2003134283-A1.  
PD 17-JUL-2003.  
PA (PETE-) PETERSON D P.  
PA (PEAR-) PEARSON C I.  
PA (COCK-) COCKS B G.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1341  
ID ADE54011 standard; cDNA; 2336 BP.  
DE Human prostate cancer cDNA #358.  
PN US2003190640-A1.  
PD 09-OCT-2003.  
PA (FARI-) FARIS M.  
PA (PEAR-) PEARSON C I.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1342  
ID AAQ20360 standard; cDNA; 2377 BP.  
DE Human pro-urokinase cDNA.  
PN DE4122688-A.  
PD 16-JAN-1992.  
PA (FARM-) FARMITALIA ERBA SRL CARLO.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1343  
ID AAQ04107 standard; cDNA; 2427 BP.  
DE Human pro-urokinase cDNA of clone pcUK176.  
PN EP365894-A.  
PD 02-MAY-1990.  
PA (FARM-) FARMITALIA ERBA SPA CARLO.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1344  
ID ADQ22641 standard; DNA; 2655 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5461.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 37.17% Conservative: 72  
Best Local Similarity: 23.79% Mismatches: 184  
Query Match: 6.67% Indels: 154  
RESULT 1345  
ID ADH41464 standard; DNA; 1368 BP.  
DE Novel human nucleic acid NOV3b.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.79% Conservative: 70  
Best Local Similarity: 24.65% Mismatches: 178  
Query Match: 6.65% Indels: 126  
RESULT 1346  
ID ADH41488 standard; DNA; 1368 BP.  
DE Novel human nucleic acid NOV3n.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.79% Conservative: 70  
Best Local Similarity: 24.65% Mismatches: 178  
Query Match: 6.65% Indels: 126  
RESULT 1347  
ID ABQ78854 standard; DNA; 1386 BP.  
DE Nucleic acid relating to the invention #1.  
PN RU2181147-C2.  
PD 10-APR-2002.  
PA (CHAR-) CHARIKOVA E V.  
Percent Similarity: 34.73% Conservative: 66  
Best Local Similarity: 22.14% Mismatches: 151  
Query Match: 6.65% Indels: 191

RESULT 1348  
 ID AAQ04742 standard; DNA; 1389 BP.  
 DE Mutant sequence encoding human factor IX (FIX).  
 PN EP373012-A.  
 PD 13-JUN-1990.  
 PA (TRGE ) TRANSGENE SA.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1349  
 ID AAV10462 standard; DNA; 1404 BP.  
 DE Human Factor X protease cDNA.  
 PN WO9747737-A1.  
 PD 18-DEC-1997.  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 Percent Similarity: 36.90%  
 Best Local Similarity: 23.19%  
 Query Match: 6.65%  
 Conservative: 68  
 Mismatches: 191  
 Indels: 123

RESULT 1350  
 ID AAI71004 standard; cDNA; 1413 BP.  
 DE Human Factor IX cDNA.  
 PN WO200198482-A2.  
 PD 27-DEC-2001.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PA (UNIW ) UNIV WASHINGTON.  
 Percent Similarity: 34.76%  
 Best Local Similarity: 21.55%  
 Query Match: 6.65%  
 Conservative: 68  
 Mismatches: 163  
 Indels: 173

RESULT 1351  
 ID AAQ76017 standard; cDNA; 1548 BP.  
 DE Human Factor-IX cDNA.  
 PN WO9429471-A1.  
 PD 22-DEC-1994.  
 PA (GENE-) GENETIC THERAPY INC.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1352  
 ID AAX88292 standard; DNA; 1548 BP.  
 DE Human Factor IX cDNA.  
 PN US5915935-A.  
 PD 10-AUG-1999.  
 PA (GENE-) GENETIC THERAPY INC.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1353  
 ID ABN84383 standard; cDNA; 1548 BP.  
 DE Human Factor IX cDNA sequence.  
 PN US2002064812-A1.  
 PD 30-MAY-2002.  
 PA (CONN/) CONNELLY S.  
 PA (KALE/) KALEKO M.  
 PA (SMIT/) SMITH T.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1354  
 ID AAX88061 standard; cDNA; 1610 BP.  
 DE Human IGF-1 cDNA.  
 PN US5925564-A.  
 PD 20-JUL-1999.  
 PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1355  
 ID ADH42200 standard; DNA; 1612 BP.  
 DE Novel human nucleic acid NOV47d.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 34.73%  
 Conservative: 66

Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Mismatches: 151  
 Indels: 191

RESULT 1356  
 ID AAN50351 standard; cDNA; 1638 BP.  
 DE Sequence encoding human factor IX.  
 PN WO8505376-A.  
 PD 05-DEC-1985.  
 PA (TRGE ) TRANSGENE SA.  
 PA (DSAL/) DE LA SALLE H.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1357  
 ID AAN50362 standard; cDNA; 1639 BP.  
 DE Sequence encoding human factor IX, called DNA FIX.  
 PN WO8505125-A.  
 PD 21-NOV-1985.  
 PA (TRGE ) TRANSGENE SA.  
 PA (JAYE/) JAYE M.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1358  
 ID AAA54034 standard; DNA; 2775 BP.  
 DE Human factor IX coding sequence.  
 PN WO200054787-A1.  
 PD 21-SEP-2000.  
 PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1359  
 ID AAN40142 standard; cDNA; 2781 BP.  
 DE Part of the sequence of human factor IX cDNA.  
 PN WO8400560-A.  
 PD 16-FEB-1984.  
 PA (NATR ) NAT RES DEV CORP.  
 PA (BROW/) BROWNLEE G G.  
 Percent Similarity: 34.76%  
 Best Local Similarity: 21.55%  
 Query Match: 6.65%  
 Conservative: 68  
 Mismatches: 163  
 Indels: 173

RESULT 1360  
 ID ABV77053 standard; DNA; 2804 BP.  
 DE Nucleotide sequence of human Factor IX.  
 PN WO200286091-A2.  
 PD 31-OCT-2002.  
 PA (REGC ) UNIV CALIFORNIA.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1361  
 ID AAM60543 standard; cDNA; 2807 BP.  
 DE Factor-IX cDNA.  
 PN WO8606408-A.  
 PD 06-NOV-1986.  
 PA (GENY ) GENETICS INST INC.  
 PA (KAUF/) KAUFMAN R J.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1362  
 ID ADH42198 standard; DNA; 2807 BP.  
 DE Novel human nucleic acid NOV47c.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 6.65%  
 Conservative: 66  
 Mismatches: 151  
 Indels: 191

RESULT 1363  
 ID ABA09219 standard; cDNA; 3421 BP.  
 DE Human corin homologue-encoding cDNA, SEQ ID NO:995.

PN WO200157188-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1364  
 ID AAZ29662 standard; cDNA; 4933 BP.  
 DE Human Serine protease, Corin cDNA.  
 PN WO9964608-A1.  
 PD 16-DEC-1999.  
 PA (SCHD) SCHERING AG.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1365  
 ID AAD13164 standard; DNA; 4933 BP.  
 DE Human corin DNA.  
 PN WO200157194-A2.  
 PD 09-AUG-2001.  
 PA (CORV-) CORVAS INT INC.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1366  
 ID ADI10397 standard; DNA; 4933 BP.  
 DE Human cell surface protease coding sequence #15.  
 PN WO200295007-A2.  
 PD 28-NOV-2002.  
 PA (CORV-) CORVAS INT INC.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1367  
 ID ADJ46921 standard; cDNA; 4933 BP.  
 DE Human transmembrane serine protease (WTSF)-related cDNA #5.  
 PN US2004001801-A1.  
 PD 01-JAN-2004.  
 PA (CORV-) CORVAS INT INC.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1368  
 ID ADR29371 standard; DNA; 4933 BP.  
 DE Human corin dopaminergic neuronal marker DNA SEQ ID NO:1.  
 PN WO2004065599-A1.  
 PD 05-AUG-2004.  
 PA (EISA) EISAI CO LTD.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1369  
 ID ADP21389 standard; DNA; 4942 BP.  
 DE Gene PRSC for screening for cardiac therapeutic preparation.  
 PN WO2004050894-A2.  
 PD 17-JUN-2004.  
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.  
 Percent Similarity: 33.13%  
 Best Local Similarity: 20.68%  
 Query Match: 266  
 Indels: 287  
 RESULT 1370  
 ID AAA53835 standard; DNA; 5753 BP.  
 DE Vector PTGFG36 comprising human clotting factor IX.  
 PN WO200049147-A1.  
 PD 24-AUG-2000.  
 PA (THER-) THERAGENE BIOMEDICAL LAB GMBH.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 151  
 Indels: 191  
 RESULT 1371  
 ID AAD18173 standard; DNA; 5753 BP.  
 DE Human wild-type factor IX protein encoding vector PTGFG36hyg.  
 PN WO200170968-A2.

PD 27-SEP-2001.  
 PA (OCTA-) OCTAGENE GMBH.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 151  
 Indels: 191  
 RESULT 1372  
 ID AAA53846 standard; DNA; 5905 BP.  
 DE Vector PTGFG53 comprising human clotting factor IX.  
 PN WO200049147-A1.  
 PD 24-AUG-2000.  
 PA (THER-) THERAGENE BIOMEDICAL LAB GMBH.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 151  
 Indels: 191  
 RESULT 1373  
 ID AAA53847 standard; DNA; 6052 BP.  
 DE Vector PTGFG64 comprising human clotting factor IX.  
 PN WO200049147-A1.  
 PD 24-AUG-2000.  
 PA (THER-) THERAGENE BIOMEDICAL LAB GMBH.  
 Percent Similarity: 34.73%  
 Best Local Similarity: 22.14%  
 Query Match: 151  
 Indels: 191  
 RESULT 1374  
 ID AAH77500 standard; DNA; 13928 BP.  
 DE Haemophilia B genetic therapy related oligonucleotide #3.  
 PN CN1302864-A.  
 PD 11-JUL-2001.  
 PA (XIAJ/) XIA J.  
 Percent Similarity: 34.76%  
 Best Local Similarity: 21.55%  
 Query Match: 163  
 Indels: 173  
 RESULT 1375  
 ID AAN93079 standard; DNA; 2266 BP.  
 DE Sequence encoding prourokinase.  
 PN EP299706-A.  
 PD 18-JAN-1989.  
 PA (COLB) COLLABORATIVE RES INC.  
 Percent Similarity: 37.17%  
 Best Local Similarity: 23.79%  
 Query Match: 72  
 Indels: 184  
 RESULT 1376  
 ID AAQ06133 standard; DNA; 1236 BP.  
 DE Sequence encoding human pro-urokinase variant.  
 PN EP398382-A.  
 PD 22-NOV-1990.  
 PA (GREC) GREEN CROSS CORP.  
 Percent Similarity: 37.30%  
 Best Local Similarity: 23.63%  
 Query Match: 70  
 Indels: 174  
 RESULT 1377  
 ID AAT61671 standard; cDNA; 1236 BP.  
 DE Human native prourokinase cDNA.  
 PN EP398361-A.  
 PD 22-NOV-1990.  
 PA (GREC) GREEN CROSS CORP.  
 Percent Similarity: 37.11%  
 Best Local Similarity: 23.63%  
 Query Match: 69  
 Indels: 175  
 RESULT 1378  
 ID AAQ0317 standard; cDNA; 1736 BP.  
 DE Sequence encoding human pre-pro tissue plasminogen activator (t-PA).  
 PN US5200340-A.  
 PD 06-APR-1993.  
 PA (ZYMO) ZYMOGENETICS INC.  
 Percent Similarity: 35.01%  
 Best Local Similarity: 21.84%  
 Query Match: 185  
 Indels: 192  
 RESULT 1379  
 ID AAX28626 standard; DNA; 2792 BP.  
 DE Nucleotide sequence of human factor IX-R338A.  
 PN WO9903496-A1.  
 PD 28-JAN-1999.

PA (UYNC-) UNIV NORTH CAROLINA.  
 PN (STAF/) STAFFORD D W.  
 PA (CHAN/) CHANG J L.  
 Percent Similarity: 34.73% Conservative: 66  
 Best Local Similarity: 22.14% Mismatches: 151  
 Query Match: 6.63% Indels: 191.  
 RESULT 1380  
 ID AAN70356 standard; cDNA to mRNA; 1475 BP.  
 DE Human urine-derived high molecular weight type urokinase A and B-chain  
 DE pre-structural gene.  
 PN EP232544-A.  
 PD 19-AUG-1987.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 39.08% Conservative: 77  
 Best Local Similarity: 24.43% Mismatches: 189  
 Query Match: 6.62% Indels: 132  
 RESULT 1381  
 ID AB235272 standard; cDNA; 2344 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 383.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 37.17% Conservative: 72  
 Best Local Similarity: 23.79% Mismatches: 184  
 Query Match: 6.62% Indels: 154  
 RESULT 1382  
 ID AAQ06134 standard; DNA; 1236 BP.  
 DE Sequence encoding human pro-urokinase variant.  
 PN EP398362-A.  
 PD 22-NOV-1990.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 37.11% Conservative: 69  
 Best Local Similarity: 23.63% Mismatches: 175  
 Query Match: 6.60% Indels: 147  
 RESULT 1383  
 ID ABN99361 standard; DNA; 2387 BP.  
 DE Human secreted protein (SCRFP) coding sequence 2.  
 PN WO200226982-A2.  
 PD 04-APR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 34.38% Conservative: 47  
 Best Local Similarity: 23.82% Mismatches: 133  
 Query Match: 6.60% Indels: 159  
 RESULT 1384  
 ID AAQ10577 standard; DNA; 1465 BP.  
 DE Coding sequence for human factor IX, contained in plasmid pHFxl.  
 PN US4994371-A.  
 PD 19-FEB-1991.  
 PA (DAVI/) DAVIE E W.  
 Percent Similarity: 34.73% Conservative: 64  
 Best Local Similarity: 22.52% Mismatches: 152  
 Query Match: 6.59% Indels: 190  
 RESULT 1385  
 ID AAN50141 standard; cDNA; 1475 BP.  
 DE Sequence encoding pro-urokinase (sequence IV).  
 PN EP154272-A.  
 PD 11-SEP-1985.  
 PA (GREC ) GREEN CROSS CORP.  
 Percent Similarity: 36.99% Conservative: 71  
 Best Local Similarity: 23.79% Mismatches: 185  
 Query Match: 6.59% Indels: 154  
 RESULT 1386  
 ID AD243392 standard; cDNA; 2304 BP.  
 DE Human uPA cDNA, SEQ ID 561.  
 PN WO2003054143-A2.  
 PD 03-JUL-2003.  
 PA (NEUR-) NEUROGENETICS INC.  
 Percent Similarity: 37.74% Conservative: 67  
 Best Local Similarity: 25.09% Mismatches: 192  
 Query Match: 6.59% Indels: 138  
 RESULT 1387  
 ID ADH54434 standard; cDNA; 2304 BP.

DE Human uPA gene cDNA sequence SeqID561.  
 PN US2003224380-A1.  
 PD 04-DEC-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Percent Similarity: 37.74% Conservative: 67  
 Best Local Similarity: 25.09% Mismatches: 192  
 Query Match: 6.59% Indels: 138  
 RESULT 1388  
 ID ACN43224 standard; cDNA; 4633 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2099.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 35.02% Conservative: 87  
 Best Local Similarity: 23.44% Mismatches: 266  
 Query Match: 6.59% Indels: 224  
 RESULT 1389  
 ID AAQ10169 standard; DNA; 1236 BP.  
 DE Encodes Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).  
 PN EP405285-A.  
 PD 02-JAN-1991.  
 PA (KTOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 37.11% Conservative: 65  
 Best Local Similarity: 24.41% Mismatches: 175  
 Query Match: 6.58% Indels: 147  
 RESULT 1390  
 ID ADH41472 standard; DNA; 1479 BP.  
 DE Novel human nucleic acid NOV3f.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 38.79% Conservative: 71  
 Best Local Similarity: 24.44% Mismatches: 178  
 Query Match: 6.58% Indels: 126  
 RESULT 1391  
 ID AAN71330 standard; DNA; 2304 BP.  
 DE Sequence encoding modified prourokinase.  
 PN EP236040-A.  
 PD 09-SEP-1987.  
 PA (COLB ) COLLABORATIVE RES INC.  
 Percent Similarity: 37.15% Conservative: 71  
 Best Local Similarity: 23.83% Mismatches: 181  
 Query Match: 6.57% Indels: 154  
 RESULT 1392  
 ID ADQ38774 standard; DNA; 2359 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 437.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 37.43% Conservative: 66  
 Best Local Similarity: 24.95% Mismatches: 195  
 Query Match: 6.57% Indels: 136  
 RESULT 1393  
 ID ADQ38775 standard; DNA; 2375 BP.  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 438.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 37.43% Conservative: 66  
 Best Local Similarity: 24.95% Mismatches: 195  
 Query Match: 6.57% Indels: 136  
 RESULT 1394  
 ID AB211297 standard; cDNA; 2505 BP.  
 DE Human polynucleotide SEQ ID NO 179.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 33.25% Conservative: 102  
 Best Local Similarity: 20.87% Mismatches: 252  
 Query Match: 6.57% Indels: 301  
 RESULT 1395  
 ID ADM43815 standard; cDNA; 2505 BP.  
 DE Novel human arginine-rich protein cDNA #179.



PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 33.25%  
Best Local Similarity: 20.87%  
Query Match: 6.57%  
RESULT 1396  
ID AAD27077 standard; DNA; 1236 BP.  
DE Human urokinase-type plasminogen activator tcuPA and scuPA DNA.  
PN WO200157752-A2.  
PD 27-DEC-2001.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Percent Similarity: 37.11%  
Best Local Similarity: 23.44%  
Query Match: 6.55%  
RESULT 1397  
ID ADE85976 standard; cDNA; 1236 BP.  
DE Human single chain urokinase plasminogen activator coding sequence.  
PN WO2003086278-A2.  
PD 23-OCT-2003.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Percent Similarity: 38.10%  
Best Local Similarity: 25.00%  
Query Match: 6.55%  
RESULT 1398  
ID ADI31601 standard; cDNA; 1236 BP.  
DE Human cDNA #927.  
PN US6607879-B1.  
PD 19-AUG-2003.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 38.10%  
Best Local Similarity: 25.00%  
Query Match: 6.55%  
RESULT 1399  
ID AAQ10224 standard; DNA; 1455 BP.  
DE Encodes human prourokinase derivative APUK (k,k).  
PN WO9015867-A.  
PD 27-DEC-1990.  
PA (NIPS) NIPPON SODA CO.  
Percent Similarity: 38.10%  
Best Local Similarity: 25.00%  
Query Match: 6.55%  
RESULT 1400  
ID AAQ81549 standard; cDNA; 1548 BP.  
DE Factor-IX cDNA.  
PN WO9505201-A1.  
PD 23-FEB-1995.  
PA (GENE-) GENETIC THERAPY INC.  
Percent Similarity: 34.54%  
Best Local Similarity: 22.14%  
Query Match: 6.55%  
RESULT 1401  
ID ABL28971 standard; DNA; 3736 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38386.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 44.91%  
Best Local Similarity: 26.32%  
Query Match: 6.55%  
RESULT 1402  
ID AAQ10282 standard; DNA; 1316 BP.  
DE Structural gene encoding single-chain urine plasminogen activator.  
PN EP408945-A.  
PD 23-JAN-1991.  
PA (CHEF) GRUENENTHAL GMBH.  
Percent Similarity: 38.46%  
Best Local Similarity: 25.19%  
Query Match: 6.54%  
RESULT 1403  
ID AAQ10168 standard; DNA; 1236 BP.  
DE Encodes Pro-urokinase derivative UK-T6 with Thr at position 155.  
PN EP405285-A.  
PD 02-JAN-1991.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 36.91%  
Best Local Similarity: 24.41%  
Query Match: 6.53%  
RESULT 1404  
ID AAQ41450 standard; DNA; 1236 BP.  
DE Mutant human prourokinase gene.  
PN EP541952-A1.  
PD 19-MAY-1993.  
PA (GREC) GREEN CROSS CORP.  
Percent Similarity: 37.70%  
Best Local Similarity: 24.80%  
Query Match: 6.53%  
RESULT 1405  
ID AAQ48228 standard; DNA; 1236 BP.  
DE PUK gene.  
PN JP05192142-A.  
PD 03-AUG-1993.  
PA (GREC) GREEN CROSS CORP.  
Percent Similarity: 37.70%  
Best Local Similarity: 24.80%  
Query Match: 6.53%  
RESULT 1406  
ID AAQ10225 standard; DNA; 1455 BP.  
DE Encodes human prourokinase derivative APUK (k,q).  
PN WO9015867-A.  
PD 27-DEC-1990.  
PA (NIPS) NIPPON SODA CO.  
Percent Similarity: 38.10%  
Best Local Similarity: 25.00%  
Query Match: 6.53%  
RESULT 1407  
ID AAN60591 standard; DNA; 2301 BP.  
DE Sequence encoding modified human pro-urokinase clone.  
PN WO8604351-A.  
PD 31-JUL-1986.  
PA (SAGA) SAGAMI CHEM RES CENTRE.  
PA (MIYA) MIYAKE T.  
PA (HODO) HODOGAYA-CHEM CO LTD.  
PA (NIPS) NIPPON SODA CO.  
PA (TOXJ) TOYO SODA MFG CO LTD.  
PA (NISC) NISSAN CHEM IND LTD.  
PA (NIPC) NIPPON CHEM IND CO LTD.  
PA (NISC) NISSAN CHEM IND LTD.  
PA (TOXJ) TOYO SODA MFG CO LTD.  
PA (NIPS) NIPPON SODA CO.  
Percent Similarity: 37.31%  
Best Local Similarity: 24.81%  
Query Match: 6.51%  
RESULT 1408  
ID AAG61734 standard; cDNA; 834 BP.  
DE cDNA encoding mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:3.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Percent Similarity: 40.85%  
Best Local Similarity: 27.45%  
Query Match: 6.50%  
RESULT 1409  
ID AAT80075 standard; cDNA; 1335 BP.  
DE Inhibitor resistant urokinase gene.  
PN US5648253-A.  
PD 15-JUL-1997.  
PA (TSIT-) TSI CORP.  
Percent Similarity: 37.11%  
Best Local Similarity: 23.44%  
Query Match: 6.50%  
RESULT 1410  
ID AAN50477 standard; cDNA; 1386 BP.  
DE Sequence encoding human pre-pro-urokinase in pULB 1000.  
Conservative: 64  
Mismatch: 176  
Indels: 147  
Conservative: 65  
Mismatch: 183  
Indels: 131  
Conservative: 65  
Mismatch: 183  
Indels: 131  
Conservative: 66  
Mismatch: 197  
Indels: 134  
Conservative: 41  
Mismatch: 116  
Indels: 65  
Conservative: 70  
Mismatch: 175  
Indels: 147

PN BE900826-A.  
PD 16-APR-1985.  
PA (UNIO ) UCB SA.  
Percent Similarity: 36.93%  
Best Local Similarity: 24.81%  
Query Match: 6.49%  
RESULT 1411  
ID ACN411794 standard; cDNA; 2113 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:669.  
PN WO2004023973-A2.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 37.75%  
Best Local Similarity: 24.11%  
Query Match: 6.49%  
RESULT 1412  
ID AAT61457 standard; DNA; 3546 BP.  
DE C-proteinase clone PCP-2.  
PN WO9706242-A1.  
PD 20-FEB-1997.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Percent Similarity: 30.25%  
Best Local Similarity: 21.85%  
Query Match: 6.49%  
RESULT 1413  
ID AA288362 standard; cDNA; 1296 BP.  
DE Human preprourokinase CT92 nucleotide sequence.  
PN WO200000624-A1.  
PD 06-JAN-2000.  
PA (CROP-) CROPTTECH DEV CORP.  
Percent Similarity: 37.17%  
Best Local Similarity: 23.79%  
Query Match: 6.46%  
RESULT 1414  
ID AAN70447 standard; cDNA; 2310 BP.  
DE Sequence of human tissue plasminogen activator (t-PA) cDNA clone.  
PN EP236209-A.  
PD 09-SEP-1987.  
PA (GENE-) GENETICA.  
Percent Similarity: 35.46%  
Best Local Similarity: 22.70%  
Query Match: 6.46%  
RESULT 1415  
ID ADQ18557 standard; DNA; 3546 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1376.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 35.98%  
Best Local Similarity: 26.27%  
Query Match: 6.46%  
RESULT 1416  
ID ABZ34743 standard; cDNA; 3552 BP.  
DE Coding sequence SEQ ID 101, downregulated in osteogenesis.  
PN WO200281745-A2.  
PD 17-OCT-2002.  
PA (AVET ) AVENTIS PHARMA SA.  
Percent Similarity: 35.98%  
Best Local Similarity: 26.27%  
Query Match: 6.46%  
RESULT 1417  
ID ABL92109 standard; cDNA; 3557 BP.  
DE Human Tumour Endothelial Marker polynucleotide SEQ ID NO 241.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Percent Similarity: 35.98%  
Best Local Similarity: 26.27%  
Query Match: 6.46%  
RESULT 1418  
ID ASX72034 standard; DNA; 3557 BP.  
DE DNA encoding human tumour endothelial marker TEM 25.  
PN WO200283874-A2.

PD 24-OCT-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
Percent Similarity: 35.98%  
Best Local Similarity: 26.27%  
Query Match: 6.46%  
RESULT 1419  
ID ADQ23028 standard; DNA; 3889 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5848.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 35.98%  
Best Local Similarity: 26.27%  
Query Match: 6.46%  
RESULT 1420  
ID AAQ06135 standard; DNA; 1236 BP.  
DE Sequence encoding human pro-urokinase variant.  
PN EP398362-A.  
PD 22-NOV-1990.  
PA (GREC ) GREEN CROSS CORP.  
Percent Similarity: 36.91%  
Best Local Similarity: 23.44%  
Query Match: 6.45%  
RESULT 1421  
ID AAQ04485 standard; DNA; 1236 BP.  
DE Plasmid pSRIUKS11d encoding UK-S1.  
PN EP370205-A.  
PD 30-MAY-1990.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 37.60%  
Best Local Similarity: 23.80%  
Query Match: 6.45%  
RESULT 1422  
ID AAQ10223 standard; DNA; 1467 BP.  
DE Encodes human prourokinase derivative AHUK (q,q).  
PN WO9015867-A.  
PD 27-DEC-1990.  
PA (NIPS ) NIPPON SODA CO.  
Percent Similarity: 38.10%  
Best Local Similarity: 24.80%  
Query Match: 6.45%  
RESULT 1423  
ID ADA50521 standard; DNA; 714 BP.  
DE Human protease gene SEQ ID NO:25.  
PN WO2003040393-A2.  
PD 15-MAY-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Percent Similarity: 44.98%  
Best Local Similarity: 29.00%  
Query Match: 6.44%  
RESULT 1424  
ID ADB58493 standard; DNA; 2045 BP.  
DE Toxicity-related gene, SEQ ID 3519.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.83%  
Best Local Similarity: 21.28%  
Query Match: 6.44%  
RESULT 1425  
ID ADB53088 standard; DNA; 2045 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3630.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 33.83%  
Best Local Similarity: 21.28%  
Query Match: 6.44%  
RESULT 1426  
ID AAQ05535 standard; DNA; 2249 BP.  
DE Plasmid plgN delta GFTPA encoding novel mutant tissue plasminogen activator (tPA).  
PN EP379890-A.

PD 01-AUG-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 37.31%  
Best Local Similarity: 24.23%  
Query Match: 6.44%  
RESULT 1427  
ID ADR44281 standard; DNA; 3405 BP.  
DE Mosquito C-type lectin (CTL) gene sequence SEQ ID NO:27.  
PD 01-SEP-2004.  
PA (EMBL-) EMBL.  
Percent Similarity: 32.17%  
Best Local Similarity: 20.87%  
Query Match: 6.44%  
RESULT 1428  
ID AAQ04486 standard; DNA; 1236 BP.  
DE Plasmid pUKS3 encoding UK-S3.  
PD EP370205-A.  
PD 30-MAY-1990.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 36.91%  
Best Local Similarity: 24.22%  
Query Match: 6.43%  
RESULT 1429  
ID AAQ32850 standard; cDNA; 2487 BP.  
DE BMP1.  
PD WO9221365-A1.  
PD 10-DEC-1992.  
PA (PROC ) PROCTER & GAMBLE CO.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.90%  
Query Match: 6.43%  
RESULT 1430  
ID ABR83959 standard; cDNA; 2487 BP.  
DE Human cDNA differentially expressed in granulocytic cells #530.  
PD WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.90%  
Query Match: 6.43%  
RESULT 1431  
ID ADP65508 standard; DNA; 2487 BP.  
DE Human bone morphogenetic protein 1 (BMP-1) mRNA DNA.  
PD WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.90%  
Query Match: 6.43%  
RESULT 1432  
ID ADP65019 standard; DNA; 2487 BP.  
DE Human bone morphogenetic protein 1 (BMP1), transcript DNA sequence.  
PD WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.90%  
Query Match: 6.43%  
RESULT 1433  
ID ADH11557 standard; cDNA; 2487 BP.  
DE Human bone morphogenetic protein (BMP) polynucleotide #6.  
PD US2003224501-A1.  
PD 04-DEC-2003.  
PA (YOUNG/) YOUNG P E.  
PA (RUBE/) RUBEN S M.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.90%  
Query Match: 6.43%  
RESULT 1434  
ID ACN38772 standard; cDNA; 2487 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA83022, SEQ ID NO:2495.  
PD WO2004030615-A2.

PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.79%  
Query Match: 6.43%  
RESULT 1435  
ID AAN80631 standard; DNA; 2500 BP.  
DE Human Bone Morphogenic Protein-1 cDNA in lambda U2OS-1.  
PD WO8800205-A.  
PD 14-JAN-1988.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 37.79%  
Best Local Similarity: 25.90%  
Query Match: 6.43%  
RESULT 1436  
ID AAN82184 standard; DNA; 1575 BP.  
DE Modified tissue plasminogen activator lacking the G region and with G-183 DE and S-186 substd for S and T resp.  
PD JP632330084-A.  
PD 26-SEP-1988.  
PA (EISA ) EISAI CO LTD.  
Percent Similarity: 37.21%  
Best Local Similarity: 23.85%  
Query Match: 6.41%  
RESULT 1437  
ID AAN81089 standard; DNA; 1680 BP.  
DE Tissue plasminogen activator analogue coding sequence.  
PD EP293934-A.  
PD 07-DEC-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (NOVO ) NOVO IND AS.  
PA (EISA ) EISA CO LTD.  
Percent Similarity: 38.46%  
Best Local Similarity: 24.18%  
Query Match: 6.41%  
RESULT 1438  
ID ACN42707 standard; cDNA; 1710 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1582.  
PD WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 41.81%  
Best Local Similarity: 26.76%  
Query Match: 6.41%  
RESULT 1439  
ID AAQ05534 standard; DNA; 2099 BP.  
DE Plasmid pLGTQTPA encoding novel mutant tissue plasminogen activator (tPA).  
PD EP379890-A.  
PD 01-AUG-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 37.59%  
Best Local Similarity: 24.29%  
Query Match: 6.41%  
RESULT 1440  
ID ABL04087 standard; cDNA; 4140 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6743.  
PD WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 38.58%  
Best Local Similarity: 23.60%  
Query Match: 6.41%  
RESULT 1441  
ID ACF05073 standard; cDNA; 948 BP.  
DE Bovine recombinant prethrombin-2 nucleotide sequence.  
PD WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 44.65%  
Best Local Similarity: 28.78%  
Query Match: 6.40%  
RESULT 1442

ID ACF05076 standard; cDNA; 956 BP.  
 DE Bovine recombinant prethrombin-2 nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 44.65%  
 Best Local Similarity: 28.78%  
 Query Match: 6.40%  
 RESULT 1443  
 ID ACF05075 standard; cDNA; 1098 BP.  
 DE Bovine recombinant prethrombin-2 nucleotide sequence.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Percent Similarity: 44.65%  
 Best Local Similarity: 28.78%  
 Query Match: 6.40%  
 RESULT 1444  
 ID AAN91133 standard; DNA; 1419 BP.  
 DE Sequence of coding region in plasmid pmTQk112.  
 PN EP302456-A.  
 PD 08-FEB-1989.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Percent Similarity: 35.91%  
 Best Local Similarity: 22.98%  
 Query Match: 6.40%  
 RESULT 1445  
 ID AAS00146 standard; cDNA; 2487 BP.  
 DE Human cDNA clone HTPFG82 encoding IgSF protein #2.  
 PN WO200118176-A1.  
 PD 15-MAR-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (NIJG/) NI J.  
 Percent Similarity: 34.94%  
 Best Local Similarity: 22.89%  
 Query Match: 6.40%  
 RESULT 1446  
 ID AAN82185 standard; DNA; 1575 BP.  
 DE Modified tissue plasminogen activator lacking F and G region and with S-DE 119 substd for M.  
 DE 119 substd for M.  
 PN JP63230084-A.  
 PD 26-SEP-1988.  
 PA (EISA ) EISAI CO LTD.  
 Percent Similarity: 36.92%  
 Best Local Similarity: 24.42%  
 Query Match: 6.39%  
 RESULT 1447  
 ID ADO09841 standard; cDNA; 10662 BP.  
 DE Human NOV2b cDNA.  
 PN US2004018970-A1.  
 PD 29-JAN-2004.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PATT/) PATTURAJAN M.  
 PA (VERM/) VERNET C A M.  
 PA (CASM/) CASMAN S J.  
 PA (NALLY/) MALYANKAR U M.  
 PA (SHEN/) SHENOY S G.  
 PA (SPYT/) SPYTEK K A.  
 PA (GANG/) GANGOLLI E A.  
 PA (MILL/) MILLER C E.  
 PA (BOLD/) BOLDOG F L.  
 PA (LILL/) LI L.  
 PA (TAUP/) TAUPIER R J.  
 PA (KEKU/) KEKUDA R.  
 PA (SMIT/) SMITHSON G.  
 PA (ZERR/) ZERHUSEN B D.  
 PA (LIUX/) LIU X.  
 PA (COLM/) COLMAN S D.  
 PA (TCHE/) TCHERNEV V T.  
 PA (SIJG/) SI J.  
 PA (EDIN/) EDINGER S R.  
 PA (STON/) STONE D J.  
 PA (SCIO/) SCORE P.

PA (MILL/) MILLET I.  
 PA (ROTH/) ROTHENBERG M E.  
 Percent Similarity: 33.48%  
 Best Local Similarity: 21.42%  
 Query Match: 6.39%  
 RESULT 1448  
 ID ACN38775 standard; cDNA; 2463 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA325072, SEQ ID NO:2501.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 39.09%  
 Best Local Similarity: 27.66%  
 Query Match: 6.38%  
 RESULT 1449  
 ID ABK31781 standard; DNA; 3387 BP.  
 DE DNA encoding novel human protease #38.  
 PN WO200200860-A2.  
 PD 03-JAN-2002.  
 PA (SUGB-) SUGEN INC.  
 Percent Similarity: 34.03%  
 Best Local Similarity: 23.73%  
 Query Match: 6.38%  
 RESULT 1450  
 ID ABK86141 standard; cDNA; 3711 BP.  
 DE cDNA encoding human protease PRTS8.  
 PN WO200238744-A2.  
 PD 16-MAY-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 34.03%  
 Best Local Similarity: 23.73%  
 Query Match: 6.38%  
 RESULT 1451  
 ID AAO04962 standard; cDNA; 1506 BP.  
 DE Sequence encoding glycosylated plasminogen activator.  
 PN JP02049586-A.  
 PD 19-FEB-1990.  
 PA (KANF ) KANEGAFUCHI CHEM KK.  
 Percent Similarity: 35.82%  
 Best Local Similarity: 22.87%  
 Query Match: 6.36%  
 RESULT 1452  
 ID ADI30831 standard; cDNA; 2152 BP.  
 DE Human cDNA #157.  
 PN US6607879-B1.  
 PD 19-AUG-2003.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 36.47%  
 Best Local Similarity: 24.62%  
 Query Match: 6.36%  
 RESULT 1453  
 ID AAZ88364 standard; cDNA; 1239 BP.  
 DE Human prourokinase CT97 nucleotide sequence.  
 PN WO200000624-A1.  
 PD 06-JAN-2000.  
 PA (CROP-) CROPTech DEV CORP.  
 Percent Similarity: 37.11%  
 Best Local Similarity: 23.44%  
 Query Match: 6.35%  
 RESULT 1454  
 ID AAZ88363 standard; cDNA; 1305 BP.  
 DE Patatin signal peptide and prourokinase CT111 nucleotide sequence.  
 PN WO200000624-A1.  
 PD 06-JAN-2000.  
 PA (CROP-) CROPTech DEV CORP.  
 Percent Similarity: 37.11%  
 Best Local Similarity: 23.44%  
 Query Match: 6.35%  
 RESULT 1455  
 ID AAN81069 standard; DNA; 1437 BP.  
 DE Mutant no. 2600: tissue plasminogen activator homologue with finger and DE growth factor domain deletions.  
 DE Growth factor domain deletions.  
 PN EP292009-A.



Percent Similarity: 32.20% Conservative: 101  
 Best Local Similarity: 19.50% Mismatches: 278  
 Query Match: 6.31% Indels: 261  
 RESULT 1472  
 ID AAD13115 standard; cDNA; 708 BP.  
 DE Human membrane-type serine protease (MTSP) 4 cDNA.  
 PN WO200157194-A2.  
 PD 09-AUG-2001.  
 PA (CORV-) CORVAS INT INC.  
 Percent Similarity: 44.94% Conservative: 43  
 Best Local Similarity: 28.84% Mismatches: 105  
 Query Match: 6.31% Indels: 42  
 RESULT 1473  
 ID AD110374 standard; DNA; 708 BP.  
 DE Human cell surface protease coding sequence #3.  
 PN WO200295007-A2.  
 PD 28-NOV-2002.  
 PA (CORV-) CORVAS INT INC.  
 Percent Similarity: 44.94% Conservative: 43  
 Best Local Similarity: 28.84% Mismatches: 105  
 Query Match: 6.31% Indels: 42  
 RESULT 1474  
 ID ADJ46898 standard; cDNA; 708 BP.  
 DE Human transmembrane serine protease (MTSP) cDNA #3.  
 PN US2004001801-A1.  
 PD 01-JAN-2004.  
 PA (CORV-) CORVAS INT INC.  
 Percent Similarity: 44.94% Conservative: 43  
 Best Local Similarity: 28.84% Mismatches: 105  
 Query Match: 6.31% Indels: 42  
 RESULT 1475  
 ID ABK31780 standard; DNA; 792 BP.  
 DE DNA encoding novel human protease #37.  
 PN WO200200860-A2.  
 PD 03-JAN-2002.  
 PA (SUGE-) SUGEN INC.  
 Percent Similarity: 44.79% Conservative: 47  
 Best Local Similarity: 26.64% Mismatches: 95  
 Query Match: 6.31% Indels: 48  
 RESULT 1476  
 ID ADJ95175 standard; DNA; 1869 BP.  
 DE Novel NOVX gene sequence #202.  
 PN WO2003040325-A2.  
 PD 15-MAY-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.38% Conservative: 96  
 Best Local Similarity: 20.30% Mismatches: 264  
 Query Match: 6.31% Indels: 226  
 RESULT 1477  
 ID ADK51027 standard; DNA; 1869 BP.  
 DE Human NOV11B gene sequence SeqID47.  
 PN WO2003083046-A2.  
 PD 09-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.38% Conservative: 96  
 Best Local Similarity: 20.30% Mismatches: 264  
 Query Match: 6.31% Indels: 226  
 RESULT 1478  
 ID ADK51031 standard; DNA; 1869 BP.  
 DE Human NOV11D gene sequence SeqID51.  
 PN WO2003083046-A2.  
 PD 09-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.38% Conservative: 96  
 Best Local Similarity: 20.30% Mismatches: 264  
 Query Match: 6.31% Indels: 226  
 RESULT 1479  
 ID ADL56819 standard; cDNA; 2037 BP.  
 DE Human NOVX cDNA #3.  
 PN US2003215449-A1.  
 PD 20-NOV-2003.  
 PA (MEZE-) MEZES P D.  
 PA (RAST-) RASTELLI L.

PA (HERR-) HERRMANN J L.  
 PA (MACD-) MACDOUGALL J R.  
 PA (ZHON-) ZHONG H.  
 PA (CASM-) CASMAN S J.  
 PA (BOLD-) BOLDOG F L.  
 PA (SHIM-) SHIMKETS R A.  
 PA (GORM-) GORMAN L.  
 PA (EISE-) EISEN A J.  
 PA (VERN-) SPADERNA S K.  
 PA (BERG-) BERGHS C.  
 PA (SPYT-) SPYTEK X A.  
 PA (DIP1-) DIPIPPO V A.  
 PA (ZERH-) ZERHUSEN B D.  
 PA (PEYM-) PEYMAN J A.  
 PA (ELLE-) ELLERMAN K.  
 PA (STON-) STONE D J.  
 PA (GROS-) GROSSE W M.  
 PA (ALSO-) ALSOBROOK J P.  
 PA (LEPL-) LEPLEY D M.  
 PA (RIEG-) RIEGER D K.  
 PA (BURG-) BURGESS C E.  
 PA (EDIN-) EDINGER S R.  
 PA (VOSS-) VOSS E Z.  
 PA (MILL-) MILLER C E.  
 Percent Similarity: 33.06% Conservative: 95  
 Best Local Similarity: 20.19% Mismatches: 261  
 Query Match: 6.31% Indels: 234  
 RESULT 1480  
 ID ASS59536 standard; cDNA; 2038 BP.  
 DE Human cDNA, homologous to Kallikrein, designated NOV3.  
 PN WO200255705-A2.  
 PD 18-JUL-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.06% Conservative: 95  
 Best Local Similarity: 20.19% Mismatches: 261  
 Query Match: 6.31% Indels: 234  
 RESULT 1481  
 ID ADJ95173 standard; DNA; 2038 BP.  
 DE Novel NOVX gene sequence #201.  
 PN WO2003040325-A2.  
 PD 15-MAY-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.06% Conservative: 95  
 Best Local Similarity: 20.19% Mismatches: 261  
 Query Match: 6.31% Indels: 234  
 RESULT 1482  
 ID ADK51025 standard; DNA; 2038 BP.  
 DE Human NOV11A gene sequence SeqID45.  
 PN WO2003083046-A2.  
 PD 09-OCT-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 33.06% Conservative: 95  
 Best Local Similarity: 20.19% Mismatches: 261  
 Query Match: 6.31% Indels: 234  
 RESULT 1483  
 ID ADO39203 standard; cDNA; 2038 BP.  
 DE Human cDNA encoding novel protein NOV3.  
 PN US2004018196-A1.  
 PD 29-JAN-2004.  
 PA (MEZE-) MEZES P D.  
 PA (RAST-) RASTELLI L.  
 PA (HERR-) HERRMANN J L.  
 PA (MACD-) MACDOUGALL J R.  
 PA (CASM-) CASMAN S J.  
 PA (BOLD-) BOLDOG F L.  
 PA (SHIM-) SHIMKETS R A.  
 PA (GORM-) GORMAN L.  
 PA (EISE-) EISEN A J.  
 PA (SPAD-) SPADERNA S K.  
 PA (VERN-) VERNET C A M.  
 PA (BERG-) BERGHS C.





Query Match: 6.30% Indels: 142  
RESULT 1498  
ID AAN91117 standard; DNA; 1314 BP.  
DE Sequence of coding region in plasmid pTQIPA delta trp.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 37.32% Conservative: 64  
Best Local Similarity: 23.90% Mismatches: 159  
Query Match: 6.30% Indels: 142  
RESULT 1499  
ID AAN91127 standard; DNA; 1314 BP.  
DE Sequence of coding region in plasmid pSTQitrp.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 37.32% Conservative: 64  
Best Local Similarity: 23.90% Mismatches: 159  
Query Match: 6.30% Indels: 142  
RESULT 1500  
ID AAN91126 standard; DNA; 1314 BP.  
DE Sequence of coding region in plasmid pSTQktrp.  
PN EP302456-A.  
PD 08-FEB-1989.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Percent Similarity: 37.32% Conservative: 64  
Best Local Similarity: 23.90% Mismatches: 159  
Query Match: 6.30% Indels: 142

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 9, 2005, 20:40:48 ; Search time 5938 Seconds  
(without alignments)  
4615.405 Million cell updates/sec

Title: US-10-063-692-38

Perfect score: 3945

Sequence: 1 MELGWTQLTFLQLLLIS.....LSTAFKVLVLPKDWIERNMK 720

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-O=/cpn2.1/USPTO.spool/US10063692/runat\_09052005.122254.4841/app.query.fasta\_1.903  
-DB=EST -QFMT=fstap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10063692 @CEN 1 1 4352 @runat\_09052005.122254.4841 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hc1: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_g881: \*  
9: gb\_g882: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3936	99.8	3165	3	HSM806734
2	3813	96.7	2850	3	AF370388
3	3612	91.6	2746	3	AK088017
4	3489.5	88.5	2214	9	AY406074
5	3211.5	81.4	2214	9	AY406076
6	2480.5	62.9	2214	9	AY406075
7	1766	44.8	2184	3	AK031254
8	1578.5	40.0	1049	5	EX399905
9	1527	38.7	952	5	BX439313

10	1492	37.8	886	5	BX337781
11	1440	36.5	1158	4	BM461342
12	1436	36.4	879	6	CD514783
13	1341	34.0	795	6	CD655367
14	1258	31.9	718	7	CF125161
15	1226	31.1	785	7	CO397557
16	1156.5	29.3	742	5	BX350293
17	1150	29.2	697	2	BB620582
18	1128	28.6	711	7	CO733882
19	1107	28.1	630	4	BM724013
20	1104	28.0	693	7	CO880461
21	1100	27.9	773	4	RG403264
22	1097.5	27.8	715	1	AL048495
23	1086	27.5	660	7	CK959441
24	1081.5	27.4	711	5	BU253929
25	1077	27.3	830	7	CK474785
26	1065	27.0	626	5	BP381335
27	1058	26.8	635	2	BB632336
28	1055	26.7	584	5	BP205877
29	1005	25.5	595	4	BI346571
30	1004.5	25.5	891	6	CB204666
31	991.5	25.1	846	7	CO387203
32	990	25.1	566	5	BP289572
33	948	24.0	774	1	AU067539
34	940	23.8	500	6	CB712029
35	924	23.4	832	5	BP464936
36	917	23.2	593	2	AW918019
37	915	23.2	547	2	BE231795
38	909	23.0	546	4	BM254217
39	908	23.0	938	5	BU383403
40	904	22.9	557	4	BM106593
41	882	22.4	590	7	CK622160
42	877	22.2	660	6	BY745962
43	860	21.8	664	7	CN059249
44	859	21.8	476	5	BM282717
45	853	21.6	633	2	AW957662
46	843.5	21.4	1100	5	BX337780
47	834	21.1	492	7	CN296855
48	812	20.6	452	2	BE048236
49	803	20.4	520	4	BI346989
50	801	20.3	520	2	BE653376
51	794	20.1	687	4	BI526460
52	791	20.1	1008	5	BX399904
53	789	20.0	468	2	AM484384
54	786	19.9	519	2	BE683792
55	784	19.9	482	5	BX515589
56	776	19.7	584	5	BP312143
57	774	19.6	463	1	AA444868
58	772	19.6	483	4	BM088773
59	752	19.1	521	2	BE910833
60	735	18.6	428	1	BF197805
61	722	18.3	458	1	AI549757
62	710	18.0	583	5	BP216550
63	704	17.8	456	7	CO260289
64	704	17.8	594	7	CN061039
65	688	17.4	814	5	BU206384
66	686	17.4	422	2	AW323842
67	685	17.4	348	7	CN334668
68	675	17.1	570	1	AI536361
69	669	17.0	489	5	BY243636
70	662	16.8	897	5	BX434191
71	653.5	16.6	662	5	BU218794
72	650	16.5	419	4	BM484683
73	642	16.3	382	6	CD707019
74	634.5	16.1	385	5	BY275139
75	632	16.0	482	5	BY243643
76	621	15.7	378	4	BM090462
77	612	15.5	410	5	BX473159
78	599	15.2	435	6	CB793309
79	594.5	15.1	494	2	BE374037
80	594	15.1	378	2	AM426139
81	586	14.9	465	5	BY244862
82	576	14.6	907	5	BU358450

83	573	14.5	371	5	BY131558	BY131558	BY131558	156	312	7.9	3035	3	AK004939	Mus muscu
84	568	14.4	421	5	BY295210	BY295210	BY295210	157	309.5	7.8	1931	3	CR653493	Tetraodon
85	565.5	14.3	395	2	AW416537	AW416537	AW416537	158	306.5	7.8	1586	3	CR606412	full-leng
86	560	14.2	959	1	AU051031	AU051031	AU051031	159	302.5	7.7	1857	3	AK089402	Mus muscu
87	559	14.2	808	5	BU359706	BU359706	BU359706	160	301	7.6	3683	3	AK033582	Mus muscu
88	554	14.0	411	7	CN296856	CN296856	CN296856	161	300	7.6	621	4	BI387043	BFL26_001
89	553	14.0	416	6	CB768218	CB768218	CB768218	162	300	7.6	642	9	AG144714	Pan trogl
90	551	14.0	343	2	AW307893	AW307893	AW307893	163	298.5	7.6	1717	3	CR653983	Tetraodon
91	546	13.8	338	1	AA375185	AA375185	AA375185	164	298	7.6	1723	3	CR634742	Tetraodon
92	539	13.7	425	5	BY266233	BY266233	BY266233	165	297.5	7.5	2511	3	AK038356	Mus muscu
93	528.5	13.4	752	5	BM879710	BM879710	BM879710	c	296	7.5	722	5	BU742056	UI-E-B01-
94	528	13.4	310	7	CN122781	CN122781	CN122781	167	292	7.4	163	7	CN334667	170005319
95	525	13.3	416	5	BY238364	BY238364	BY238364	168	291	7.4	380	5	BY035258	BY035258
96	520	13.2	427	5	BY273129	BY273129	BY273129	169	289.5	7.3	2498	5	CR623908	full-leng
97	515	13.1	791	5	B0316123	B0316123	B0316123	c	289	7.3	722	5	BQ014522	UI-H-ED1-
98	510	12.9	348	7	R47049	R47049	R47049	170	287	7.3	1618	3	CR725571	Tetraodon
99	510	12.9	756	7	CN334669	CN334669	CN334669	171	287	7.3	1618	3	CR725571	Tetraodon
100	508	12.9	404	5	BY271161	BY271161	BY271161	172	286	7.2	2079	3	CR652267	Tetraodon
101	501	12.7	851	7	CO394970	CO394970	CO394970	173	285.5	7.2	1676	3	CR637804	Tetraodon
102	493	12.5	643	8	BZ245624	BZ245624	BZ245624	174	285	7.2	185	2	BF366351	IL2-NT009
103	479	12.1	414	5	BY282746	BY282746	BY282746	c	285	7.2	1237	6	CD497665	CD429-B05
104	476.5	12.1	749	4	BM105355	BM105355	BM105355	176	285	7.2	1584	3	CR648830	Tetraodon
105	476	12.1	482	4	BM105355	BM105355	BM105355	177	284.5	7.2	807	4	BI834499	BI844199
106	475.5	12.1	427	5	BY265763	BY265763	BY265763	178	284	7.2	1438	3	CR639903	Tetraodon
107	471	11.9	410	5	BY287911	BY287911	BY287911	179	284	7.2	1538	3	CR634681	Tetraodon
108	471	11.9	714	7	CF525168	CF525168	CF525168	180	284	7.2	1559	3	CR634333	Tetraodon
109	470	11.9	386	2	BF451877	BF451877	BF451877	181	282.5	7.2	1706	3	CR634000	Tetraodon
110	470	11.9	504	1	AA199196	AA199196	AA199196	182	282.5	7.2	1707	3	CR639050	Tetraodon
c	111	466	817	7	CK775452	CK775452	CK775452	183	282	7.1	1966	3	CR638621	Tetraodon
112	463.5	11.7	333	7	TS2085	TS2085	TS2085	184	281.5	7.1	1056	5	BM919200	BM919200
113	460	11.7	381	7	CR772910	CR772910	CR772910	185	280.5	7.1	795	5	AY414006	Homo sapi
114	459.5	11.6	369	1	AA833210	AA833210	AA833210	186	279.5	7.1	921	4	BI833975	603085088
115	459	11.6	3787	3	AK031598	AK031598	AK031598	187	278	7.0	1434	3	CR623031	full-leng
116	453	11.5	425	5	BY295062	BY295062	BY295062	188	278	7.0	1467	3	CR607773	full-leng
117	447	11.3	423	5	BY259943	BY259943	BY259943	c	276	7.0	264	2	BB585844	BB585844
118	435	11.0	262	2	AW431829	AW431829	AW431829	189	276	7.0	1066	8	CC229783	CC229783
119	433	11.0	410	2	BF920134	BF920134	BF920134	191	275.5	7.0	674	5	BU488601	604126955
120	432	11.0	297	2	AW483167	AW483167	AW483167	192	275.5	7.0	746	5	BX540841	BX540841
121	427	10.8	258	1	AL701986	AL701986	AL701986	c	275.5	7.0	850	6	CD508999	CD493-H10
122	421	10.7	358	5	BY128083	BY128083	BY128083	c	275.5	7.0	857	6	CD507437	CD485-A11
123	417	10.6	359	6	BY783505	BY783505	BY783505	c	275.5	7.0	855	6	CD508999	CD493-H10
124	417	10.6	2751	3	AK050052	AK050052	AK050052	c	275.5	7.0	860	6	CD504920	CD504920
125	416.5	10.6	757	5	BM884986	BM884986	BM884986	c	275.5	7.0	890	6	CD504919	CD504919
126	413	10.5	633	5	BY252479	BY252479	BY252479	198	275.5	7.0	890	6	CD508998	CD508998
127	408	10.3	357	5	BY339892	BY339892	BY339892	199	275.5	7.0	894	5	BU487901	BU487901
128	408	10.3	359	5	BY341239	BY341239	BY341239	200	275.5	7.0	894	5	BU487901	603972106
129	403.5	10.2	4266	3	CR749540	CR749540	CR749540	201	275.5	7.0	1421	3	CR633905	Tetraodon
130	392.5	9.9	327	5	BY289536	BY289536	BY289536	c	274	6.9	1429	3	CR732608	Tetraodon
131	392	9.9	327	2	AW353000	AW353000	AW353000	c	273.5	6.9	882	6	CB561012	AGENCOURT
132	389	9.9	611	5	BU477941	BU477941	BU477941	c	273.5	6.9	896	6	CD499146	CD499146
133	385	9.8	325	2	AG957673	AG957673	AG957673	c	273.5	6.9	1116	6	CD499146	CD499146
c	134	382	9.7	731	9	AW511653	AW511653	c	273.5	6.9	1130	6	CD499724	CD499724
135	377	9.6	389	4	BM876043	BM876043	BM876043	c	273.5	6.9	1164	6	CD504975	CD504975
136	377	9.6	409	5	BY264071	BY264071	BY264071	c	273.5	6.9	1181	6	CD502179	CD502179
137	369	9.4	2876	3	AK087522	AK087522	AK087522	c	273.5	6.9	1212	6	CD498397	CD498397
c	138	367.5	569	7	CO631899	CO631899	CO631899	c	273.5	6.9	1215	6	CD504505	CD504505
139	365	9.3	399	1	AJ696577	AJ696577	AJ696577	c	273.5	6.9	1232	6	CD503870	CD503870
140	358	9.1	2386	3	BC046065	BC046065	BC046065	c	273.5	6.9	1409	3	CR608439	CR608439
c	141	357	9.0	539	9	CG991118	CG991118	c	273.5	6.9	2686	3	CR749503	Homo sapi
142	352.5	8.9	776	9	CC530365	CC530365	CC530365	c	273	6.9	778	5	BM081500	BM081500
143	352	8.9	352	5	BY310228	BY310228	BY310228	c	273	6.9	797	5	BM081500	BM081500
144	350	8.9	373	1	AA126930	AA126930	AA126930	c	273	6.9	805	4	BJ714778	BJ714778
145	349.5	8.9	688	8	AZ794032	AZ794032	AZ794032	c	273	6.9	1571	7	CF110615	Shultzomi
c	146	349	8.8	740	5	BQ009840	BQ009840	c	272.5	6.9	878	6	CD508601	CD508601
147	343	8.7	702	5	BM282919	BM282919	BM282919	c	271.5	6.9	925	3	CR636671	Tetraodon
148	337	8.5	188	5	BQ694586	BQ694586	BQ694586	c	271.5	6.9	838	7	CN156901	CN156901
149	333	8.4	506	1	AA266124	AA266124	AA266124	c	271	6.9	1423	3	CR654263	CR654263
150	327	8.3	382	3	AK081081	AK081081	AK081081	c	270	6.8	1201	3	CR639571	CR639571
c	151	323	723	5	BQ014545	BQ014545	BQ014545	c	270	6.8	1967	3	CR730923	Tetraodon
152	320	8.1	507	1	AA043793	AA043793	AA043793	c	269.5	6.8	840	7	CO928471	CO928471
153	318.5	8.1	3248	3	BC008514	BC008514	BC008514	c	269.5	6.8	968	3	CR651513	Tetraodon
154	318.5	8.1	4017	3	AK052738	AK052738	AK052738	c	269.5	6.8	1136	3	CR642844	Tetraodon
155	318	8.1	241	5	BU788909	BU788909	BU788909	c	269.5	6.8	2044	3	CR647409	Tetraodon

229	268.5	6.8	952	3	CR648349	Tetraodon	CR648349	302	265.5	6.7	963	3	CR635040	Tetraodon	CR635040
230	268.5	6.8	958	3	CR643383	Tetraodon	CR643383	303	265.5	6.7	963	3	CR653362	Tetraodon	CR653362
c 231	268.5	6.8	966	6	CD498092	CD431-F04	CD498092	304	265.5	6.7	963	3	CR654376	Tetraodon	CR654376
232	268.5	6.8	968	3	CR645716	Tetraodon	CR645716	305	265.5	6.7	963	3	CR655625	Tetraodon	CR655625
233	268.5	6.8	991	6	CD498091	CD431-F04	CD498091	306	265.5	6.7	964	3	CR635805	Tetraodon	CR635805
234	268.5	6.8	1024	6	CD506086	CD477-C09	CD506086	307	265.5	6.7	964	3	CR652426	Tetraodon	CR652426
235	268.5	6.8	1075	3	CR637860	Tetraodon	CR637860	308	265.5	6.7	965	3	CR636493	Tetraodon	CR636493
c 236	268	6.8	891	6	CD499352	CD438-H02	CD499352	309	265.5	6.7	965	3	CR642503	Tetraodon	CR642503
c 237	268	6.8	981	6	CD506087	CD477-C09	CD506087	310	265.5	6.7	965	3	CR642503	Tetraodon	CR642503
238	267.5	6.8	924	7	CK409299	AUF_IfLvr	CK409299	311	265.5	6.7	965	3	CR645376	Tetraodon	CR645376
239	267.5	6.8	944	5	BM919892	AGENCOURT	BM919892	312	265.5	6.7	966	3	CR642902	Tetraodon	CR642902
240	266.5	6.8	870	3	CR645650	Tetraodon	CR645650	313	265.5	6.7	966	3	CR646996	Tetraodon	CR646996
241	266.5	6.8	974	3	CR656477	Tetraodon	CR656477	314	265.5	6.7	967	3	CR642781	Tetraodon	CR642781
242	266.5	6.8	1741	3	CR641480	Tetraodon	CR641480	315	265.5	6.7	967	3	CR648557	Tetraodon	CR648557
243	266	6.7	749	5	BU488413	60412747	BU488413	316	265.5	6.7	967	3	CR653274	Tetraodon	CR653274
244	266	6.7	801	7	CN510309	AGENCOURT	CN510309	317	265.5	6.7	967	3	CR653075	Tetraodon	CR653075
245	265.5	6.7	843	3	CR636630	Tetraodon	CR636630	318	265.5	6.7	968	3	CR655105	Tetraodon	CR655105
246	265.5	6.7	906	3	CR638127	Tetraodon	CR638127	319	265.5	6.7	971	3	CR638949	Tetraodon	CR638949
247	265.5	6.7	907	3	CR656092	Tetraodon	CR656092	320	265.5	6.7	971	3	CR639592	Tetraodon	CR639592
248	265.5	6.7	915	3	CR640949	Tetraodon	CR640949	321	265.5	6.7	971	3	CR643673	Tetraodon	CR643673
249	265.5	6.7	919	3	CR641090	Tetraodon	CR641090	322	265.5	6.7	971	3	CR643965	Tetraodon	CR643965
250	265.5	6.7	919	3	CR644534	Tetraodon	CR644534	323	265.5	6.7	971	3	CR653075	Tetraodon	CR653075
251	265.5	6.7	920	3	CR647695	Tetraodon	CR647695	324	265.5	6.7	972	3	CR649003	Tetraodon	CR649003
252	265.5	6.7	924	3	CR646003	Tetraodon	CR646003	325	265.5	6.7	973	3	CR634877	Tetraodon	CR634877
253	265.5	6.7	927	3	CR649278	Tetraodon	CR649278	326	265.5	6.7	973	3	CR642156	Tetraodon	CR642156
254	265.5	6.7	929	3	CR649904	Tetraodon	CR649904	327	265.5	6.7	974	3	CR654336	Tetraodon	CR654336
255	265.5	6.7	932	3	CR641687	Tetraodon	CR641687	328	265.5	6.7	975	3	CR651274	Tetraodon	CR651274
256	265.5	6.7	938	3	CR644946	Tetraodon	CR644946	329	265.5	6.7	975	3	CR656121	Tetraodon	CR656121
257	265.5	6.7	938	3	CR648301	Tetraodon	CR648301	330	265.5	6.7	976	3	CR637198	Tetraodon	CR637198
258	265.5	6.7	939	3	CR655652	Tetraodon	CR655652	331	265.5	6.7	977	3	CR642541	Tetraodon	CR642541
259	265.5	6.7	941	3	CR653581	Tetraodon	CR653581	332	265.5	6.7	977	3	CR648403	Tetraodon	CR648403
260	265.5	6.7	943	3	CR638500	Tetraodon	CR638500	333	265.5	6.7	978	3	CR735011	Tetraodon	CR735011
261	265.5	6.7	943	3	CR645523	Tetraodon	CR645523	334	265.5	6.7	981	3	CR646070	Tetraodon	CR646070
262	265.5	6.7	943	3	CR649221	Tetraodon	CR649221	335	265.5	6.7	1039	3	CR644082	Tetraodon	CR644082
263	265.5	6.7	944	3	CR646188	Tetraodon	CR646188	336	265.5	6.7	1197	3	CR640066	Tetraodon	CR640066
264	265.5	6.7	945	3	CR643027	Tetraodon	CR643027	337	265.5	6.7	1201	3	CR645235	Tetraodon	CR645235
265	265.5	6.7	945	3	CR648151	Tetraodon	CR648151	338	265.5	6.7	1209	3	CR729660	Tetraodon	CR729660
266	265.5	6.7	948	3	CR643117	Tetraodon	CR643117	339	265.5	6.7	1217	3	CR652649	Tetraodon	CR652649
267	265.5	6.7	949	3	CR655908	Tetraodon	CR655908	340	265.5	6.7	1390	3	CR649867	Tetraodon	CR649867
268	265.5	6.7	950	3	CR643289	Tetraodon	CR643289	341	265.5	6.7	1399	3	CR727544	Tetraodon	CR727544
269	265.5	6.7	952	3	CR636594	Tetraodon	CR636594	342	265.5	6.7	1988	3	CR592485	full-leng	CR592485
270	265.5	6.7	953	3	CR637521	Tetraodon	CR637521	343	265	6.7	774	5	BX083148	BX083148	BX083148
271	265.5	6.7	953	3	CR637531	Tetraodon	CR637531	344	265	6.7	779	5	BX078970	BX078970	BX078970
272	265.5	6.7	953	3	CR639263	Tetraodon	CR639263	345	265	6.7	850	5	BX078583	BX078583	BX078583
273	265.5	6.7	953	3	CR647021	Tetraodon	CR647021	346	265	6.7	854	6	CR565651	AGENCOURT	CR565651
274	265.5	6.7	954	3	CR653165	Tetraodon	CR653165	c 347	265	6.7	854	6	CR565651	AGENCOURT	CR565651
275	265.5	6.7	954	3	CR635344	Tetraodon	CR635344	348	265	6.7	1106	3	CR645231	Tetraodon	CR645231
276	265.5	6.7	954	3	CR655952	Tetraodon	CR655952	349	264.5	6.7	774	7	CV488433	AGENCOURT	CV488433
277	265.5	6.7	955	3	CR635542	Tetraodon	CR635542	c 350	264.5	6.7	877	7	CK406791	AUF_IfLvr	CK406791
278	265.5	6.7	955	3	CR644574	Tetraodon	CR644574	351	264.5	6.7	959	3	CR637196	Tetraodon	CR637196
279	265.5	6.7	956	3	CR635540	Tetraodon	CR635540	352	264.5	6.7	964	3	CR655278	Tetraodon	CR655278
280	265.5	6.7	956	3	CR637602	Tetraodon	CR637602	353	264.5	6.7	966	3	CR645072	Tetraodon	CR645072
281	265.5	6.7	957	3	CR635227	Tetraodon	CR635227	354	264	6.7	2073	3	AK007987	MUS muscu	AK007987
282	265.5	6.7	957	3	CR640159	Tetraodon	CR640159	355	263.5	6.7	798	5	BX074786	BX074786	BX074786
283	265.5	6.7	957	3	CR646990	Tetraodon	CR646990	356	263.5	6.7	832	7	CN180066	AGENCOURT	CN180066
284	265.5	6.7	958	3	CR638822	Tetraodon	CR638822	357	263.5	6.7	881	7	CK409600	AUF_IfLvr	CK409600
285	265.5	6.7	958	3	CR639620	Tetraodon	CR639620	358	263.5	6.7	894	7	CK402317	AUF_IfLvr	CK402317
286	265.5	6.7	958	3	CR653201	Tetraodon	CR653201	359	263.5	6.7	925	7	CK406767	AUF_IfLvr	CK406767
287	265.5	6.7	959	3	CR637270	Tetraodon	CR637270	360	263.5	6.7	939	3	CR638380	Tetraodon	CR638380
288	265.5	6.7	959	3	CR643681	Tetraodon	CR643681	361	263.5	6.7	942	3	CR647663	Tetraodon	CR647663
289	265.5	6.7	959	3	CR650507	Tetraodon	CR650507	362	263.5	6.7	967	6	CD363253	AGENCOURT	CD363253
290	265.5	6.7	959	3	CR651405	Tetraodon	CR651405	363	263.5	6.7	1450	3	CR603372	full-leng	CR603372
291	265.5	6.7	959	3	CR651712	Tetraodon	CR651712	364	263.5	6.7	1502	3	CR649600	Tetraodon	CR649600
292	265.5	6.7	959	3	CR652069	Tetraodon	CR652069	c 365	263	6.7	760	7	CV484847	AGENCOURT	CV484847
293	265.5	6.7	960	3	CR635690	Tetraodon	CR635690	c 366	263	6.7	850	7	CF284554	AGENCOURT	CF284554
294	265.5	6.7	960	3	CR643347	Tetraodon	CR643347	367	263	6.7	963	7	CN317696	AGENCOURT	CN317696
295	265.5	6.7	961	3	CR653969	Tetraodon	CR653969	368	262.5	6.7	957	3	CR635563	Tetraodon	CR635563
296	265.5	6.7	961	3	CR636815	Tetraodon	CR636815	369	262.5	6.7	1018	6	CD507436	CD485-A11	CD507436
297	265.5	6.7	961	3	CR654102	Tetraodon	CR654102	370	262.5	6.7	1476	9	CR644996	Tetraodon	CR644996
298	265.5	6.7	962	3	CR635908	Tetraodon	CR635908	c 371	262	6.6	570	3	CR841478	GR0AA75D	CR841478
299	265.5	6.7	962	3	CR636196	Tetraodon	CR636196	372	261.5	6.6	853	7	CK407561	AUF_IfLvr	CK407561
300	265.5	6.7	962	3	CR637964	Tetraodon	CR637964	373	261.5	6.6	853	7	CO960318	AGENCOURT	CO960318
301	265.5	6.7	962	3	CR641763	Tetraodon	CR641763	374	261.5	6.6	855	5	BQ733682	AGENCOURT	BQ733682

375	261.5	6.6	954	3	CR633957	CR633957 Tetraodon	448	255	6.5	860	3	CR644603	CR644603 Tetraodon
376	261.5	6.6	959	3	CR645823	CR645823 Tetraodon	449	255	6.5	863	3	CR654851	CR654851 Tetraodon
377	261.5	6.6	965	3	CR718326	CR718326 Tetraodon	450	255	6.5	864	3	CR642012	CR642012 Tetraodon
378	261.5	6.6	1051	4	BM547198	BM547198 AGENCOURT	451	255	6.5	864	3	CR655196	CR655196 Tetraodon
379	261.5	6.6	1138	3	CR636401	CR636401 Tetraodon	452	255	6.5	874	3	CR655655	CR655655 Tetraodon
380	261.5	6.6	1567	3	CR645935	CR645935 Tetraodon	453	255	6.5	877	3	CR653848	CR653848 Tetraodon
381	260.5	6.6	795	9	AY414007	AY414007 Pan trogl	c 454	255	6.5	886	7	CF375630	CF375630 AGENCOURT
382	260.5	6.6	815	4	BJ714978	BJ714978 Tetraodon	455	255	6.5	928	7	CR864509	CR864509 AGENCOURT
383	260.5	6.6	820	5	BM081126	BM081126 Tetraodon	456	255	6.5	977	3	CR720946	CR720946 Tetraodon
384	260.5	6.6	822	5	BM079673	BM079673 Tetraodon	457	255	6.5	1046	3	CR633733	CR633733 Tetraodon
385	260.5	6.6	926	3	CR643380	CR643380 Tetraodon	458	255	6.5	1086	6	CD499351	CD499351 CDA38-H02
386	260.5	6.6	957	3	CR639412	CR639412 Tetraodon	459	255	6.5	1114	3	CR647072	CR647072 Tetraodon
387	260.5	6.6	974	3	CR650791	CR650791 Tetraodon	460	255	6.5	1126	3	CR637589	CR637589 Tetraodon
388	260.5	6.6	1188	3	CR727891	CR727891 Tetraodon	461	255	6.5	1200	3	CR640466	CR640466 Tetraodon
c 389	260	6.6	676	7	CV491738	CV491738 AGENCOURT	462	254.5	6.5	807	7	CV484837	CV484837 AGENCOURT
390	260	6.6	771	5	BM073544	BM073544 Tetraodon	463	254.5	6.5	971	3	CR636724	CR636724 Tetraodon
391	260	6.6	787	5	BM073699	BM073699 Tetraodon	464	254.5	6.5	1085	5	BM919045	BM919045 AGENCOURT
392	260	6.6	829	7	CO250114	CO250114 AGENCOURT	465	254.5	6.5	1210	5	CR647865	CR647865 Tetraodon
393	259.5	6.6	768	5	BM077913	BM077913 Tetraodon	466	254.5	6.5	1519	3	CR641286	CR641286 Tetraodon
394	259.5	6.6	782	7	CF347656	CF347656 AGENCOURT	467	254	6.4	506	8	AQ150311	AQ150311 HS 3178_B
395	259.5	6.6	786	5	BM072919	BM072919 Tetraodon	468	254	6.4	738	5	BM083513	BM083513 BX083513
396	259.5	6.6	848	7	CO915858	CO915858 AGENCOURT	469	254	6.4	763	5	BM083864	BM083864 BX083864
397	259.5	6.6	882	3	CR650843	CR650843 Tetraodon	470	254	6.4	794	5	BU487543	BU487543 604126191
398	259.5	6.6	2041	4	BJ498457	BJ498457 full-leng	471	254	6.4	817	5	BM076781	BM076781 BX076781
399	259	6.6	645	4	BJ498457	BJ498457 Tetraodon	472	254	6.4	860	3	CR643444	CR643444 Tetraodon
400	259	6.6	822	5	BM081087	BM081087 Tetraodon	473	254	6.4	878	7	CF225589	CF225589 AGENCOURT
401	259	6.6	844	5	BM078668	BM078668 Tetraodon	474	254	6.4	995	3	CR644564	CR644564 Tetraodon
402	259	6.6	1223	3	AK014645	AK014645 Mus muscu	475	254	6.4	1065	3	CR651738	CR651738 Tetraodon
403	259	6.6	1869	3	CR633979	CR633979 Tetraodon	476	253.5	6.4	749	5	BU486703	BU486703 604127811
404	258.5	6.6	812	7	CV491817	CV491817 AGENCOURT	477	253.5	6.4	797	5	BU076220	BU076220 BX076220
c 405	258	6.5	717	7	CV491804	CV491804 AGENCOURT	478	253.5	6.4	801	5	BU417196	BU417196 603671644
406	258	6.5	752	5	BM077057	BM077057 Tetraodon	479	253.5	6.4	809	5	BU417370	BU417370 603671273
407	258	6.5	770	7	CF998216	CF998216 AGENCOURT	480	253.5	6.4	853	5	BU487073	BU487073 604126372
408	258	6.5	788	5	BM077756	BM077756 Tetraodon	c 481	253.5	6.4	917	7	CF582693	CF582693 AGENCOURT
409	258	6.5	793	5	BU488539	BU488539 604124870	482	253.5	6.4	922	3	CR652681	CR652681 Tetraodon
410	258	6.5	818	5	BM076890	BM076890 Tetraodon	483	253.5	6.4	1152	3	CR658453	CR658453 Tetraodon
411	258	6.5	824	7	CN322770	CN322770 AGENCOURT	484	253	6.4	1152	3	BU416681	BU416681 603671141
412	258	6.5	876	3	CR635090	CR635090 Tetraodon	485	253	6.4	782	4	BJ715033	BJ715033 BX715033
413	258	6.5	1477	3	CR643003	CR643003 Tetraodon	486	253	6.4	866	3	CR642780	CR642780 Tetraodon
414	257.5	6.5	830	5	BM075027	BM075027 Tetraodon	487	253	6.4	883	3	CR654193	CR654193 Tetraodon
415	257.5	6.5	848	7	CO959111	CO959111 AGENCOURT	488	253	6.4	998	3	CR643074	CR643074 Tetraodon
416	257.5	6.5	954	3	CR642576	CR642576 Tetraodon	489	253	6.4	5901	9	AY407075	AY407075 Mus muscu
c 417	257.5	6.5	1106	6	CD509145	CD509145 CDA94-G02	490	252.5	6.4	693	5	BM189458	BM189458 BW189458
418	257.5	6.5	1136	3	CR645632	CR645632 Tetraodon	491	252.5	6.4	805	5	BU417083	BU417083 603671453
419	257.5	6.5	1218	3	CR644124	CR644124 Tetraodon	492	252.5	6.4	892	3	CR643850	CR643850 Tetraodon
420	257	6.5	767	6	CA350208	CA350208 620902_NC	493	252.5	6.4	901	3	CR645646	CR645646 Tetraodon
421	257	6.5	782	7	CK026016	CK026016 AGENCOURT	494	252.5	6.4	904	3	CR640189	CR640189 Tetraodon
422	257	6.5	823	5	BM074929	BM074929 Tetraodon	495	252.5	6.4	904	3	CR642568	CR642568 Tetraodon
423	256.5	6.5	795	9	AY414008	AY414008 Mus muscu	496	252.5	6.4	905	3	CR639582	CR639582 Tetraodon
424	256.5	6.5	868	3	AK009019	AK009019 Mus muscu	497	252.5	6.4	906	3	CR637481	CR637481 Tetraodon
425	256.5	6.5	2742	3	BC044626	BC044626 Homo sapi	498	252.5	6.4	909	3	CR655333	CR655333 Tetraodon
426	256	6.5	716	5	BM074928	BM074928 Tetraodon	499	252.5	6.4	909	3	CR655881	CR655881 Tetraodon
427	256	6.5	723	5	BM073538	BM073538 Tetraodon	500	252.5	6.4	911	3	CR644035	CR644035 Tetraodon
428	256	6.5	727	5	BM078251	BM078251 BX078251	501	252.5	6.4	911	3	CR645585	CR645585 Tetraodon
429	256	6.5	733	5	BM084289	BM084289 Tetraodon	502	252.5	6.4	911	3	CR650663	CR650663 Tetraodon
430	256	6.5	768	5	BM078667	BM078667 Tetraodon	503	252.5	6.4	912	3	CR654453	CR654453 Tetraodon
431	256	6.5	775	5	BM076322	BM076322 Tetraodon	504	252.5	6.4	913	3	CR652478	CR652478 Tetraodon
432	256	6.5	779	5	BM079925	BM079925 Tetraodon	505	252.5	6.4	915	3	CR655403	CR655403 Tetraodon
433	256	6.5	825	5	BM073854	BM073854 Tetraodon	506	252.5	6.4	916	3	CR633664	CR633664 Tetraodon
434	256	6.5	831	7	CN322308	CN322308 AGENCOURT	507	252.5	6.4	917	3	CR639740	CR639740 Tetraodon
c 435	256	6.5	858	7	CF284556	CF284556 AGENCOURT	508	252.5	6.4	919	3	CR639446	CR639446 Tetraodon
436	256	6.5	908	7	CN156107	CN156107 943469_WA	509	252.5	6.4	919	3	CR650874	CR650874 Tetraodon
437	256	6.5	1082	3	CR655570	CR655570 Tetraodon	510	252.5	6.4	920	3	CR635099	CR635099 Tetraodon
438	256	6.5	1174	3	CR729399	CR729399 Tetraodon	511	252.5	6.4	920	3	CR635994	CR635994 Tetraodon
439	255.5	6.5	833	7	CO960543	CO960543 AGENCOURT	512	252.5	6.4	920	3	CR641802	CR641802 Tetraodon
440	255.5	6.5	939	3	CR634185	CR634185 Tetraodon	513	252.5	6.4	920	3	CR646673	CR646673 Tetraodon
441	255.5	6.5	967	3	CR710965	CR710965 Tetraodon	514	252.5	6.4	920	3	CR646862	CR646862 Tetraodon
442	255	6.5	701	5	BU417312	BU417312 603670839	515	252.5	6.4	922	3	CR640332	CR640332 Tetraodon
443	255	6.5	711	5	BM083229	BM083229 Tetraodon	516	252.5	6.4	923	3	CR635331	CR635331 Tetraodon
444	255	6.5	759	7	CF522916	CF522916 AGENCOURT	517	252.5	6.4	923	3	CR643185	CR643185 Tetraodon
445	255	6.5	772	5	BU416382	BU416382 603670632	518	252.5	6.4	924	3	CR645044	CR645044 Tetraodon
c 446	255	6.5	774	7	CV483748	CV483748 AGENCOURT	519	252.5	6.4	924	3	CR650125	CR650125 Tetraodon
447	255	6.5	816	5	BM078622	BM078622 Tetraodon	520	252.5	6.4	925	3	CR634177	CR634177 Tetraodon

521	252.5	6.4	925	3	CR638868	Tetraodon	CR638868	594	249.5	6.3	871	3	CR728114	Tetraodon	CR728114
522	252.5	6.4	926	3	CR642728	Tetraodon	CR642728	595	249.5	6.3	901	3	CR642443	Tetraodon	CR642443
523	252.5	6.4	927	3	CR649071	Tetraodon	CR649071	596	249.5	6.3	905	5	BU488572	Tetraodon	BU488572
524	252.5	6.4	928	3	CR644693	Tetraodon	CR644693	597	249.5	6.3	906	3	CR636996	Tetraodon	CR636996
525	252.5	6.4	927	3	CR649839	Tetraodon	CR649839	598	249.5	6.3	908	3	CR641726	Tetraodon	CR641726
526	252.5	6.4	927	3	CR650861	Tetraodon	CR650861	599	249.5	6.3	920	3	CR645319	Tetraodon	CR645319
527	252.5	6.4	929	3	CR650703	Tetraodon	CR650703	600	249.5	6.3	924	3	CR633589	Tetraodon	CR633589
528	252.5	6.4	929	3	CR651331	Tetraodon	CR651331	601	249.5	6.3	925	3	CR651690	Tetraodon	CR651690
529	252.5	6.4	930	3	CR653042	Tetraodon	CR653042	602	249.5	6.3	928	3	CR641657	Tetraodon	CR641657
530	252.5	6.4	930	3	CR656522	Tetraodon	CR656522	603	249.5	6.3	929	3	CR652631	Tetraodon	CR652631
531	252.5	6.4	931	3	CR643809	Tetraodon	CR643809	604	249.5	6.3	931	3	CR639501	Tetraodon	CR639501
532	252.5	6.4	932	3	CR639229	Tetraodon	CR639229	605	249.5	6.3	932	3	CR639294	Tetraodon	CR639294
533	252.5	6.4	933	3	CR652196	Tetraodon	CR652196	606	249.5	6.3	1141	5	BM918816	AGENCYCOURT	BM918816
534	252.5	6.4	934	3	CR635034	Tetraodon	CR635034	607	249	6.3	693	7	CF778907	AGENCYCOURT	CF778907
535	252.5	6.4	934	3	CR639892	Tetraodon	CR639892	608	249	6.3	728	4	BJ714567	BJ714567	BJ714567
536	252.5	6.4	934	3	CR644641	Tetraodon	CR644641	609	249	6.3	729	4	BJ707845	BJ707845	BJ707845
537	252.5	6.4	939	3	CR651400	Tetraodon	CR651400	610	249	6.3	730	4	BJ709178	BJ709178	BJ709178
538	252.5	6.4	940	3	CR646689	Tetraodon	CR646689	611	249	6.3	731	4	BJ708245	BJ708245	BJ708245
539	252.5	6.4	941	3	CR655890	Tetraodon	CR655890	612	249	6.3	731	4	BJ711604	BJ711604	BJ711604
540	252.5	6.4	1049	5	BM919345	AGENCYCOURT	BM919345	613	249	6.3	732	4	BJ709989	BJ709989	BJ709989
541	252.5	6.4	1200	3	CR635412	Tetraodon	CR635412	614	249	6.3	732	4	BJ710455	BJ710455	BJ710455
542	252.5	6.4	1458	3	CR641256	Tetraodon	CR641256	615	249	6.3	732	4	BJ713493	BJ713493	BJ713493
543	252	6.4	735	4	BJ707169	BJ707169	616	249	6.3	736	4	BJ708003	BJ708003	BJ708003	
544	252	6.4	818	6	CB560134	AGENCYCOURT	CB560134	617	249	6.3	740	4	BJ708327	BJ708327	BJ708327
545	252	6.4	834	7	CF376371	AGENCYCOURT	CF376371	618	249	6.3	776	6	CA771814	CA771814	CA771814
546	252	6.4	838	5	BX075937	AGENCYCOURT	BX075937	619	249	6.3	798	6	CA777464	CA777464	CA777464
547	252	6.4	860	3	CR635188	Tetraodon	CR635188	620	249	6.3	827	5	BX077184	BX077184	BX077184
548	252	6.4	862	3	CR638045	Tetraodon	CR638045	621	249	6.3	847	6	CD508696	CD508696	CD508696
549	252	6.4	1058	7	CF591286	AGENCYCOURT	CF591286	622	249	6.3	856	7	CF581209	CF581209	CF581209
550	251.5	6.4	830	5	BU492586	Tetraodon	BU492586	623	249	6.3	874	6	BY708812	BY708812	BY708812
551	251.5	6.4	850	5	BU479980	AUF_Iflvr	BU479980	624	249	6.3	876	3	AK007765	AK007765	AK007765
552	251.5	6.4	888	5	BU417435	Tetraodon	BU417435	625	249	6.3	877	3	AK003079	AK003079	AK003079
553	251.5	6.4	907	3	CR645518	Tetraodon	CR645518	626	249	6.3	877	3	AK007815	AK007815	AK007815
554	251.5	6.4	920	3	CR656594	Tetraodon	CR656594	627	249	6.3	877	3	AK008729	AK008729	AK008729
555	251.5	6.4	923	7	CF381134	Tetraodon	CF381134	628	249	6.3	877	3	AK008927	AK008927	AK008927
556	251	6.4	797	7	CF348030	AGENCYCOURT	CF348030	629	249	6.3	879	3	AK008888	AK008888	AK008888
557	221	6.4	845	7	CF374141	AGENCYCOURT	CF374141	630	249	6.3	882	7	CF581178	CF581178	CF581178
558	221	6.4	856	7	CF378642	AGENCYCOURT	CF378642	631	249	6.3	891	3	AK008644	AK008644	AK008644
559	221	6.4	860	3	CR642136	Tetraodon	CR642136	632	249	6.3	892	7	CF580743	CF580743	CF580743
560	221	6.4	902	4	BI752107	Tetraodon	BI752107	633	249	6.3	909	7	CF581329	CF581329	CF581329
561	221	6.4	1037	3	CR639656	Tetraodon	CR639656	634	249	6.3	910	7	CF586044	CF586044	CF586044
562	221	6.4	1515	3	CR645042	Tetraodon	CR645042	635	249	6.3	916	7	CF580742	CF580742	CF580742
563	221	6.4	4379	3	BC053923	Tetraodon	BC053923	636	249	6.3	943	5	BQ222778	BQ222778	BQ222778
564	250.5	6.3	722	7	CO882996	BOVGen_11	CO882996	637	249	6.3	2487	3	AK007765	AK007765	AK007765
565	250.5	6.3	768	7	CK177303	AGENCYCOURT	CK177303	638	248.5	6.3	2487	3	AK007765	AK007765	AK007765
566	250.5	6.3	783	5	BX073778	AGENCYCOURT	BX073778	639	248.5	6.3	669	7	CN563024	CN563024	CN563024
567	250.5	6.3	788	3	CR646057	Tetraodon	CR646057	640	248.5	6.3	769	5	BX860661	BX860661	BX860661
568	250.5	6.3	804	5	BU417486	Tetraodon	BU417486	641	248.5	6.3	852	7	CO936690	CO936690	CO936690
569	250.5	6.3	811	7	CK176944	AGENCYCOURT	CK176944	642	248.5	6.3	1305	6	CD502467	CD502467	CD502467
570	250.5	6.3	814	7	CK175861	AGENCYCOURT	CK175861	643	248	6.3	643	4	BJ492843	BJ492843	BJ492843
571	250.5	6.3	818	7	CK190772	AGENCYCOURT	CK190772	644	248	6.3	732	4	BJ709656	BJ709656	BJ709656
572	250.5	6.3	839	7	CO249929	AGENCYCOURT	CO249929	645	248	6.3	749	4	BJ707512	BJ707512	BJ707512
573	250.5	6.3	844	5	BU416522	AGENCYCOURT	BU416522	646	248	6.3	798	5	BU487405	BU487405	BU487405
574	250.5	6.3	844	7	CO933077	AGENCYCOURT	CO933077	647	248	6.3	846	6	CD497919	CD497919	CD497919
575	250.5	6.3	889	7	CK409519	AUF_Iflvr	CK409519	648	248	6.3	912	6	BY708787	BY708787	BY708787
576	250.5	6.3	900	7	CK409575	AUF_Iflvr	CK409575	649	248	6.3	919	7	CF581262	CF581262	CF581262
577	250.5	6.3	908	7	CK408339	AUF_Iflvr	CK408339	650	248	6.3	931	7	CF577601	CF577601	CF577601
578	250.5	6.3	912	3	CR641542	Tetraodon	CR641542	651	247.5	6.3	738	6	CA345943	CA345943	CA345943
579	250.5	6.3	920	7	CR651608	Tetraodon	CR651608	652	247.5	6.3	741	7	CV487080	CV487080	CV487080
580	250.5	6.3	920	7	CK407536	AUF_Iflvr	CK407536	653	247.5	6.3	744	5	BX081286	BX081286	BX081286
581	250.5	6.3	925	3	CR653117	Tetraodon	CR653117	654	247.5	6.3	770	5	BX072759	BX072759	BX072759
582	250.5	6.3	928	7	CF581264	AGENCYCOURT	CF581264	655	247.5	6.3	780	4	BJ720412	BJ720412	BJ720412
583	250.5	6.3	932	7	CK408003	AUF_Iflvr	CK408003	656	247.5	6.3	784	5	BX074176	BX074176	BX074176
584	250.5	6.3	935	7	CK407783	AUF_Iflvr	CK407783	657	247.5	6.3	790	7	CK173411	CK173411	CK173411
585	250.5	6.3	1000	1	AL532786	AUF_Iflvr	AL532786	658	247.5	6.3	808	5	BX074661	BX074661	BX074661
586	250.5	6.3	1035	3	CK5080KX	Single re	CK5080KX	659	247.5	6.3	823	5	BX079297	BX079297	BX079297
587	250.5	6.3	1883	3	CR641415	Tetraodon	CR641415	660	247.5	6.3	828	5	CK180142	CK180142	CK180142
588	250	6.3	679	4	BJ502290	AGENCYCOURT	BJ502290	661	247.5	6.3	836	5	BX079926	BX079926	BX079926
589	249.5	6.3	973	3	CR716391	Tetraodon	CR716391	662	247.5	6.3	849	6	CD496157	CD496157	CD496157
590	249.5	6.3	748	4	BI836955	Tetraodon	BI836955	663	247.5	6.3	908	3	CR644464	CR644464	CR644464
591	249.5	6.3	749	4	BJ726902	AGENCYCOURT	BJ726902	664	247.5	6.3	917	3	CR648546	CR648546	CR648546
592	249.5	6.3	818	5	BX079902	AGENCYCOURT	BX079902	665	247.5	6.3	920	3	CR654011	CR654011	CR654011
593	249.5	6.3	820	5	BU416925	AGENCYCOURT	BU416925	666	247.5	6.3	944	6	CD796235	CD796235	CD796235



C 667	247	6.3	614	7	CF101857	CF101857 hac32c10.	C 740	245.5	6.2	773	4	BJ726614	BJ726614
C 668	247	6.3	647	6	CD015434	CD015434 hac21f03.	C 741	245.5	6.2	774	4	BJ715378	BJ715378
C 669	247	6.3	648	6	CD014428	CD014428 hac31n09.	C 742	245.5	6.2	776	4	BJ718243	BJ718243
C 670	247	6.3	770	5	BU490853	BU490853 604129946	C 743	245.5	6.2	776	5	EX074785	EX074785
C 671	247	6.3	844	7	CF581226	CF581226 AGENCOURT	C 744	245.5	6.2	777	4	BJ717871	BJ717871
C 672	247	6.3	848	7	CF586043	CF586043 AGENCOURT	C 745	245.5	6.2	779	4	BJ716216	BJ716216
C 673	247	6.3	870	6	CD506832	CD506832 CDA81-E08	C 746	245.5	6.2	794	4	BJ719963	BJ719963
C 674	247	6.3	874	7	CF581314	CF581314 AGENCOURT	C 747	245.5	6.2	798	4	BJ720317	BJ720317
C 675	247	6.3	882	6	CD500632	CD500632 CDA46-B04	C 748	245.5	6.2	852	7	CO933440	CO933440
C 676	247	6.3	893	7	CF580422	CF580422 AGENCOURT	C 749	245.5	6.2	893	3	CR645057	CR645057
C 677	247	6.3	915	7	CF580726	CF580726 AGENCOURT	C 750	245.5	6.2	911	3	CR646918	CR646918
C 678	247	6.3	1008	3	CNS098PT	BU047002 Single re	C 751	245.5	6.2	911	3	CR649923	CR649923
C 679	247	6.3	1051	3	CR655901	CR655901 Tetraodon	C 752	245.5	6.2	912	3	CR649923	CR649923
C 680	247	6.3	1070	6	CD505254	CD505254 CDA72-F12	C 753	245.5	6.2	912	3	CR655471	CR655471
C 681	246.5	6.2	779	5	BU416569	BU416569 603671624	C 754	245.5	6.2	913	3	CR639696	CR639696
C 682	246.5	6.2	783	7	CO915425	CO915425 AGENCOURT	C 755	245.5	6.2	913	3	CR650510	CR650510
C 683	246.5	6.2	817	5	BU489309	BU489309 604129260	C 756	245.5	6.2	914	3	CR644712	CR644712
C 684	246.5	6.2	820	5	BU417081	BU417081 603671152	C 757	245.5	6.2	915	3	CR642478	CR642478
C 685	246.5	6.2	888	7	AK007333	Mus muscu	C 758	245.5	6.2	916	3	CR633670	CR633670
C 686	246.5	6.2	888	7	CNS11336	CNS11336 AGENCOURT	C 759	245.5	6.2	916	3	CR635159	CR635159
C 687	246.5	6.2	908	3	CR639515	Tetraodon	C 760	245.5	6.2	917	3	CR641924	CR641924
C 688	246.5	6.2	916	3	CR644691	CR644691 Tetraodon	C 761	245.5	6.2	917	3	CR652850	CR652850
C 689	246.5	6.2	916	3	CR652423	CR652423 Tetraodon	C 762	245.5	6.2	918	3	CR637918	CR637918
C 690	246.5	6.2	918	3	CR650862	CR650862 Tetraodon	C 763	245.5	6.2	918	3	CR642059	CR642059
C 691	246.5	6.2	919	3	CR645747	CR645747 Tetraodon	C 764	245.5	6.2	918	3	CR646866	CR646866
C 692	246.5	6.2	919	3	CR732093	CR732093 Tetraodon	C 765	245.5	6.2	920	3	CR640305	CR640305
C 693	246.5	6.2	925	3	CR636483	CR636483 Tetraodon	C 766	245.5	6.2	920	3	CR646500	CR646500
C 694	246.5	6.2	926	3	CR642894	CR642894 Tetraodon	C 767	245.5	6.2	921	3	CR634303	CR634303
C 695	246.5	6.2	927	3	CR638224	CR638224 Tetraodon	C 768	245.5	6.2	921	3	CR646833	CR646833
C 696	246.5	6.2	927	3	CR653272	CR653272 Tetraodon	C 769	245.5	6.2	921	3	CR647938	CR647938
C 697	246.5	6.2	928	3	CR638651	CR638651 Tetraodon	C 770	245.5	6.2	921	3	CR648374	CR648374
C 698	246.5	6.2	929	3	CR643837	CR643837 Tetraodon	C 771	245.5	6.2	922	3	CR639603	CR639603
C 699	246.5	6.2	930	3	CR649255	CR649255 Tetraodon	C 772	245.5	6.2	923	3	CR646823	CR646823
C 700	246.5	6.2	935	3	CR655306	CR655306 Tetraodon	C 773	245.5	6.2	923	3	CR651452	CR651452
C 701	246.5	6.2	936	3	CR637185	CR637185 Tetraodon	C 774	245.5	6.2	924	3	CR634150	CR634150
C 702	246.5	6.2	936	3	CR639122	CR639122 Tetraodon	C 775	245.5	6.2	925	3	CR633696	CR633696
C 703	246.5	6.2	1020	3	CR655414	CR655414 Tetraodon	C 776	245.5	6.2	925	3	CR638053	CR638053
C 704	246.5	6.2	1052	5	BM925522	BM925522 AGENCOURT	C 777	245.5	6.2	925	3	CR643848	CR643848
C 705	246.5	6.2	1473	3	CR655736	CR655736 Tetraodon	C 778	245.5	6.2	925	3	CR645030	CR645030
C 706	246	6.2	741	5	BX540472	BX540472 BX540472	C 779	245.5	6.2	925	3	CR651356	CR651356
C 707	246	6.2	744	5	BU416638	BU416638 603671357	C 780	245.5	6.2	926	3	CR653755	CR653755
C 708	246	6.2	799	5	AX076088	AX076088 BX076088	C 781	245.5	6.2	926	3	CR635794	CR635794
C 709	246	6.2	811	5	BU417493	BU417493 603671392	C 782	245.5	6.2	926	3	CR642588	CR642588
C 710	246	6.2	817	4	BJ716525	BJ716525 BJ716525	C 783	245.5	6.2	926	3	CR643840	CR643840
C 711	246	6.2	826	6	CD506833	CD506833 CDA81-E08	C 784	245.5	6.2	926	3	CR648762	CR648762
C 712	246	6.2	876	3	AK007566	AK007566 Mus muscu	C 785	245.5	6.2	926	3	CR649853	CR649853
C 713	246	6.2	885	5	BY707387	BY707387 BX707387	C 786	245.5	6.2	927	3	CR637181	CR637181
C 714	246	6.2	900	6	BY703467	BY703467 BY703467	C 787	245.5	6.2	927	3	CR638875	CR638875
C 715	246	6.2	907	7	CF581371	CF581371 AGENCOURT	C 788	245.5	6.2	927	3	CR649174	CR649174
C 716	246	6.2	913	7	CF581274	CF581274 AGENCOURT	C 789	245.5	6.2	927	3	CR655117	CR655117
C 717	246	6.2	913	7	CF578058	CF578058 AGENCOURT	C 790	245.5	6.2	928	3	CR634111	CR634111
C 718	246	6.2	914	7	CF581324	CF581324 AGENCOURT	C 791	245.5	6.2	928	3	CR637946	CR637946
C 719	245.5	6.2	686	4	BJ706506	BJ706506 BJ706506	C 792	245.5	6.2	928	3	CR639510	CR639510
C 720	245.5	6.2	731	4	BJ723231	BJ723231 BJ723231	C 793	245.5	6.2	928	3	CR645366	CR645366
C 721	245.5	6.2	735	1	AV906915	AV906915 AV906915	C 794	245.5	6.2	928	3	CR652215	CR652215
C 722	245.5	6.2	744	4	BJ724325	BJ724325 BJ724325	C 795	245.5	6.2	929	3	CR635930	CR635930
C 723	245.5	6.2	747	4	BJ720611	BJ720611 BJ720611	C 796	245.5	6.2	929	3	CR639664	CR639664
C 724	245.5	6.2	747	4	BJ724412	BJ724412 BJ724412	C 797	245.5	6.2	929	3	CR642856	CR642856
C 725	245.5	6.2	747	4	BJ726569	BJ726569 BJ726569	C 798	245.5	6.2	929	3	CR635731	CR635731
C 726	245.5	6.2	748	4	BJ716014	BJ716014 BJ716014	C 799	245.5	6.2	930	3	CR636527	CR636527
C 727	245.5	6.2	748	4	BJ716963	BJ716963 BJ716963	C 800	245.5	6.2	930	3	CR642584	CR642584
C 728	245.5	6.2	748	4	BJ721670	BJ721670 BJ721670	C 801	245.5	6.2	932	3	CR633598	CR633598
C 729	245.5	6.2	750	4	BJ724827	BJ724827 BJ724827	C 802	245.5	6.2	932	3	CR635120	CR635120
C 730	245.5	6.2	751	4	BJ721319	BJ721319 BJ721319	C 803	245.5	6.2	932	3	CR647728	CR647728
C 731	245.5	6.2	751	4	BJ721860	BJ721860 BJ721860	C 804	245.5	6.2	932	3	CR649884	CR649884
C 732	245.5	6.2	752	4	BJ725497	BJ725497 BJ725497	C 805	245.5	6.2	933	3	CR640933	CR640933
C 733	245.5	6.2	757	4	BJ723169	BJ723169 BJ723169	C 806	245.5	6.2	933	3	CR647323	CR647323
C 734	245.5	6.2	760	4	BJ726635	BJ726635 BJ726635	C 807	245.5	6.2	933	3	CR651528	CR651528
C 735	245.5	6.2	765	4	BJ715465	BJ715465 BJ715465	C 808	245.5	6.2	933	3	CR656731	CR656731
C 736	245.5	6.2	771	4	BJ719672	BJ719672 BJ719672	C 809	245.5	6.2	934	3	CR653273	CR653273
C 737	245.5	6.2	772	4	BJ719248	BJ719248 BJ719248	C 810	245.5	6.2	935	3	CR652266	CR652266
C 738	245.5	6.2	773	4	BJ717746	BJ717746 BJ717746	C 811	245.5	6.2	937	3	CR653488	CR653488
C 739	245.5	6.2	773	4	BJ718606	BJ718606 BJ718606	C 812	245.5	6.2	938	3	CR647700	CR647700

813	245.5	6.2	939	3	CR653655	Tetraodon	CR653655	886	243	6.2	847	7	CO960123	AGENCYCOURT
814	245.5	6.2	940	3	CR634548	Tetraodon	CR634548	887	243	6.2	908	3	CR638917	Tetraodon
815	245.5	6.2	940	3	CR654861	Tetraodon	CR654861	888	243	6.2	1115	5	BM918560	AGENCYCOURT
816	245.5	6.2	943	3	CR656736	Tetraodon	CR656736	889	243	6.2	1630	3	CR648863	Tetraodon
817	245.5	6.2	943	3	CR640353	Tetraodon	CR640353	c 890	242.5	6.1	776	4	BJ716484	BJ716484
818	245.5	6.2	943	3	CR649462	Tetraodon	CR649462	891	242.5	6.1	799	7	CO936831	AGENCYCOURT
819	245.5	6.2	945	3	CR635020	Tetraodon	CR635020	892	242.5	6.1	890	3	CR644201	Tetraodon
820	245.5	6.2	961	3	CR644090	Tetraodon	CR644090	893	242.5	6.1	901	3	CR655134	Tetraodon
821	245.5	6.2	1013	3	CR6408SVR	Single re	CR6408SVR	894	242.5	6.1	918	3	CR653996	Tetraodon
822	245.5	6.2	1203	3	CR641198	Single re	CR641198	895	242.5	6.1	1238	9	AY408326	Mus muscu
823	245.5	6.2	1207	3	CR647047	Tetraodon	CR647047	896	242.5	6.1	1848	3	CR654394	Tetraodon
824	245.5	6.2	1726	3	CR653279	Tetraodon	CR653279	897	242	6.1	797	5	BU417007	Tetraodon
825	245.5	6.2	1894	3	CR626692	full-leng	CR626692	898	242	6.1	806	7	CO927000	Tetraodon
826	245	6.2	727	4	BJ712430	BJ712430	BJ712430	899	242	6.1	811	5	BU417059	Tetraodon
827	245	6.2	730	4	BJ708144	BJ708144	BJ708144	900	242	6.1	819	5	BU416369	Tetraodon
828	245	6.2	781	5	BU492581	604130334	BU492581	901	242	6.1	871	5	BX077714	BX077714
829	245	6.2	789	7	CF662498	CGLL02a06	CF662498	c 902	242	6.1	1144	6	CD5077354	CD5077354
830	245	6.2	874	5	BU486885	603972212	BU486885	903	242	6.1	1253	3	CR592280	full-leng
831	245	6.2	880	6	CD497918	CD430-F03	CD497918	904	242	6.1	6030	9	AY407073	Homo sapi
832	245	6.2	909	6	CD505684	CD475-A11	CD505684	905	241.5	6.1	708	4	BJ705989	BJ705989
833	245	6.2	918	3	CR644892	Tetraodon	CR644892	906	241.5	6.1	709	4	BJ705756	BJ705756
834	245	6.2	942	3	CR734060	Tetraodon	CR734060	907	241.5	6.1	709	4	BJ706011	BJ706011
835	245	6.2	1089	3	AK016509	Mus muscu	AK016509	908	241.5	6.1	710	4	BJ706306	BJ706306
836	245	6.2	1128	4	BI757320	603029535	BI757320	909	241.5	6.1	710	4	BJ714703	BJ714703
837	245	6.2	1139	3	CR636750	Tetraodon	CR636750	910	241.5	6.1	711	4	BJ704593	BJ704593
838	245	6.2	3048	9	AY411207	Homo sapi	AY411207	911	241.5	6.1	711	4	BJ705039	BJ705039
839	244.5	6.2	725	4	BJ706958	BJ706958	BJ706958	912	241.5	6.1	712	4	BJ714674	BJ714674
840	244.5	6.2	777	7	CK873031	AGENCYCOURT	CK873031	913	241.5	6.1	722	4	BJ712631	BJ712631
841	244.5	6.2	781	5	BX081322	BX081322	BX081322	914	241.5	6.1	724	4	BJ714304	BJ714304
842	244.5	6.2	790	5	BU491739	604128370	BU491739	915	241.5	6.1	726	4	BJ712324	BJ712324
843	244.5	6.2	797	6	CD498003	CD431-B05	CD498003	916	241.5	6.1	730	4	BJ708039	BJ708039
844	244.5	6.2	810	5	BU492339	604129362	BU492339	917	241.5	6.1	735	5	BU486806	BU486806
845	244.5	6.2	884	7	CF507659	AGENCYCOURT	CF507659	918	241.5	6.1	792	5	BX914864	BX914864
846	244.5	6.2	897	7	CF581269	AGENCYCOURT	CF581269	c 919	241.5	6.1	794	5	BM388081	BM388081
847	244.5	6.2	905	3	CR733827	Tetraodon	CR733827	920	241.5	6.1	820	5	BU487247	BU487247
848	244.5	6.2	909	3	CR651501	Tetraodon	CR651501	921	241.5	6.1	852	3	CK0509MU1	Single re
849	244.5	6.2	925	3	CR650208	Tetraodon	CR650208	922	241.5	6.1	868	7	CK015897	AGENCYCOURT
850	244.5	6.2	925	3	CR644791	Tetraodon	CR644791	c 923	241.5	6.1	876	6	CB562993	AGENCYCOURT
851	244	6.2	695	5	BX073443	BX073443	BX073443	924	241.5	6.1	915	3	CR656100	Tetraodon
852	244	6.2	734	5	BX674560	BX674560	BX674560	925	241.5	6.1	916	3	CR646536	Tetraodon
853	244	6.2	740	7	CN169918	AGENCYCOURT	CN169918	926	241.5	6.1	921	3	CR635696	Tetraodon
854	244	6.2	750	5	BX076323	BX076323	BX076323	927	241.5	6.1	929	3	CR655848	Tetraodon
855	244	6.2	784	4	BJ724595	BJ724595	BJ724595	928	241.5	6.1	961	3	CR644045	Tetraodon
856	244	6.2	774	6	CA774808	ip12f10.x	CA774808	c 930	241	6.1	595	7	CF101863	Single re
857	244	6.2	799	5	BU490424	604131761	BU490424	c 931	241	6.1	595	7	CF102254	hac34d01
858	244	6.2	885	3	AK003060	Mus muscu	AK003060	c 932	241	6.1	735	7	CO882924	BOVGen 11
859	244	6.2	908	7	CF581361	AGENCYCOURT	CF581361	933	241	6.1	756	7	CO574502	AGENCYCOURT
860	244	6.2	928	3	CR638839	Tetraodon	CR638839	934	241	6.1	821	7	CO959505	AGENCYCOURT
861	244	6.2	1480	3	CR650638	Tetraodon	CR650638	935	241	6.1	874	7	CF374140	AGENCYCOURT
862	243.5	6.2	650	4	BG172830	pqlin.pk0	BG172830	936	241	6.1	887	3	CR648357	Tetraodon
863	243.5	6.2	757	7	CK176945	EST766265	CK176945	c 937	241	6.1	920	7	CF581286	AGENCYCOURT
864	243.5	6.2	764	4	BJ726859	BJ726859	BJ726859	938	240.5	6.1	740	4	BJ724753	BJ724753
865	243.5	6.2	775	7	CK029489	AGENCYCOURT	CK029489	c 939	240.5	6.1	757	5	BM588890	BM588890
866	243.5	6.2	784	4	BJ718142	BJ718142	BJ718142	940	240.5	6.1	807	7	CN321900	AGENCYCOURT
867	243.5	6.2	816	5	BX914956	BX914956	BX914956	941	240.5	6.1	814	7	CN323058	AGENCYCOURT
868	243.5	6.2	852	7	CF266485	AGENCYCOURT	CF266485	c 942	240.5	6.1	829	4	BU1521986	BU1521986
869	243.5	6.2	877	7	CK406949	AUF iflvr	CK406949	943	240.5	6.1	832	5	BU416693	BU416693
870	243.5	6.2	879	7	CK407045	AUF iflvr	CK407045	944	240.5	6.1	835	5	BU489163	BU489163
871	243.5	6.2	904	3	CR634091	Tetraodon	CR634091	945	240.5	6.1	901	3	CR640301	Tetraodon
872	243.5	6.2	905	3	CR734219	Tetraodon	CR734219	946	240.5	6.1	903	3	CR635831	Tetraodon
873	243.5	6.2	905	7	CK406448	AUF iflvr	CK406448	947	240.5	6.1	907	3	CR649952	Tetraodon
874	243.5	6.2	916	3	CR649458	Tetraodon	CR649458	948	240.5	6.1	911	3	CR636786	Tetraodon
875	243.5	6.2	916	3	CR641262	Tetraodon	CR641262	949	240.5	6.1	912	3	CR649775	Tetraodon
876	243.5	6.2	927	3	CR647064	Tetraodon	CR647064	950	240.5	6.1	915	3	CR647813	Tetraodon
877	243.5	6.2	934	3	CR635918	Tetraodon	CR635918	951	240.5	6.1	918	3	CR638345	Tetraodon
878	243.5	6.2	934	3	CR638649	Tetraodon	CR638649	952	240.5	6.1	921	3	CR656065	Tetraodon
879	243.5	6.2	935	7	CR646129	Tetraodon	CR646129	953	240.5	6.1	921	3	CR647144	Tetraodon
880	243.5	6.2	957	7	CK408890	AUF iflvr	CK408890	954	240.5	6.1	925	3	CR653326	Tetraodon
881	243	6.2	689	5	BX083735	BX083735	BX083735	955	240.5	6.1	932	3	CR641267	Tetraodon
882	243	6.2	780	4	BI838552	603086213	BI838552	956	240.5	6.1	935	3	CK044832	Single re
883	243	6.2	786	5	BX083163	BX083163	BX083163	957	240.5	6.1	940	3	CR646211	Tetraodon
884	243	6.2	822	5	CF346385	AGENCYCOURT	CF346385	958	240.5	6.1	944	3	CR651701	Tetraodon
885	243	6.2	842	7	CF346385	AGENCYCOURT	CF346385							

959	240.5	6.1	946	3	CR652182	Tetraodon	CR652182	1032	238.5	6.0	940	3	CR731036	Tetraodon
960	240.5	6.1	947	3	CR646891	Tetraodon	CR646891	1033	238.5	6.0	969	3	CNS0954U	Single re
961	240.5	6.1	948	3	CR641038	Tetraodon	CR641038	1034	238.5	6.0	975	3	CNS09CNO	Single re
962	240.5	6.1	958	3	CR642655	Tetraodon	CR642655	c1035	238.5	6.0	1172	6	CD508404	CD508404
963	240.5	6.1	961	3	CR649860	Tetraodon	CR649860	1036	238.5	6.0	2873	9	AY411208	AY411208 Pan trogl
964	240.5	6.1	964	3	CNS093BK	Single re	CR649860	1037	238	6.0	698	5	BM437706	BM437706
965	240.5	6.1	970	3	CR656705	Tetraodon	CR656705	c1038	238	6.0	701	6	CB492844	CB492844 onykrbna5
966	240.5	6.1	3388	3	AK004995	Mus muscu	AK004995	1039	238	6.0	746	5	BM431504	BM431504
967	240	6.1	749	5	BM076018	Mus muscu	BM076018	1040	238	6.0	756	4	BM070730	BM070730
968	240	6.1	751	5	BM076018	Mus muscu	BM076018	1041	238	6.0	788	5	BM070730	BM070730
969	240	6.1	754	5	BM076018	Mus muscu	BM076018	1042	238	6.0	788	7	BM070730	BM070730
970	240	6.1	832	4	BM076018	Mus muscu	BM076018	1043	238	6.0	788	7	BM070730	BM070730
971	240	6.1	832	4	BM076018	Mus muscu	BM076018	1044	238	6.0	884	7	BM070730	BM070730
972	240	6.1	832	4	BM076018	Mus muscu	BM076018	1045	238	6.0	908	3	BM070730	BM070730
973	240	6.1	1407	3	CR683082	Tetraodon	CR683082	1046	238	6.0	1156	3	BM070730	BM070730
974	240	6.1	1407	3	CR683082	Tetraodon	CR683082	1047	238	6.0	2348	9	BM070730	BM070730
975	239.5	6.1	1407	3	CR683082	Tetraodon	CR683082	1048	237.5	6.0	658	5	BM070730	BM070730
976	239.5	6.1	732	4	BM0708107	Homo sapi	BM0708107	1049	237.5	6.0	708	4	BM0708107	BM0708107
977	239.5	6.1	732	4	BM0708107	Homo sapi	BM0708107	1050	237.5	6.0	748	4	BM0708107	BM0708107
978	239.5	6.1	753	7	CR631172	AK001	CR631172	c1051	237.5	6.0	758	5	BM0708107	BM0708107
979	239.5	6.1	758	5	BM081136	BM081136	BM081136	c1052	237.5	6.0	762	7	BM0708107	BM0708107
980	239.5	6.1	790	5	BM081136	BM081136	BM081136	c1053	237.5	6.0	774	4	BM0708107	BM0708107
981	239.5	6.1	811	7	CR6326143	AGENCYCOURT	CR6326143	1054	237.5	6.0	789	5	BM0708107	BM0708107
982	239.5	6.1	839	5	BU417215	603671003	BU417215	c1055	237.5	6.0	794	5	BM0708107	BM0708107
983	239.5	6.1	854	5	BU416893	603671026	BU416893	c1056	237.5	6.0	807	7	BM0708107	BM0708107
984	239.5	6.1	889	7	CF589938	AGENCYCOURT	CF589938	1057	237.5	6.0	881	7	BM0708107	BM0708107
985	239.5	6.1	896	7	CF589938	AGENCYCOURT	CF589938	1058	237.5	6.0	908	7	BM0708107	BM0708107
986	239.5	6.1	907	7	CF589938	AGENCYCOURT	CF589938	1059	237.5	6.0	916	3	BM0708107	BM0708107
987	239.5	6.1	917	7	CF589938	AGENCYCOURT	CF589938	1060	237.5	6.0	920	3	BM0708107	BM0708107
988	239.5	6.1	930	3	CR646196	Tetraodon	CR646196	1061	237.5	6.0	932	7	BM0708107	BM0708107
989	239.5	6.1	1042	5	BM426922	BM426922	BM426922	1062	237.5	6.0	979	3	BM0708107	BM0708107
990	239.5	6.1	1155	3	CR645634	Tetraodon	CR645634	c1063	237	6.0	660	4	BM0708107	BM0708107
991	239.5	6.1	1323	3	CR615568	full-leng	CR615568	1064	237	6.0	719	5	BM0708107	BM0708107
992	239.5	6.1	1323	3	CR615568	full-leng	CR615568	c1065	237	6.0	731	4	BM0708107	BM0708107
993	239.5	6.1	1334	3	CR622185	full-leng	CR622185	1066	237	6.0	752	7	BM0708107	BM0708107
994	239.5	6.1	1342	3	CR601129	full-leng	CR601129	1067	237	6.0	769	5	BM0708107	BM0708107
995	239.5	6.1	1345	3	CR613780	full-leng	CR613780	1068	237	6.0	784	5	BM0708107	BM0708107
996	239.5	6.1	1347	3	CR591153	full-leng	CR591153	1069	237	6.0	790	6	BM0708107	BM0708107
997	239.5	6.1	1352	3	CR611613	full-leng	CR611613	1070	237	6.0	796	5	BM0708107	BM0708107
998	239.5	6.1	1352	3	CR622185	full-leng	CR622185	1071	237	6.0	804	5	BM0708107	BM0708107
999	239.5	6.1	1354	3	CR593594	full-leng	CR593594	1072	237	6.0	810	5	BM0708107	BM0708107
1000	239.5	6.1	1355	3	CR597047	full-leng	CR597047	1073	237	6.0	811	5	BM0708107	BM0708107
1001	239.5	6.1	1358	3	CR599000	full-leng	CR599000	1074	237	6.0	822	5	BM0708107	BM0708107
1002	239.5	6.1	1360	3	CR608843	full-leng	CR608843	1075	237	6.0	831	4	BM0708107	BM0708107
1003	239.5	6.1	1365	3	CR601475	full-leng	CR601475	1076	237	6.0	852	5	BM0708107	BM0708107
1004	239.5	6.1	1367	3	CR615236	full-leng	CR615236	1077	237	6.0	868	5	BM0708107	BM0708107
1005	239.5	6.1	1369	3	CR611617	full-leng	CR611617	1078	237	6.0	878	7	BM0708107	BM0708107
1006	239.5	6.1	1993	3	CR602253	full-leng	CR602253	1079	237	6.0	884	5	BM0708107	BM0708107
c1007	239	6.1	594	7	CF101840	hac32b04	CF101840	1080	237	6.0	914	7	BM0708107	BM0708107
1008	239	6.1	701	5	BM0708107	hac32b04	BM0708107	c1081	237	6.0	936	7	BM0708107	BM0708107
1009	239	6.1	737	5	BM0708107	hac32b04	BM0708107	1082	237	6.0	936	7	BM0708107	BM0708107
c1010	239	6.1	751	4	BM0708107	hac32b04	BM0708107	1083	237	6.0	1917	9	BM0708107	BM0708107
1011	239	6.1	760	5	BU491755	604128508	BU491755	1084	237	6.0	2841	3	BM0708107	BM0708107
1012	239	6.1	847	7	CF581438	AGENCYCOURT	CF581438	1085	237	6.0	544	2	BM0708107	BM0708107
c1013	239	6.1	890	7	CF581438	AGENCYCOURT	CF581438	1086	236.5	6.0	597	7	BM0708107	BM0708107
1014	239	6.1	1239	3	CR654513	Tetraodon	CR654513	1087	236.5	6.0	706	4	BM0708107	BM0708107
1015	239	6.1	1842	3	CR653520	Tetraodon	CR653520	1088	236.5	6.0	750	5	BM0708107	BM0708107
1016	238.5	6.0	687	5	BM036510	BM036510	BM036510	1089	236.5	6.0	753	7	BM0708107	BM0708107
1017	238.5	6.0	690	5	BM079128	BM079128	BM079128	1090	236.5	6.0	763	7	BM0708107	BM0708107
1018	238.5	6.0	707	4	BM0714071	BM0714071	BM0714071	c1091	236.5	6.0	775	5	BM0708107	BM0708107
1019	238.5	6.0	707	6	BM0714071	BM0714071	BM0714071	1092	236.5	6.0	783	5	BM0708107	BM0708107
c1020	238.5	6.0	762	4	BM0726029	BM0726029	BM0726029	1093	236.5	6.0	792	5	BM0708107	BM0708107
c1021	238.5	6.0	764	4	BM0719808	BM0719808	BM0719808	c1094	236.5	6.0	912	3	BM0708107	BM0708107
c1022	238.5	6.0	764	4	BM0726180	BM0726180	BM0726180	1095	236.5	6.0	912	3	BM0708107	BM0708107
1023	238.5	6.0	773	7	CF581438	AGENCYCOURT	CF581438	1096	236.5	6.0	613	6	BM0708107	BM0708107
1024	238.5	6.0	775	7	CF581438	AGENCYCOURT	CF581438	c1097	236	6.0	682	5	BM0708107	BM0708107
1025	238.5	6.0	796	4	BM0714839	BM0714839	BM0714839	1098	236	6.0	682	5	BM0708107	BM0708107
1026	238.5	6.0	861	7	CF586989	AGENCYCOURT	CF586989	1099	236	6.0	744	5	BM0708107	BM0708107
1027	238.5	6.0	865	7	CF591847	AGENCYCOURT	CF591847	1100	236	6.0	752	5	BM0708107	BM0708107
1028	238.5	6.0	918	7	CF581372	AGENCYCOURT	CF581372	c1101	236	6.0	775	4	BM0708107	BM0708107
c1029	238.5	6.0	920	7	CF581372	AGENCYCOURT	CF581372	1102	236	6.0	786	7	BM0708107	BM0708107
1030	238.5	6.0	922	3	CR639360	Tetraodon	CR639360	1103	236	6.0	848	5	BM0708107	BM0708107
1031	238.5	6.0	923	3	CR654160	Tetraodon	CR654160	c1104	236	6.0	873	7	BM0708107	BM0708107

1105	236	6.0	901	7	CF581310	AGENCY	236	5.9	783	5	BW381901	BW381901
1106	236	6.0	920	7	CF581281	AGENCY	1179	5.9	798	5	BW416406	BW416406
1107	235.5	6.0	768	7	CK846337	968823 MA	1180	234.5	802	5	BW488019	BW488019
1108	235.5	6.0	778	7	CK328977	AGENCY	1181	234.5	808	5	BW416766	BW416766
1109	235.5	6.0	791	5	BK085069	BK085069	1182	234.5	808	5	BW489614	BW489614
1110	235.5	6.0	816	7	CF346384	AGENCY	1183	234.5	811	7	CK036585	AGENCY
1111	235.5	6.0	843	6	CD495456	CD495456	1184	234.5	812	6	CD497616	CD497616
1112	235.5	6.0	847	5	BW486913	604128437	1185	234.5	816	5	BW416324	BW416324
1113	235.5	6.0	852	7	CK326599	AGENCY	1186	234.5	830	7	CF516452	AGENCY
1114	235.5	6.0	861	5	BK084717	BK084717	1187	234.5	831	7	CF577942	AGENCY
1115	235.5	6.0	887	7	CO919178	AGENCY	1188	234.5	831	7	CO350417	DR AOV FL
1116	235.5	6.0	888	7	CK407348	AUF IFLVR	1189	234.5	835	7	CF581323	AGENCY
1117	235.5	6.0	910	7	CK407839	AUF IFLVR	1190	234.5	851	5	BW417208	603671611
1118	235.5	6.0	958	7	CK421858	AUF IFLVR	1191	234.5	855	6	CD507088	CD507088
1119	235.5	6.0	973	1	AL532541	AL532541	1192	234.5	857	7	CF578099	AGENCY
1120	235.5	6.0	976	3	CK099200	CK099200	1193	234.5	864	6	CD503222	CD503222
1121	235	6.0	668	5	BK076087	BK076087	1194	234.5	864	6	CD508294	CD508294
1122	235	6.0	692	5	BK083245	BK083245	1195	234.5	874	7	CF581293	CF581293
1123	235	6.0	696	4	BK0719517	BK0719517	1196	234.5	879	7	CF581242	CF581242
1124	235	6.0	716	4	BK0724290	BK0724290	1197	234.5	884	7	CK407570	CK407570
1125	235	6.0	734	5	BK089873	604130802	1198	234.5	885	6	CD503390	CD503390
1126	235	6.0	739	4	BK0720668	BK0720668	1199	234.5	889	3	CF581384	CF581384
1127	235	6.0	741	4	BK0709342	BK0709342	1200	234.5	892	7	CK422293	AUF Ipspn
1128	235	6.0	741	4	BK0716386	BK0716386	1201	234.5	890	7	CK634480	Tetraodon
1129	235	6.0	741	4	BK0716629	BK0716629	1202	234.5	891	6	CD507087	CD507087
1130	235	6.0	743	4	BK0726389	BK0726389	1203	234.5	895	6	CD503221	CD503221
1131	235	6.0	743	4	BK0726813	BK0726813	1204	234.5	902	7	CF581237	AGENCY
1132	235	6.0	743	4	BK0726935	BK0726935	1205	234.5	917	7	CF581384	AGENCY
1133	235	6.0	744	4	BK0710738	BK0710738	1206	234.5	924	7	CK422293	AUF Ipspn
1134	235	6.0	744	4	BK0715838	BK0715838	1207	234.5	927	3	CK634480	Tetraodon
1135	235	6.0	745	4	BK0720093	BK0720093	1208	234.5	928	3	CF734879	Tetraodon
1136	235	6.0	747	4	BK0709201	BK0709201	1209	234.5	931	7	CF581439	AGENCY
1137	235	6.0	747	4	BK0720444	BK0720444	1210	234.5	953	7	CF581207	AGENCY
1138	235	6.0	748	4	BK0717972	BK0717972	1211	234.5	1452	3	CK616676	full-leng
1139	235	6.0	749	4	BK0719140	BK0719140	1212	234	1452	3	AK005546	Mus muscu
1140	235	6.0	754	4	BK0723286	BK0723286	1213	234	754	5	BX082451	BX082451
1141	235	6.0	754	4	BK0717755	BK0717755	1214	234	757	5	BX276201	BX276201
1142	235	6.0	759	4	BK0718064	BK0718064	1215	234	760	5	BW487758	BW487758
1143	235	6.0	760	4	BK0719011	BK0719011	1216	234	763	4	BK0723745	BK0723745
1144	235	6.0	760	4	BK0725468	BK0725468	1217	234	769	7	CF348317	AGENCY
1145	235	6.0	761	4	BK0719652	BK0719652	1218	234	774	5	BW416308	BW416308
1146	235	6.0	766	4	BK0722152	BK0722152	1219	234	783	7	CO936234	AGENCY
1147	235	6.0	770	4	BK0720324	BK0720324	1220	234	825	4	BI757376	603029305
1148	235	6.0	770	4	BK0722144	BK0722144	1221	234	840	7	CF581456	AGENCY
1149	235	6.0	771	4	BK0718099	BK0718099	1222	234	842	7	CO936023	AGENCY
1150	235	6.0	773	4	BK0719394	BK0719394	1223	234	860	7	CO916767	AGENCY
1151	235	6.0	774	4	BK0725643	BK0725643	1224	234	897	3	CNS0900P	AGENCY
1152	235	6.0	776	4	BK0721985	BK0721985	1225	234	920	7	CK406808	AGENCY
1153	235	6.0	777	4	BK0717147	BK0717147	1226	234	927	7	CF581452	AGENCY
1154	235	6.0	778	4	BK0721208	BK0721208	1227	234	948	2	BF314703	601901648
1155	235	6.0	785	4	BK0726255	BK0726255	1228	233.5	1050	3	AK006271	Mus muscu
1156	235	6.0	787	4	BK0718273	BK0718273	1229	233.5	606	7	CV023565	534 Full
1157	235	6.0	787	4	BK0718450	BK0718450	1230	233.5	631	5	BW362216	BW362216
1158	235	6.0	787	4	BK0720814	BK0720814	1231	233.5	674	5	BX263618	BX263618
1159	235	6.0	788	4	BK0721988	BK0721988	1232	233.5	689	2	BE314082	BE314082
1160	235	6.0	791	4	BK0715849	BK0715849	1233	233.5	689	2	BE314082	601146273
1161	235	6.0	794	4	BK0719192	BK0719192	1234	233.5	737	7	CK867609	AGENCY
1162	235	6.0	794	4	CF2852235	AGENCY	1235	233.5	737	7	CF999911	AGENCY
1163	235	6.0	819	6	CA588481	hab64c07	1236	233.5	750	5	CF999911	AGENCY
1164	235	6.0	832	5	BAU16582	603671618	1237	233.5	753	5	BW489998	604128417
1165	235	6.0	835	6	CD500955	CD48-B03	1238	233.5	759	5	BW489998	604128417
1166	235	6.0	845	7	CF581283	AGENCY	1239	233.5	774	4	BG862841	6032797508
1167	235	6.0	846	5	BW490789	604129350	1240	233.5	790	5	BW490314	604131408
1168	235	6.0	855	7	CF581183	AGENCY	1241	233.5	792	5	BW492574	604131101
1169	235	6.0	856	6	CA778232	1p15g12.y	1242	233.5	814	5	BW491344	604129379
1170	235	6.0	858	6	CD508293	CD490-A07	1243	233.5	814	5	BW491344	604129379
1171	235	6.0	1386	6	CD013940	90134942	1244	233.5	822	3	CNS080KC	AGENCY
1172	234.5	5.9	723	5	BK873612	BK873612	1245	233.5	858	3	BE379487	601237592
1173	234.5	5.9	727	4	BK0718156	BK0718156	1246	233.5	872	2	BE379487	601237592
1174	234.5	5.9	729	4	BK0720948	BK0720948	1247	233.5	884	7	CF375629	AGENCY
1175	234.5	5.9	735	6	CF523551	AGENCY	1248	233.5	886	7	CF375629	AGENCY
1176	234.5	5.9	758	6	CA371410	651831 NC	1249	233.5	896	7	CK407731	AGENCY
1177	234.5	5.9	777	5	BK073284	BK073284	1250	233.5	906	7	CK407731	AGENCY

1251	233.5	5.9	936	3	CR650622	Tetraodon	cl324	231	5.9	759	4	BJ720597
1252	233.5	5.9	942	7	CK407882	AUF_Iflvr	1325	231	5.9	759	5	BU489621
1253	233.5	5.9	949	7	CK409345	AUF_Iflvr	1326	231	5.9	777	5	BU492087
1254	233.5	5.9	953	7	CK408923	AUF_Iflvr	1327	231	5.9	777	5	BU492087
1255	233.5	5.9	953	3	BQ278177	AGENCYCOURT	1328	231	5.9	785	5	EX084985
1256	233.5	5.9	938	5	CR651108	Tetraodon	1329	231	5.9	785	5	EX082093
1257	233	5.9	681	6	CA044889	esaplbn5	1330	231	5.9	906	3	CF581449
1258	233	5.9	769	5	BU490592	604132366	1331	231	5.9	906	3	CR645466
1259	233	5.9	811	7	CV480267	AGENCYCOURT	1332	231	5.9	1580	3	CR649827
1260	233	5.9	823	7	CO580622	ILLUMIGEN	1333	231	5.9	1580	3	CR649827
1261	233	5.9	861	7	CK407019	AUF_Iflvr	1334	230.5	5.8	3042	9	AY411209
1262	233	5.9	873	2	BF313551	601900179	1335	230.5	5.8	544	2	BE012596
1263	233	5.9	916	7	CF581227	AGENCYCOURT	1336	230.5	5.8	593	4	BI900802
1264	233	5.9	921	3	CR653827	Tetraodon	1337	230.5	5.8	661	4	BJ706475
1265	233	5.9	1110	4	BI715986	ic64b09.y	1338	230.5	5.8	691	4	BG270309
1266	232.5	5.9	578	4	BI715986	ic64b09.y	1339	230.5	5.8	696	6	CB888497
1267	232.5	5.9	592	4	BI713261	ic86b11.y	1340	230.5	5.8	696	6	CB888497
1268	232.5	5.9	710	5	BU487317	604125540	1341	230.5	5.8	704	4	BJ713184
1269	232.5	5.9	757	7	CF999621	AGENCYCOURT	1342	230.5	5.8	704	4	BJ714577
1270	232.5	5.9	768	5	BU489088	604131220	1343	230.5	5.8	705	4	BJ708106
1271	232.5	5.9	771	5	BU487650	604124925	1344	230.5	5.8	706	4	BJ705779
1272	232.5	5.9	774	5	BU417316	603671161	1345	230.5	5.8	707	4	BJ706274
1273	232.5	5.9	775	7	CV512147	kc80d09.y	1346	230.5	5.8	707	4	BJ708473
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Wan,D.F., and Gu,J.R.  
TITLE Novel human cDNA clones with function of inhibiting cancer cell  
growth  
JOURNAL Unpublished  
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AUTHORS Qin,W.X., Wan,D.F., Zhou,X.M., Zhang,P.P., Jiang,H.Q., Huang,Y.,  
Zhao,X.T., and Gu,J.R.  
TITLE Direct Submission  
JOURNAL Submitted (16-APR-2001) National Laboratory For Oncogenes & Related  
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai  
200032, P. R. China

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1 High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
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RIKEN integrated sequence analysis (RISA) system--384-Format  
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Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
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4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 695-690 (2001)  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2746)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
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Muramatsu, M. and Hayaashizaki, Y.

# TITLE JOURNAL

Submitted (16-APR-2002) Yoshihide Hayaashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: http://genome.gsc.riken.jp/; Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC Building Adenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.

## FEATURES

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AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
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JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2214)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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US-10-063-692-38 (1-720) x AY406074 (1-2214)
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Db 1348 GCGAAGTGGAGTGGCGGCGGACCATCTGATCCCTATCTGCGGAAATTTGAGACATC 1407  
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Db 1468 AGCGGGTGCATGACGCGAGCTTACAAAGGAGCGTGGTTCTTAGTCTCGACGGGTGCC 1577  
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DEFINITION genomic survey sequence.  
ACCESSION AY406076  
VERSION AY406076.1 GI:39762050  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 2214)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarilwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,  
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios



JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 2214)  
 AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, P., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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 Percent Similarity: 82.94% Conservative: 33  
 Best Local Similarity: 78.57% Mismatches: 74  
 Query Match: 81.41% Indels: 55  
 DB: 9 Gaps: 3  
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 DB 1 ATGGAGCTAGACAGATGGCGCAGTTGGGGCTGGTCTCTCGAGCTCTTCTCATCTCA 60  
 QY 21 SerLeuProArgGluTrpThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40  
 DB 61 TCGTTCGCAAGAGAGTACACGGTCAATATGAAGCTGTCCGGAGCTGAGTGGGAACATC 120  
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QY 585 ArgAspLeuSerThrSerPheGlnGluSerHisIleThrValAlaGlyTrpAsnValLeu 604
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QY 625 ValAspSerLeuLeuCysGluGlnHisGluAspHisGlyIleProValSerValThr 644
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QY 645 AspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThrAlaGlu 664
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LOCUS Pan troglodytes HCM2436 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406075
VERSION AY406075.1 GI:39762049
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 2214)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2214)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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 Query Match: 62.88% Indels: 39  
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US-10-063-692-38 (1-720) x AY406075 (1-2214)

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QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
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REFERENCE  
AUTHORS

6 (bases 1 to 2184)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tonaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

TITLE  
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome cDNA library as part of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/

## FEATURES

## source

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## ORIGIN

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 Best Local Similarity: 90.41% Mismatches: 18  
 Query Match: 44.77% Indels: 1  
 DB: 3 Gaps: 0

US-10-063-692-38 (1-720) x AK031254 (1-2184)

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## RESULT 8

QY BX399905 1049 bp mRNA linear EST 29-APR-2004  
 DB BX399905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CS0D1086Y021 5-PRIME, mRNA sequence.  
 QY BX399905  
 DB BX399905.2 GI:46876619  
 QY EST.  
 DB Homo sapiens (human)  
 QY Homo sapiens  
 DB Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 QY 1 (bases 1 to 1049)  
 DB Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 QY Full-length cDNA libraries and normalization  
 DB Unpublished (2001)  
 QY On May 13, 2003 this sequence version replaced gi:30622029.  
 DB COMMENT

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5757.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DI086AH11QP1&c=5757.r.

## FEATURES

## source

Location/Qualifiers  
1..1049  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI086YO21"  
/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.58e-142 Length: 1049  
Score: 1578.50 Matches: 291  
Percent Similarity: 92.09% Conservative: 0  
Best Local Similarity: 92.09% Mismatches: 7  
Query Match: 40.01% Indels: 20  
DB: 5 Gaps: 2

US-10-063-692-38 (1-720) x BX399905 (1-1049)

QY 1 MetGluLeuGlyCysThrPheGlnLeuGlyLeuThrPheLeuLeuLeuSer 20  
DB 13 ATGGAGCTGGTGGTGGAGCGAGTGGGGCTCACATTTCTCAGCTCCTTCATCTCG 72  
QY 21 SerLeuProArgGluThrValIleAsnGluAlaCysProGlyAlaGluTrpAnile 40  
DB 73 TCCTTCCAGAGAGTACACAGTCATTAATGAAGCTGCGCTGAGCAGAGTGAATATC 132  
QY 41 MetCysArgGluCysCysGluThrPheGlnLeuGluCysValCysProGlyLysArgGlu 60  
DB 133 ATGTGTCGGAGTGTCTGAATATGATCAGATTGAGTGGCTGTGCGCCCGGAAAGAGGAA 192  
QY 61 ValValGlyThrThrileProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80  
DB 193 GTCGTGGGTATACCATCCCTTCTGTCAGGAATGAGGAGATGAGTGTGACTCCTGCTG 252  
QY 81 IleHisProGlyCysThrilePheGluAsnGlySerCysArgAsnGlySerTrpGly 100  
DB 253 ATCCACCCAGTGTGACCATCTTTGAAACCTGCAGAGCTGCCGAATGCTCATGGGG 312  
QY 101 GlyThrLeuAspPheThrValLysGlyPheThrCysAlaGluCysArgAlaGlyTrp 120  
DB 313 GGTACCTTGGATGACTTCTATGTGAAGGGGTCTTACTGTGACAGAGTCCGAGCAGCTGG 372  
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnLeu 140  
DB 373 TAGCGAGGAGACTGCATGCCATGTGGCCAGGTCTTCCGAGCCCAAGAGGTTCAGATTTC 432  
QY 141 LeuGluSerThrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPhe 160  
DB 433 TTGGAAAGCTATCCCTTAATGTCTACTGTGAATGAGCACTTCATGCTAAACCTGGTTT 492  
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspThrMetCysGlnThrAsp 180  
DB 493 GTCATCCAACTAAGATTGTGATGTTGAGCCTGGAGTTTGACTACATGTGCCAGTATGAC 552  
QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200

DB 553 TATGTTGAGTTCGTGATCGAGACACCGCATGCGCAGATCATCAAGCGTGTCTGTGGC 612  
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220  
DB 613 AACGAGCGCCAGCTCTTATCCAGAGCATAGGATCTCTACTCCAGCTCTCTTCCACTCC 672  
QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleThrGluGluIleThrAlaCysSer 240  
DB 673 GATGCTCCAGAAATTTTACCGTTTCCATGCAATTTATGAGGAGATCAGCATGCTCC 732  
QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerThrLysCys 260  
DB 733 TCATCCCTTGTTCATGACGCGCAS-TGCGTTCTTGACAGAGCTGGATCTTACAAGTGT 791  
QY 261 AlaCysLeuAlaGlyThrThrGlyGlnArgCysGluAsnLeu----- 274  
DB 792 GCCTGCTTGGCAGGCTATACTGGCAGCGCTGTGAAAATCTTCTGGRGGCTGGGAAGTCC 851  
QY 275 -----LeuGluGluArgAsnCysSerAspPro 283  
DB 852 MAGATCAAGCGCTCAGAAGATCATTTGCTGTGTTGAAGAAGAAAYGCTCAGA--CCT 909  
QY 284 GlyGlyProValAsnGlyThrGlnLysIleThrGlyGlyProGlyLeu 299  
DB 910 GGGGGGCCAGTCAATGGGTACAAAAA---TAMAGGGGGCCYGGGCTT 954

## RESULT 9

## BX439313

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## CONTACT

## Genoscope

## Centre National de Sequencage

## 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

## Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

## 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

## end enriched, double-strand cDNA was digested with Not I and cloned

## into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

## was not normalized. Library was constructed by Life Technologies, a

## division of Invitrogen.

## This sequence belongs to sequence cluster 5757.r

## For more information about this cluster, see

## http://www.genoscope.cns.fr/cdna?s=CS0DE009CB01QP1&amp;c=5757.r.

## Location/Qualifiers

## 1..952

## /organism="Homo sapiens"

## /mol\_type="mRNA"

## /db\_xref="taxon:9606"

## /clone="CS0DE009YD01"

## /tissue\_type="PLACENTA"

## /clone\_lib="Homo sapiens PLACENTA"

## /note="Vector: pCMVSPORT\_6; 1st strand cDNA was primed

## with a NotI-oligo(dT) primer. Five prime end enriched,

## double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector.

## Library was not normalized."

## ORIGIN

## Alignment Scores:

## Pred. No.:

## 2.25e-137

## Length:

## 952

Score: 1527.00 Matches: 283  
Percent Similarity: 91.40% Conservative: 4  
Best Local Similarity: 90.13% Mismatches: 17  
Query Match: 38.71% Indels: 12  
DB: 5 Gaps: 2

US-10-063-692-38 (1-720) x BX439313 (1-952)

QY 1 MetGluLeuGlyCysThrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20  
DB 13 ATGGAGCTGGTCTCGAGCA-TTGGGGCTCACTTTCTCAGCTCCTCTCATCTCG 71  
QY 21 SerLeuProArgGluTyrThrValIleAsnGluLaCysProGlyAlaGluTrpAsnIle 40  
DB 72 TCCTTGCCAAAGAGAGTACACAGTCATTAAAGAGCCCTGCCCTGGAGCAGAGTGGAAATATC 131  
QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60  
DB 132 ATGTCTGGAGTCTGTGAATATGATCAGATTGAGTGGCTGTGCCCGGAAGAGGAA 191  
QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80  
DB 192 GTCTGGGTTATACCATCCCTTCTGTCAGCAATGAGGAGAAATGAGTGTGACTCCTGCCTG 251  
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100  
DB 252 ATCCACCCAGGTTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAATGGCTCATGGGG 311  
QY 101 GlyThrLeuAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120  
DB 312 GGTACCTTGATGACTTCTATGTGAAGGGGTCTACTGTGCAGAGTCCCGAGCGCTGG 371  
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeu 140  
DB 372 TACGGAGGAGCTGCATGCGATGTGGCCAGGTTCTGCGAGCCCAAGGTCAGATTGG 431  
QY 141 LeuGluSerTyrProLeuAsnAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe 160  
DB 432 TTGGAAGAGTATCCCTTAAATGCTCACTGTGAATGGACCAATCATGTAACCTGGGTTT 491  
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180  
DB 492 GTATCCACTTAGATTGTTCATGTTGAGCGCTGAGTTTACTGTACATGTCCTCACTCC 551  
QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleLysArgValCysGly 200  
DB 552 TATGTTGAGTTCTGTATGAGACCAACCGGATGGCCAGATCATCAAGCGTGTCTGGC 611  
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220  
DB 612 AACGAGCGGCAGCTCTATCCAGAGCATAGGATCCTCACTCCACGCTCTCTTCCACTCC 671  
QY 221 AspGlySerLysAsnAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240  
DB 672 GATGGCTCCCAAGAAATTTGACGGTTTCCATGCCATTTATGAGAGATCACAGATGCTCC 731  
QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCys 260  
DB 732 TCATCCCTCTGTTCCATGACGGCACTGGTCTTTCACAGAGCTGGATCTTACAGTGT 791  
QY 261 AlaCysLeuAlaGlyTyrThrGlyGlnArgCysGluAsnLeuLeuGluArgAsnCys 280  
DB 792 GCCTGCTTGGCAGCTAATACTATGGGCGCGCTGTGAAATCGATTAAGAGATAC-GAATGT 850  
QY 281 SerAspProGlyGlyProValAsnGlyTyrGlnLysIle----- 293  
DB 851 ACAGAC-----ACCGTGGTGGCCACCGAAGTGTGATCAACACCTTGGAAATGAGT 901  
QY 294 ThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaLysIle 307  
DB 902 TCTGGAGCCTTGGAGTCCAGATCAGAGCGTCAGAGATT 943

Score: 1527.00 Matches: 283  
Percent Similarity: 91.40% Conservative: 4  
Best Local Similarity: 90.13% Mismatches: 17  
Query Match: 38.71% Indels: 12  
DB: 5 Gaps: 2

US-10-063-692-38 (1-720) x BX337781 (1-886)

QY 1 MetGluLeuGlyCysThrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20  
DB 63 ATGGAGCTGGTGTCTGGAGCAGTGGGGCTCACTTTTCTCAGCTCCTCTCATCTCG 122  
QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40  
DB 123 TCCTTGCCCAAGAGAGTACACAGTCATTATGAAGCTGCCCTGGAGCAGAGTGGAAATATC 182  
QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60  
DB 183 ATGTCTGGGAGTGTGTGAAATATGATCAGATTGAGTGGCTGTGCCCGGAAGAGGAA 242  
QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80  
DB 243 GTCTGGGTTATACCATCCCTTGTCTGAGGAAATGAGGAGAAATGAGTGTGACTCCTGCCTG 302  
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100  
DB 303 ATCCACCCAGGTTGTACCATCTTTGAAAACTCCAGAGCTGCCGAAATGGCTCATGGGG 362  
QY 101 GlyThrLeuAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120

Score: 1527.00 Matches: 283  
Percent Similarity: 91.40% Conservative: 4  
Best Local Similarity: 90.13% Mismatches: 17  
Query Match: 38.71% Indels: 12  
DB: 5 Gaps: 2

US-10-063-692-38 (1-720) x BX337781 (1-886)

QY 1 MetGluLeuGlyCysThrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20  
DB 63 ATGGAGCTGGTGTCTGGAGCAGTGGGGCTCACTTTTCTCAGCTCCTCTCATCTCG 122  
QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40  
DB 123 TCCTTGCCCAAGAGAGTACACAGTCATTATGAAGCTGCCCTGGAGCAGAGTGGAAATATC 182  
QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60  
DB 183 ATGTCTGGGAGTGTGTGAAATATGATCAGATTGAGTGGCTGTGCCCGGAAGAGGAA 242  
QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80  
DB 243 GTCTGGGTTATACCATCCCTTGTCTGAGGAAATGAGGAGAAATGAGTGTGACTCCTGCCTG 302  
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100  
DB 303 ATCCACCCAGGTTGTACCATCTTTGAAAACTCCAGAGCTGCCGAAATGGCTCATGGGG 362  
QY 101 GlyThrLeuAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120

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Db 363 GGTACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTCCGAGCAGCTGG 422
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProlysGlyGlnIleLeu 140
Db 423 TACGGAGGAGACTGTCATGCATGTGGCCAGAGTTCTCGAGAGCCCAAGGGTCCAGATTTTG 482
QY 141 LeuGluSerTyProLeuAsnAlaHisCysGluTyrThrIleHisAlaLysProGlyPh 160
Db 483 TTGAAAGCTATCCCTTAATGCTCACTGTGAATGAGCACCATTATGCTAAACCTGGGGT 542
QY 160 eValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAs 180
Db 543 TGTCACTCAACTAAGATTGTTCATGTTGAGCCTGGAGTTTGACTACATGTGCCAGATGA 602
QY 180 pTyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGl 200
Db 603 CTATGTTGAGTTTCGTGATGGAGACCAACCGCATGCCAGATCATCAAGCGTGTCTGTGG 662
QY 200 yAsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSe 220
Db 663 CAACGAGCGGCCAGCTTCCTATCCAGAGCATAGGATCCTCACTCCAGCTCTCTTCACATC 722
QY 220 rAspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSe 240
Db 723 CGATGGCTCCAGAAATTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTC 782
QY 240 rSerSerProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyrLysCy 260
Db 783 CTCATCCCTTTGTTCCATGACGCGACGTCGTGCTTGACAGGCTGGATCTTTACAAGTG 842
QY 260 sAlaCysLeuAlaGlyTyrThrGlyGlnArgCysGlu 272
Db 843 TGCCTGCTGGCAGC-TATACTGGGCGAGCS-TGTGAA 877

RESULT 11
BM461342 1158 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6419728 NCI_CGAP_Ov44 Mus musculus cDNA clone
DEFINITION IMAGE:5504093 5', mRNA sequence.
ACCESSION BM461342
VERSION 1
KEYWORDS EST.
SOURCE BM461342.1 GI:18510382
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1158)
NIH-MGC http://mgi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Aaron Hueh
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12144 row: o column: 06
High quality sequence stop: 709.
Location/Qualifiers
1. 1158
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5504093"
/lab_host="DH10B (11 phage-resistant)"
/clone_lib="NCI_CGAP_Ov44"
/note="Organ: ovary, PMSG-treated; Vector: pCMV-SPORT6.1;
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 2.2 kb. Library
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constructed by Life Technologies. Note: this is a NCI_CGAP
Library."
ORIGIN
Alignment Scores: 9,02e-129 Length: 1158
Pred. No.: 1440,00 Matches: 285
Score: 85,34% Conservativeness: 12
Percent Similarity: 81,90% Mismatches: 41
Best Local Similarity: 36,50% Indels: 12
Query Match: 4 Gaps: 3
DB:
US-10-063-692-38 (1-720) x BM461342 (1-1158)
QY 1 MetGluLeuGlyCysTyrThrGlnLeuGlyLeuThrPheLeuGlnLeuLeuLeuSer 20
Db 101 ATGGAGCTAGACAGATGGGGCTGGTTCCTGCAGCTCCTTCTCATCTCA 160
QY 21 SerLeuProArgGluTyrThrValIleAsnGluAlaCysProGlyAlaGluTrpAsnIle 40
Db 161 TCGTTGCCAAGAGAGTACACGGTCATTATGAAGCCTGTCCCGAGCTGAGTGAACATC 220
QY 41 MetCysArgGluCysCysGluTyrAspGlnIleGluCysValCysProGlyLysArgGlu 60
Db 221 ATGTGTAGAGAGTGTGTGAATATGATCAGATTGAATGCTCTGCCAGGAAAGAGAA 280
QY 61 ValValGlyTyrThrIleProCysCysArgAsnGluGluAsnGluCysAspSerCysLeu 80
Db 281 GTGGTGGGTGTACACCATCCATGCTGCAGGATAGGATATGAATGACTCCTGTCTA 340
QY 81 IleHisProGlyCysThrIlePheGluAsnCysLysSerCysArgAsnGlySerTrpGly 100
Db 341 ATTCACCCAGGTGTACCATCTTTGAAACTCTCAAGAGCTGCCGAATGGCTCTGGGGC 400
QY 101 GlyThrLeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrp 120
Db 401 GGAACCTCTGGATGACTTCTACGTGAAGGGATTTCTACTGCGAAGAGTGCAGGGCAGCTGG 460
QY 121 TyrGlyGlyAspCysMetArgCysGlyGlnValLeuArgAlaProlysGlyGlnIleLeu 140
Db 461 TACGGAGGAGACTGCGATGCGATGTGGCCAGGTTCTTCGAGCTTCAAGGGTCAAGTCTTG 520
QY 141 LeuGluSerTyProLeuAsnAlaHisCysGluTyrThrIleHisAlaLysProGlyPhe 160
Db 521 TTGGAGAGCTATCCCTTAAATGCTCACTGTGAATGAGCTATTTCATGCCAGACCTGGGTT 580
QY 161 ValIleGlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAsp 180
Db 581 ATCATCCAGTTGAGGTTTGGCATGTTGAGCCTAGAGTTTGAGCTACATGTGCCAGTATGAC 640
QY 181 TyrValGluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGly 200
Db 641 TATGTGGAGTCCGCGATGGGATATAGTAGCAGGCCCTATCATCAAGCGTTTCTGTGGC 700
QY 201 AsnGluArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSer 220
Db 701 AACGAGAGCCAGCTCCCATCANGAGCAGCTGGCTCTTCACTCCATGTCTCTTTCCATCT 760
QY 221 AspGlySerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSer 240
Db 761 GATGGCTCCAAAGAACTTCGATGGCTTTTCACGCTGTTTTCAGAGAGATCACAGGGTGTCTC 820
QY 241 SerSerProCysPheHisAspGlyThrCysValLeuAsp-LysAlaGlySerTyrLys-C 260
Db 821 TCATCCCTTGTTC-CATGATGGCAGATGCCCTCTTTCACACCAACTGGGGTCTTTTAAGGT 879
QY 260 yAlaCysLeuAlaGlyTyrThr-GlyGlnArgCysGluAsnLeuLeuGluArgAsn 279
Db 880 GTCCCTGGCTGGCTGCTACACTGGCCAGCGCTGTGAAACCTACTTTGAAGAAAGAAA- 938
QY 280 CysSerAspPro---GlyGlyProValAsnGlyTyrGlnLysIleThrGlyGlyProGly 298
Db 939 TGCTCCCGACCTTTTGGGGGGGCCAGTCAATGGGTACAGAAATATCCCAAAAGGGCCCTGA 998
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QY 299 LeuIleAsnGlyArgHisAla-IysIleGlyThrValValSer---PhePheCysAsn-A 317  
 ::|||  
 Db 999 ACTTCTCATGAGGCCCTGTAAAAAATTGGCGCCGTCGGGGCCCTTCTTTGGGAACGG 1058  
 QY 317 snSerTyrrVal-LeuSerGlyAsnGluLysArgThrCys---GlnGlnAsnGlyGlu-Tr 335  
 ::|||  
 Db 1059 GTTCATACCTTTCTTGGGGGGGAAGGAAAAACCAATTGCCCCCCCAAAATGGGAAATG 1118

QY 335 pSerGlyLys 338  
 ::|||  
 Db 1119 GGCCGGGAAA 1128

## RESULT 12

CD514783  
 LOCUS AGENCOURT\_14376424 NIH\_MGC\_181 Homo sapiens cDNA clone EST 06-JUN-2003  
 DEFINITION IMAGE:30396311 5', mRNA sequence.

ACCESSION CD514783  
 VERSION CD514783.1 GI:31446501  
 KEYWORDS EST.

## SOURCE

ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 879)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

## COMMENT

Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgabs-t@mail.nih.gov](mailto:cgabs-t@mail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: ND4M477 row: m column: 24  
 High quality sequence stop: 613.

## FEATURES

## source

1..879  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30396311"  
 /tissue\_type="White Matter"  
 /dev\_stage="Unknown"  
 /lab\_host="DH10B-Ton A (T1 and T5 phage resistances)"  
 /clone\_lib="NIH\_MGC\_181"  
 /note="Vector: pCMV-SPORT6.1; Site\_1: NotI; Site\_2: EcoRV  
 (destroyed); Library is oligo-dr primed and directionally  
 cloned (EcoRV site is destroyed upon cloning). Average  
 insert size 1.42 kb. Library was constructed by  
 (Invitrogen). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1..4e-128 Length: 879  
 Score: 1436.00 Matches: 282  
 Percent Similarity: 97.92% Conservative: 0  
 Best Local Similarity: 97.92% Mismatches: 2  
 Query Match: 36.40% Indels: 4  
 DB: 6 Gaps: 0

US-10-063-692-38 (1-720) x CD514783 (1-879)

QY 310 valValSerPhePheCysAsnAsnSerTyrrValLeuSerGlyAsnGluLysArgThrCys 329  
 ::|||  
 Db 2 GTGGTGCTCTTTCTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTGC 61

QY 330 GlnGlnAsnGlyGluTrpSerGlyLysGlnProIleCysIleLysAlaCysArgGluPro 349  
 ::|||  
 Db 62 CAGCAGAAATGGAGAGTGGTCAGGAAACAGCCCATCTGCATAAAAGCCTGCCGAGAACCA 121  
 QY 350 LysIleSerAspLeuValArgArgValLeuPrometGlnValGlnSerArgGluThr 369  
 ::|||  
 Db 122 AAGATTTCAGACCTGTGTGAGAGAGAGATTCTTCCCATGCGAGTTCTAGTCAAGGGAGACA 181  
 QY 370 ProLeuHisGlnLeuTyrrSerAlaAlaPheSerLysGlnLysLeuGlnSerAlaProThr 389  
 ::|||  
 Db 182 CCATTACACAGCTATCTCAGCGGCTTCAGCAGCAGGAAATCTGACAGATGCGCCCTACC 241  
 QY 390 LysLysProAlaLeuProPheGlyAspLeuPrometGlyTyrrGlnHisLeuHisThrGln 409  
 ::|||  
 Db 242 AAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAG 301  
 QY 410 LeuGlnTyrrGluCysIleSerProPheTyrrArgArgLeuGlySerSerArgArgThrCys 429  
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 Db 302 CTCAGTATGAGTGCATCTCACCCCTTCTACCGCCGCTGGGCAGCAGCAGGAGCATGT 361  
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 Db 362 CTGAGGACCTGGGAAGTGGAGTGGCGGGCAGCACCATCTGCATCCCTATCTCGGGGAAATT 421  
 QY 450 GluAsnIleThrAlaProLysThrGlnGlyLeuArgTrpProTrpGlnAlaIleTyrr 469  
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 QY 490 SerGlyAlaLeuValAsnGluArgThrValValAlaAlaHisCysValThrAspLeu 509  
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 Db 542 AGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGCTGCCCATCTGTGTACTGACCTG 601  
 QY 510 GlyLysValThrMetIleLysThrAlaAspLeuLysValValLeuGlyLysPheTyrrArg 529  
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 Db 602 NCGAAGGTCAACATGATCAAGCAGCAGCAGACCTGANNAGTTGTTTTGGGGAAATTTCTACC 661  
 QY 530 AspAspArgAspGluLysThrIleGlnSerLeuGlnIleSerAlaIleLeuHis 549  
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 Db 662 GATGATGACCGGATGAGAGACCATTCAGAGCCTACAGATTTCTCTCATCTATCTGTCAT 721  
 QY 550 ProAsnTyrrAspProIleLeuAspAlaAspIleAlaIleLeuLysLeuLeuAspLys 569  
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 Db 722 CCCAACTATGACCCCATCTCTTGTATGCTGACATCGCCATCTCTGAGAGCTCTTAGACAG 781  
 QY 570 AlaArg-IleSerThrArgValGlnProIle-CysLeuAlaAla-SerArgAspLeuSer 588  
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 Db 782 GCCCGTTATCAGCACCACCGAGTCCAGCCCATCTTGCCTCGTCCAGTCCGAGTCTCAGC 841  
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## RESULT 13

## CD655367

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

CD655367 795 bp mRNA linear EST 18-JUN-2003  
 AGENCOURT\_14552770 NTA Human H1 Embryonic Stem Cell cDNA Library  
 (Long) Homo sapiens cDNA clone IMAGE:30426503 5', mRNA sequence.

CD655367

CD655367.1 GI:31895529

EST.

Homo sapiens (human)

Homo sapiens

1 (bases 1 to 795)

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)



## COMMENT

Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA  
cDNA Library Preparation: Yulan Piao and Minoru Ko  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC c lone distribution information  
can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM512 row: g column: 24  
High quality sequence stop: 676.  
Location/Qualifiers

## FEATURES

## source

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/clone="IMAGE:30426503"  
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/cell\_line="WA01"  
/lab\_host="DH10B ('T1 phage-resistant')"  
/clone\_lib="NIA Human H1 Embryonic Stem Cell cDNA Library (Long)"  
/notes="Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI;  
This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199] from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MSF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLK3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 x 6cm dishes were treated with 1 mg/ml collagenase, type IV  
(Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with Trizol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID: 11544199] Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTCTTTT-3'] from 3.49 of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-Sport6 plasmid vector. The average insert size is about 3.6kb."

## ORIGIN

Alignment Scores:  
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Best Local Similarity: 98.81% Mismatches: 2  
Query Match: 33.99% Indels: 2  
DB: 6 Gaps: 0

US-10-063-692-38 (1-720) x CD655367 (1-795)

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Qy 228 GlyPheHisAlaIleTyrGluGluIleThrAlaCysSerSerProCysPheHisAsp 247

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Db 133 GGCAGTGGCTCTTGACAAGCTGGATCTTCAAGTGTGCTGTCTGGCAGCTATACT 192  
Qy 268 GlyGlnArgCysGluAsnLeuLeuGluArgAsnCysSerAspProGlyGlyProVal 287  
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Qy 288 AsnGlyTyrGlnLysIleThrGlyGlyProGlyLeuIleAsnGlyArgHisAlaIle 307  
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Db 313 GGCACCGTGTGTCTCTTTTGTAACTCTTATGAGTGTCTTAGTGGCAATGAGAAAAGA 372  
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Qy 348 GluProLysIleSerAspLeuValArgArgValLeuProMetGlnValGlnSerArg 367  
Db 433 GAACCAAGATTCAGACCTGGTGAGAGCAGAGTTCTTCCGATGCGGTTCACTCAAGG 492  
Qy 368 GluThrProLeuHisGlnLeuTyrSerAlaAlaPheSerIysGlnLysLeuGlnSerAla 387  
Db 493 GAGACACCATTAACACAGCTATCTACAGCGGCTTCAGCAAGCAGAAATCGCAGATGCC 552  
Qy 388 ProThrLysLysProAlaLeuProPheGlyAspLeuProMetGlyTyrGlnHisLeuHis 407  
Db 553 CTTACCAAGAGCCGCCCTTCCCTTTGAGATCTGCCCATGGGATACCAACATCTGCAT 612  
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Db 733 AAATTGAGAC-ATCACTGCTCCAAAGACCAAGGT 767

CF125161 718 bp mRNA linear EST 05-AUG-2003  
UI-HP-EL0-avm-p-18-0-UI.r1 NIH\_MGC\_212 Homo sapiens CDNA clone  
IMAGE:30558617 5', mRNA sequence.

CF125161  
CF125161.1 GI:33201111  
EST.

Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

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Fax: 319 335 9565

Email: bento-soares@uiowa.edu





Percent Similarity: 94.92% Conservative: 17  
Best Local Similarity: 88.28% Mismatches: 13  
Query Match: 31.08% Indels: 0  
DB: 7 Gaps: 0

US-10-063-692-38 (1-720) x C0397557 (1-785)

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QY 437 GlyArgAlaProSerCysIleProIleCysGlyLysIleGluAsnIleThrAlaProLys 456
DB 62 GGGCGGGCCCGCTCTGTATCCAACTCTGTGGAAAATCGAGAGCGTGTCTCCAAAG 121
QY 457 ThrGlnGlyLeuArgTrpProTrpGlnAlaAlaIleTyrArgArgThrSerGlyValHis 476
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DB 182 GACGGTGGTCTGCACAAAGGTGATGGTCTGTGAGTGGTCCCTGGTGAATGAG 241
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DB 362 ACCATCCAGAAATTACGGATTTCTGTATCATTTCTGACCCCACTATGACCTATCCTG 421
QY 557 LeuAspAlaAspIleAlaIleLeuLysLeuAspLysAlaArgIleSerThrArgVal 576
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QY 597 ThrValAlaGlyTrpAsnValLeuAlaAspValArgSerProGlyPheLysAsnAspThr 616
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QY 617 LeuArgSerGlyValValSerValValAspSerLeuLeuGluGlnHisGluAsp 636
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 9, 2005, 23:40:28 ; Search time 1063 Seconds  
(without alignments)  
4141.570 Million cell updates/sec

Perfect score: 3945  
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Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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560	3945	100.0	2846	16	US-10-174-587-169	Sequence 169, App
624	3945	100.0	2846	16	US-10-063-742-37	Sequence 37, Appl
739	3945	100.0	2846	19	US-10-972-717-37	Sequence 37, Appl
740	3939	99.8	2306	14	US-10-004-551-3	Sequence 3, Appl
741	3939	99.8	2306	16	US-10-098-871-25	Sequence 25, Appl
742	3932	99.7	2845	15	US-10-101-510-644	Sequence 644, App
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746	2946.5	74.7	2259	13	US-10-067-422-2	Sequence 2, Appl
747	2678.5	67.9	2142	15	US-10-037-270-1006	Sequence 1006, Ap
748	2678.5	67.9	2142	17	US-10-117-722-1006	Sequence 1006, Ap
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750	2678.5	67.9	2144	17	US-10-117-722-969	Sequence 969, App
751	821.5	20.8	997	11	US-09-876-143-1083	Sequence 1083, Ap
752	672	17.0	3467	14	US-10-183-992-3	Sequence 3, Appl
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754	665	16.9	3438	14	US-10-183-992-7	Sequence 7, Appl
755	665	16.9	3438	18	US-10-480-254-7	Sequence 7, Appl
756	665	16.9	3448	18	US-10-638-125-3	Sequence 3, Appl
757	665	16.9	4182	14	US-10-183-992-5	Sequence 5, Appl
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760	496.5	12.6	432	11	US-09-876-143-696	Sequence 696, App
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762	473	12.0	403	10	US-09-918-995-6744	Sequence 6744, Ap
763	471	11.9	3895	16	US-10-148-671-4	Sequence 4, Appl
764	459.5	11.6	369	10	US-09-903-393-1	Sequence 1, Appl
765	429	10.7	2416	19	US-10-764-420-513	Sequence 513, App
766	424	10.7	2037	19	US-10-764-420-513	Sequence 513, App
767	408.5	10.4	3064	15	US-10-101-510-599	Sequence 599, App
768	405	10.3	2475	9	US-09-874-198-3	Sequence 3, Appl
769	405	10.3	2475	9	US-09-874-238-3	Sequence 3, Appl
770	403.5	10.2	2386	9	US-09-808-602-92	Sequence 92, Appl
771	403.5	10.2	2386	10	US-09-800-198-79	Sequence 79, Appl
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779	396.5	10.1	296	18	US-10-723-860-4638	Sequence 4638, Ap
780	396.5	10.1	554	13	US-10-027-632-275184	Sequence 275184, Sequence 275184,
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783	351	8.9	2647	17	US-10-172-118-655	Sequence 655, App
784	351	8.9	2647	17	US-10-342-887-655	Sequence 472, App
785	350	8.9	2659	13	US-10-044-090-472	Sequence 15, Appl
786	350	8.9	2659	15	US-10-084-817-15	Sequence 101, App
787	348.5	8.8	3115	16	US-10-252-157-101	Sequence 448, App
788	347	8.8	3115	17	US-10-276-774-448	Sequence 404, App
c 789	347	8.8	3115	17	US-10-296-115-404	Sequence 883, App
790	346	8.8	2647	17	US-10-453-827-893	Sequence 182, App
791	342	8.7	2725	9	US-09-925-301-182	Sequence 1348, Ap
792	340.5	8.6	2908	9	US-09-917-800A-1348	Sequence 812, App
793	340.5	8.6	2908	17	US-10-191-803-812	Sequence 1421, Ap
794	340.5	8.6	2908	17	US-10-152-319A-1421	Sequence 157, App
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796	336.5	8.5	3149	17	US-10-295-027-968	Sequence 968, App
797	336.5	8.5	3149	17	US-10-342-887-157	Sequence 157, App
798	336.5	8.5	3159	18	US-10-729-807-19	Sequence 19, Appl
799	335.5	8.5	2838	17	US-10-072-012-43	Sequence 43, Appl
800	335.5	8.5	3147	10	US-09-776-191-1	Sequence 1, Appl
801	335.5	8.5	3147	10	US-09-776-191-49	Sequence 49, Appl
802	335.5	8.5	3147	14	US-10-099-700A-1	Sequence 1, Appl
803	335.5	8.5	3147	14	US-10-099-700A-3	Sequence 3, Appl
804	335.5	8.5	3147	15	US-10-190-030B-1	Sequence 1, Appl
805	335.5	8.5	3147	15	US-10-190-030B-3	Sequence 3, Appl

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807	335.5	8.5	3147	15	US-10-302-840A-3	Sequence 3, Appli	880	289.5	7.3	2672	17	US-09-776-191-9	Sequence 9, Appli
808	335.5	8.5	3147	15	US-10-267-219-1	Sequence 1, Appli	881	289.5	7.3	2672	10	US-10-156-214A-9	Sequence 9, Appli
809	335.5	8.5	3147	15	US-10-267-219-3	Sequence 3, Appli	882	289.5	7.3	2859	10	US-09-814-353-19992	Sequence 19992, A
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811	335.5	8.5	3147	16	US-10-112-221A-3	Sequence 3, Appli	884	289.5	7.3	3104	17	US-10-156-214A-7	Sequence 7, Appli
812	335.5	8.5	3147	16	US-10-104-271-1	Sequence 1, Appli	885	288.5	7.3	2409	9	US-09-888-615-54	Sequence 54, Appli
813	335.5	8.5	3147	16	US-10-104-271-3	Sequence 3, Appli	886	288.5	7.3	3143	14	US-10-167-749-168	Sequence 168, App
814	335.5	8.5	3147	17	US-10-147-211A-1	Sequence 1, Appli	887	288.5	7.3	3143	17	US-10-170-481A-168	Sequence 168, App
815	335.5	8.5	3147	17	US-10-147-211A-3	Sequence 3, Appli	888	288.5	7.3	3143	17	US-10-210-028-168	Sequence 168, App
816	335.5	8.5	3147	17	US-10-156-214A-1	Sequence 1, Appli	889	288.5	7.3	3143	17	US-10-162-521A-168	Sequence 168, App
817	335.5	8.5	3147	17	US-10-600-187-1	Sequence 1, Appli	890	288.5	7.3	3143	19	US-10-918-851-168	Sequence 168, App
818	335.5	8.5	3147	17	US-10-600-187-18	Sequence 18, Appli	891	288.5	7.3	3143	19	US-10-805-667-168	Sequence 168, App
819	334.5	8.5	3147	16	US-10-252-157-102	Sequence 102, App	892	288.5	7.3	3143	19	US-10-897-359-168	Sequence 168, App
820	331.5	8.4	3696	10	US-09-776-191-63	Sequence 63, Appli	893	288.5	7.3	3143	19	US-10-893-802-168	Sequence 168, App
821	331.5	8.4	3696	15	US-10-157-031-266	Sequence 266, App	894	288.5	7.3	3143	19	US-10-897-360-168	Sequence 168, App
822	331.5	8.4	3696	17	US-10-156-214A-30	Sequence 30, Appli	895	288.5	7.3	3547	17	US-10-926-083-3	Sequence 3, Appli
823	328.5	8.3	4506	17	US-10-467-043-27	Sequence 27, Appli	896	287	7.3	1401	17	US-10-406-031-6	Sequence 6, Appli
824	328.5	8.3	5598	16	US-10-276-934-1	Sequence 1, Appli	897	287	7.3	1404	17	US-10-406-031-4	Sequence 4, Appli
825	328.5	8.3	5667	16	US-10-276-934-4	Sequence 4, Appli	898	286	7.2	1689	9	US-10-741-600-83	Sequence 83, Appli
826	328.5	8.3	6145	16	US-10-276-934-2	Sequence 2, Appli	899	286	7.2	1689	9	US-09-969-271-6	Sequence 6, Appli
827	328.5	8.3	6409	16	US-10-276-934-3	Sequence 3, Appli	900	286	7.2	1726	17	US-10-411-037-25	Sequence 25, Appli
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830	327.5	8.3	2063	9	US-09-925-302-169	Sequence 169, App	903	286	7.2	1726	18	US-10-410-949-25	Sequence 25, Appli
831	327.5	8.3	2063	10	US-09-925-302-169	Sequence 169, App	904	286	7.2	1726	18	US-10-410-930-25	Sequence 25, Appli
832	324	8.2	2900	17	US-10-600-187-9	Sequence 9, Appli	905	286	7.2	1726	18	US-10-410-977-25	Sequence 25, Appli
833	323	8.2	8010	17	US-10-016-248-3	Sequence 3, Appli	906	286	7.2	1726	18	US-10-411-012-25	Sequence 25, Appli
834	323	8.2	10136	17	US-10-016-248-1	Sequence 1, Appli	907	286	7.2	1726	18	US-10-287-994-25	Sequence 25, Appli
835	319.5	8.1	1365	17	US-10-406-031-18	Sequence 18, Appli	908	286	7.2	1726	18	US-10-410-913-25	Sequence 25, Appli
836	319.5	8.1	1401	17	US-10-406-031-16	Sequence 16, Appli	909	286	7.2	1726	18	US-10-410-980-25	Sequence 25, Appli
837	318.5	8.1	2756	9	US-09-925-301-351	Sequence 351, App	910	286	7.2	2461	17	US-10-172-118-541	Sequence 541, App
838	318.5	8.1	3106	9	US-09-900-751-1	Sequence 1, Appli	911	286	7.2	2461	17	US-10-342-887-541	Sequence 541, App
839	314.5	8.0	1362	17	US-10-406-031-12	Sequence 12, Appli	912	283.5	7.2	1486	19	US-10-764-420-2390	Sequence 2390, Ap
840	314.5	8.0	1365	17	US-10-406-031-10	Sequence 10, Appli	913	281.5	7.1	901	17	US-10-330-051A-21	Sequence 21, Appli
841	312.5	7.9	1843	9	US-09-880-107-3670	Sequence 3670, Ap	914	281	7.1	1467	15	US-10-348-504-43	Sequence 43, Appli
842	312.5	7.9	1843	9	US-10-349-858-17	Sequence 17, Appli	915	281	7.1	1467	16	US-10-407-123-26	Sequence 26, Appli
843	312	7.9	1386	17	US-10-168-407-11	Sequence 11, Appli	916	280.5	7.1	1184	18	US-09-969-347-210	Sequence 210, App
844	312	7.9	1401	17	US-10-406-031-9	Sequence 9, Appli	917	280.5	7.1	1184	18	US-10-283-975A-47	Sequence 47, App
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846	312	7.9	3096	17	US-10-451-168-29	Sequence 29, Appli	919	280.5	7.1	1184	18	US-10-617-619-9	Sequence 9, Appli
847	311.5	7.9	2580	17	US-10-104-047-1934	Sequence 1934, Ap	920	279.5	7.1	2106	18	US-10-097-340-311	Sequence 311, App
848	311	7.9	1386	17	US-10-168-407-9	Sequence 9, Appli	921	279.5	7.1	3112	14	US-10-097-340-311	Sequence 10, Appli
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850	310.5	7.9	1245	17	US-10-670-628-1	Sequence 1, Appli	923	279	7.1	3522	17	US-10-363-937-23	Sequence 23, Appli
851	310.5	7.9	1257	10	US-09-997-623-3	Sequence 3, Appli	924	278.5	7.1	1877	10	US-09-978-418-33	Sequence 33, Appli
852	310.5	7.9	1257	10	US-09-978-917A-3	Sequence 3, Appli	925	278.5	7.1	1440	17	US-10-375-741-13	Sequence 13, Appli
853	310.5	7.9	1260	14	US-10-182-263-7	Sequence 7, Appli	926	278.5	7.1	2462	9	US-09-964-824A-289	Sequence 289, App
854	310.5	7.9	1260	14	US-10-182-263-7	Sequence 7, Appli	927	278.5	7.1	2462	9	US-09-880-107-2251	Sequence 2251, Ap
855	310.5	7.9	1359	17	US-10-406-031-15	Sequence 15, Appli	928	278.5	7.1	2462	17	US-10-375-716-25	Sequence 25, Appli
856	310.5	7.9	1383	10	US-09-997-623-1	Sequence 1, Appli	929	278.5	7.1	2462	17	US-10-349-858-14	Sequence 14, Appli
857	310.5	7.9	1383	10	US-09-978-917A-1	Sequence 1, Appli	930	278.5	7.1	2462	19	US-10-843-641A-5592	Sequence 5592, Ap
858	310.5	7.9	1386	14	US-10-182-263-8	Sequence 8, Appli	931	278	7.0	1502	17	US-10-406-031-26	Sequence 26, Appli
859	310.5	7.9	1386	17	US-10-168-407-8	Sequence 8, Appli	932	278	7.0	1507	15	US-10-101-510-433	Sequence 433, App
860	310.5	7.9	1395	17	US-10-406-031-13	Sequence 13, Appli	933	278.5	7.1	1507	17	US-10-101-510-433	Sequence 13, Appli
861	310	7.9	1386	14	US-10-182-263-11	Sequence 11, Appli	934	278	7.0	1507	18	US-10-283-975A-81	Sequence 81, Appli
862	310	7.9	1386	14	US-10-182-263-12	Sequence 12, Appli	935	278	7.0	1570	18	US-10-897-360-170	Sequence 170, App
863	310	7.9	1386	17	US-10-168-407-10	Sequence 10, Appli	936	278	7.0	1570	18	US-10-162-521A-170	Sequence 170, App
864	309	7.8	1386	14	US-10-182-263-9	Sequence 9, Appli	937	277	7.0	1327	19	US-10-805-667-170	Sequence 170, App
865	308	7.8	1386	14	US-10-182-263-10	Sequence 10, Appli	938	277	7.0	1327	19	US-10-893-359-170	Sequence 170, App
866	301	7.6	2795	19	US-10-741-600-81	Sequence 81, Appli	939	277	7.0	1327	19	US-10-897-360-170	Sequence 170, App
867	300.5	7.6	1850	19	US-10-764-420-2429	Sequence 2429, Ap	940	277	7.0	1327	19	US-10-897-360-170	Sequence 170, App
868	299.5	7.6	1401	17	US-10-406-031-3	Sequence 3, Appli	941	277	7.0	1327	19	US-10-918-851-170	Sequence 170, App
869	299.5	7.6	1404	17	US-10-406-031-1	Sequence 1, Appli	942	277	7.0	1327	19	US-10-805-667-170	Sequence 170, App
870	297.5	7.5	2641	9	US-09-974-298-144	Sequence 69, Appli	943	277	7.0	1327	19	US-10-893-359-170	Sequence 170, App
871	297.5	7.5	2641	9	US-09-917-800A-1575	Sequence 1575, Ap	944	277	7.0	1327	19	US-10-897-360-170	Sequence 170, App
872	294.5	7.5	1543	9	US-10-152-319A-1544	Sequence 1544, Ap	945	277	7.0	1327	19	US-09-783-587B-2	Sequence 2, Appli
873	294.5	7.5	1543	9	US-10-152-319A-1544	Sequence 1544, Ap	946	277	7.0	1327	19	US-09-783-587B-4	Sequence 4, Appli
874	293	7.4	3121	16	US-10-114-153-49	Sequence 49, Appli	947	276.5	7.0	2036	9	US-09-954-456-552	Sequence 552, App
875	289.5	7.3	2509	14	US-10-193-656-7	Sequence 7, Appli	948	276.5	7.0	2036	9	US-09-880-107-1612	Sequence 1612, App
876	289.5	7.3	2519	17	US-09-969-271-5	Sequence 5, Appli	949	276.5	7.0	2036	9	US-09-880-107-1612	Sequence 3579, Ap
877	289.5	7.3	2519	17	US-10-172-118-540	Sequence 540, App	950	276.5	7.0	2036	9	US-10-843-641A-3579	Sequence 12, Appli
878	289.5	7.3	2519	17	US-10-342-887-540	Sequence 540, App	951	276.5	7.0	2040	18	US-10-617-619-12	Sequence 12, Appli

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1121	275.5	7.0	1332	17	US-10-411-037-7	Sequence 7, Appl	1194	263	6.7	1475	9	US-09-735-705-122	Sequence 122, App
1122	275.5	7.0	1332	17	US-10-411-026-7	Sequence 7, Appl	1195	263	6.7	1475	9	US-09-850-716A-122	Sequence 122, App
1123	275.5	7.0	1332	17	US-10-410-966-7	Sequence 7, Appl	1196	263	6.7	1475	9	US-09-897-778-122	Sequence 122, App
1124	275.5	7.0	1332	17	US-10-411-049-7	Sequence 7, Appl	1197	263	6.7	1475	10	US-09-466-366A-122	Sequence 122, App
1125	275.5	7.0	1332	18	US-10-410-930-7	Sequence 7, Appl	1198	263	6.7	1475	14	US-10-007-700-122	Sequence 122, App
1126	275.5	7.0	1332	18	US-10-410-997-7	Sequence 7, Appl	1199	263	6.7	1475	15	US-10-117-982-122	Sequence 122, App
1127	275.5	7.0	1332	18	US-10-411-012-7	Sequence 7, Appl	1200	263	6.7	1475	15	US-10-101-510-159	Sequence 159, App
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1134	275.5	7.0	2422	18	US-10-738-777-1	Sequence 1, Appl	1207	263	6.7	1475	18	US-10-410-997-33	Sequence 33, Appl
1135	275.5	7.0	4496	15	US-10-234-406-5	Sequence 5, Appl	1208	263	6.7	1475	18	US-10-411-012-33	Sequence 33, Appl
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1137	275	7.0	1683	9	US-09-912-559-1	Sequence 1, Appl	1210	263	6.7	1475	18	US-10-410-913-33	Sequence 33, Appl
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1144	275	7.0	1683	19	US-10-930-754-2	Sequence 2, Appl	1217	263	6.7	2294	9	US-09-850-716A-123	Sequence 123, App
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1148	274	6.9	4276	15	US-10-234-406-7	Sequence 7, Appl	1221	263	6.7	2294	15	US-10-117-983-123	Sequence 123, App
1149	272	6.9	1645	15	US-10-101-510-420	Sequence 420, App	1222	263	6.7	2294	17	US-10-313-986-123	Sequence 123, App
1150	271.5	6.9	1506	10	US-09-873-367C-501	Sequence 501, App	1223	263	6.7	2294	17	US-10-641-643-1217	Sequence 1217, Ap
1151	271.5	6.9	1506	14	US-10-097-340-168	Sequence 168, App	1224	263	6.7	2294	18	US-10-775-972-123	Sequence 123, App
1152	271.5	6.9	1506	14	US-10-282-907-1	Sequence 1, Appl	1225	263	6.7	2294	13	US-10-087-192-593	Sequence 593, App
1153	271.5	6.9	1506	14	US-10-282-907-3	Sequence 3, Appl	1226	263	6.7	2304	14	US-10-171-311-183	Sequence 183, App
1154	271.5	6.9	1506	15	US-10-101-510-167	Sequence 167, App	1227	263	6.7	2304	15	US-10-301-822-160	Sequence 160, App
1155	271.5	6.9	1506	15	US-10-301-822-96	Sequence 96, Appl	1228	263	6.7	2304	17	US-10-388-360-335	Sequence 335, App
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1158	271.5	6.9	1506	16	US-10-394-087-55	Sequence 55, Appl	1231	263	6.7	2304	17	US-10-159-563-121	Sequence 121, App
1159	271.5	6.9	1506	17	US-10-172-118-814	Sequence 814, App	1232	263	6.7	2304	19	US-10-645-756-37	Sequence 37, Appl
1160	271.5	6.9	1506	17	US-10-295-027-529	Sequence 529, App	1233	263	6.7	2304	19	US-09-971-392-45	Sequence 45, Appl
1161	271.5	6.9	1506	17	US-10-173-999-130	Sequence 130, App	1234	263	6.7	2336	15	US-10-101-510-458	Sequence 458, App
1162	271.5	6.9	1506	17	US-10-342-887-814	Sequence 814, App	1235	263	6.7	2336	16	US-10-252-157-358	Sequence 358, App
1163	271.5	6.9	1506	17	US-10-300-820-11	Sequence 11, Appl	1236	263	6.7	2336	16	US-10-252-157-358	Sequence 358, App
1164	271.5	6.9	1506	18	US-10-757-262-27	Sequence 27, Appl	1237	263	6.7	2655	18	US-10-723-860-5461	Sequence 5461, Ap
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1166	271.5	6.9	3162	17	US-10-210-130-61	Sequence 61, Appl	1239	262.5	6.7	1548	9	US-09-150-811-6	Sequence 6, Appl
1167	270	6.8	200	10	US-09-903-393-2	Sequence 2, Appl	1240	262.5	6.7	1548	15	US-10-073-064-6	Sequence 6, Appl
1168	267	6.8	1389	18	US-10-416-952-1	Sequence 1, Appl	1241	262.5	6.7	2091	15	US-10-841-250-9	Sequence 9, Appl
1169	267	6.8	1437	17	US-10-375-716-26	Sequence 26, Appl	1242	262.5	6.7	2091	17	US-10-349-858-16	Sequence 16, Appl
1170	267	6.8	1437	17	US-10-408-695-1	Sequence 1, Appl	1243	262.5	6.7	2773	17	US-10-132-829-2	Sequence 2, Appl
1171	267	6.8	1437	17	US-10-411-037-9	Sequence 9, Appl	1244	262.5	6.7	2804	14	US-10-133-907-2	Sequence 2, Appl
1172	267	6.8	1437	17	US-10-411-026-9	Sequence 9, Appl	1245	262.5	6.7	2804	16	US-10-133-907-2	Sequence 1, Appl
1173	267	6.8	1437	17	US-10-410-962-9	Sequence 9, Appl	1246	262.5	6.7	3129	18	US-10-865-978-1	Sequence 1, Appl
1174	267	6.8	1437	17	US-10-410-962-9	Sequence 9, Appl	1247	262.5	6.7	3421	17	US-10-276-774-995	Sequence 995, App
1175	267	6.8	1437	18	US-10-410-930-9	Sequence 9, Appl	1248	262.5	6.7	4933	17	US-09-776-191-61	Sequence 61, Appl
1176	267	6.8	1437	18	US-10-410-997-9	Sequence 9, Appl	1249	262.5	6.7	4933	17	US-10-156-214A-28	Sequence 28, Appl
1177	267	6.8	1437	18	US-10-411-012-9	Sequence 9, Appl	1250	262.5	6.7	4933	17	US-10-926-083-1	Sequence 1, Appl
1178	267	6.8	1437	18	US-10-287-994-9	Sequence 9, Appl	1251	262.5	6.7	5753	17	US-10-239-498A-6	Sequence 6, Appl
1179	267	6.8	1437	18	US-10-410-913-9	Sequence 9, Appl	1252	262.5	6.7	13928	17	US-10-362-916-1	Sequence 1, Appl
1180	267	6.8	1437	19	US-10-410-980-9	Sequence 9, Appl	1253	261	6.6	2792	9	US-09-118-748-1	Sequence 1, Appl
1181	265.5	6.7	1359	17	US-10-432-989-3	Sequence 3, Appl	1254	260.5	6.6	2344	15	US-10-104-510-383	Sequence 383, App
1182	265.5	6.7	3318	9	US-09-808-602-91	Sequence 91, Appl	1255	260	6.6	2387	18	US-10-398-037-69	Sequence 69, Appl
1183	265.5	6.7	3318	17	US-09-800-198-78	Sequence 78, Appl	1256	260	6.6	2304	17	US-10-282-174-561	Sequence 561, App
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1191	263.5	6.7	1691	9	US-09-808-602-18	Sequence 18, Appl	1264	258.5	6.6	1236	17	US-10-407-821-1	Sequence 1, Appl
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